Salata 121713

SEQ 1

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq1asq.res made by  on Fri 19 May 95 8:38:34-PDT.


Query sequence being compared:US-08-121-713B-1 (1-6)
Number of sequences searched:                53402
Number of scores above cutoff:                4639

     Results of the initial comparison of US-08-121-713B-1 (1-6) with:
   Data bank : A-GeneSeq 18, all entries

100000-
      -
N     -
U50000-
M     *
B     -
E     -
R     -                                  *
      -
O     -
F10000-
      -
S     -
E 5000-
Q     -
U     -
E     -
N     -
C     -                                                  *
E     -
S 1000-
      -
      -
   500-
      -
      -
      -
      -
      -
      -
   100-
      -
      -
    50-
      -
      -
      -
      -
      -
      -
    10-
      -
      -
```



```
     5-
      -
      -
      -
      -
      -
      -
      -
     0-------------------------------------------------------------------------
      ||     |      |  |   |      |    | |      |      |      |      |
SCORE 0|     0      1  |   1      2    | 2      3      3      4      4
STDEV  1               2              3
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	0	1	1.08

Times:	CPU	Total Elapsed
	00:00:32.01	00:00:32.00

Number of residues:	6354270
Number of sequences searched:	53402
Number of scores above cutoff:	4639

Cut-off raised to 2.
Cut-off raised to 3.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 3 standard deviations above mean ****					
1. R57006	N-terminal fragment of human	10	4	4	3.70	0
2. R32437	Human thrombospondin type I r	10	4	6	3.70	0
3. P91647	Sequence deduced from human p	11	4	4	3.70	0
4. P80008	Synthetic peptide Sp-23 with	11	4	4	3.70	0
5. R03394	Fragment of pertussis toxin S	11	4	4	3.70	0
6. R05524	Tumour necrosis factor derive	12	4	4	3.70	0
7. P10340	Somatostatin deriv. A50.	13	4	4	3.70	0
8. R06485	N-terminal of plasma protein	13	4	4	3.70	0

9.	R41498	TNF inhibitory peptide X.	14	4	4	3.70	0
10.	R57135	Recombinant mature xenoxin-1	15	4	4	3.70	0
11.	R51437	Circumsporozoite protein regi	15	4	6	3.70	0
12.	R09375	Sequence of peptide TPI used	15	4	4	3.70	0
13.	P91752	Antigenic N-terminal peptide	15	4	4	3.70	0
14.	R32709	N terminal of haematopoietic	16	4	4	3.70	0
15.	R47008	IFN-alpha receptor position 2	17	4	4	3.70	0
16.	P97787	Sequence encoded by a genetic	17	4	4	3.70	0
17.	R51436	Circumsporozoite protein regi	19	4	6	3.70	0
18.	R30935	Peptide 43 corresponding to i	19	4	4	3.70	0
19.	R26535	Sequence of peptide P3 which	19	4	4	3.70	0
20.	R26534	Sequence of peptide P2 which	20	4	4	3.70	0
21.	R13689	Scatter factor N-terminal.	20	4	4	3.70	0
22.	R13688	Scatter factor N-terminal.	20	4	4	3.70	0
23.	R04980	Papilloma virus type 16 L1 pe	20	4	4	3.70	0
24.	R04981	Papilloma virus type 16 L1 pe	20	4	4	3.70	0
25.	R13629	Thrombospondin peptide p11.	23	4	6	3.70	0
26.	R47725	HIV epitope #58.	24	4	4	3.70	0
27.	R40077	Hib OMP P2 peptide OMP2-7 (17	27	4	4	3.70	0
28.	R10144	Hepatocyte growth factor beta	27	4	4	3.70	0
29.	R42872	Halystatin fragment.	28	4	4	3.70	0
30.	R09376	Sequence of peptide TPQ used	30	4	4	3.70	0
31.	R03358	Arginine deiminase.	30	4	4	3.70	0
32.	R25690	Exon XIII of human hepatocyte	33	4	4	3.70	0
33.	R35388	Amphiphilic peptide #119 used	35	4	4	3.70	0
34.	P94254	Cecropin B.	35	4	4	3.70	0
35.	R53573	Spider venom calcium channel	36	4	4	3.70	0
36.	P91331	Amino acid sequence of Mod. S	36	4	4	3.70	0
37.	P91330	Amino acid sequence of SB-37	36	4	4	3.70	0
38.	P91063	Amino acid sequence of cecrop	36	4	4	3.70	0
39.	P94255	Semisynthetic Cecropin B gene	37	4	4	3.70	0
40.	R53353	Hyalophora cecropia Cecropin	38	4	4	3.70	0
41.	R07734	Lytic peptide with proliferat	38	4	4	3.70	0
42.	R46945	pAGbeta2-101 platelet aggrega	39	4	4	3.70	0
43.	R46944	pAGbeta1-101 platelet aggrega	39	4	4	3.70	0
44.	R46943	pAGbeta107 platelet aggregati	39	4	4	3.70	0
45.	R46942	pAGbeta106 platelet aggregati	39	4	4	3.70	0

1. US-08-121-713B-1 (1-6)
R57006 N-terminal fragment of human histo-blood group A t

ID R57006 standard; peptide; 10 AA.
AC R57006;
DT 15-FEB-1995 (first entry)
DE N-terminal fragment of human histo-blood group A transferase.
KW Blood; group; determinant; antigen; erythrocyte; oligosaccharide;
KW glycoconjugate; glycosphingolipid; glycoprotein; glycosyltransferase;
KW transferase.
OS Homo sapiens.
PN US5326857-A.
PD 05-JUL-1994.
PF 31-AUG-1989; 402695.
PR 31-AUG-1989; US-402695.
PR 29-AUG-1991; US-752101.
PA (BIOM-) BIOMEMBRANE INST.
PI Clausen H, Hakomori S, White T, Yamamoto F;
DR WPI; 94-217098/26.
PT Isolated DNA molecules - encode human histo-blood groups A-, B-
PT and O-glycotransferases

PS Example 2; Column 41-42; 63pp; English.
CC The histo-blood group ABH determinants are major allogeneic antigens
CC in both erythrocytes and tissues of humans. They generally
CC constitute peripheral parts of the oligosaccharide chains of
CC glycoconjugates i.e.linked to lipids (glycosphingolipids) or to
CC proteins (glycoproteins). It was proposed that the A and B
CC phenotypes were associated with glycosyltransferases that converted
CC the H substance associated with the O phenotype to A and B
CC respectively, through the addition of alpha1-3-N-acetylgalactosamine
CC or alpha1-3-galactosyl residues to the H antigen Fuc-alpha1-2Gal-
CC beta1-R. Hence, the primary products of the histo-blood group A
CC and B genes are the respective glycosyltransferases. This is a
CC fragment of the A group transferase. See also R56995-R57010.
SQ Sequence 10 AA;
SQ 2 A; 0 R; 1 N; 1 D; 0 B; 0 C; 1 Q; 1 E; 0 Z; 1 G; 0 H;
SQ 1 I; 0 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 0 Y; 2 V;

Initial Score	=	4	Optimized Score	=	4	Significance	= 3.70
Residue Identity	=	33%	Matches	=	2	Mismatches	= 4
Gaps	=	0	Conservative Substitutions				= 0

```
     X    X
     XCXNXI
       | |
    VDQANGIEAV
     X    X 10
```

2. US-08-121-713B-1 (1-6)
R32437 Human thrombospondin type I repeat-derived peptide

ID R32437 standard; peptide; 10 AA.
AC R32437;
DT 10-JUN-1993 (first entry)
DE Human thrombospondin type I repeat-derived peptide #8.
KW thrombosis; coagulation; heparin binding inhibitor; type I repeat.
OS Synthetic.
PN US7801812-A.
PD 15-DEC-1992.
PF 06-DEC-1991; 801812.
PR 06-DEC-1991; US-801812.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
PI Roberts DD;
DR WPI; 93-067439/08.
PT New sulphated glyco-conjugate binding peptide(s) - from type 1
PT repeats of human thrombo:spondin, preventing interaction of the
PT glyco-conjugates with adhesion molecules, growth factors, etc.
PS Disclosure; Page 13; 64pp; English.
CC This peptide was obtained from the adhesive glycoprotein thrombo-
CC spondin. It is adjacent to an active, preferred peptide of the
CC invention which lacks the cluster of basic amino acids which fit
CC the consensus sequences of many heparin-binding proteins but which
CC have binding constants of approximately 10 to 100-fold higher than
CC the proteins having the basic consensus sequences. The pref.
CC peptides all contain a subsequence WSXW (X=P, E, H, A, S) with a
CC substantial lack of an electrical charge. They act as inhibitors of
CC heparin- or related sulphated glycoconjugate-binding to adhesion
CC molecules, growth factors, etc. This flanking sequence does not
CC have inhibitory activity.
SQ Sequence 10 AA;

```
 SQ   0  A; 1  R; 1  N; 0  D; 0  B; 1  C; 2  Q; 0  E; 0  Z; 2  G; 0  H;
 SQ   1  I; 0  L; 0  K; 0  M; 0  F; 0  P; 1  S; 1  T; 0  W; 0  Y; 0  V;

Initial Score    =      4  Optimized Score  =      6  Significance =  3.70
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

     X    X
     XCXNXI
      | | |
    TSCGNGIQQR
     X    X 10
```

3. US-08-121-713B-1 (1-6)
   P91647 Sequence deduced from human papillomavirus (HPV) o

```
 ID   P91647 standard; peptide; 11 AA.
 AC   P91647;
 DT   11-MAR-1992  (first entry)
 DE   Sequence deduced from human papillomavirus (HPV) open reading
 DE   frame.
 KW   Diagnosis; wart; condylomas; cervical cancer; antigen.
 OS   Human papillomavirus.
 PN   EP-344940-A.
 PD   06-DEC-1989.
 PF   15-MAY-1989; 304874.
 PR   16-MAY-1988; US-194407.
 PR   13-MAR-1989; US-323614.
 PA   (SCRI-) SCRIPPS CLINIC RES.
 PI   Dillner J, Lerner RA, Smith R, Parks DE;
 DR   WPI; 89-358324/49.
 PT   Antigenic polypeptide(s) useful as immunogens - for producing
 PT   antibodies to papillomavirus agent proteins
 PS   Claim 3; Page 49; 60pp; English.
 CC   The peptides of the invention are useful for generating antibodies
 CC   that immunoreact with papillomavirus latent protein. Inocula
 CC   typically contain polypeptide or protein concns. of 10mcg to 500mcg
 CC   per dose (pref. 50mcg-50mg).
 SQ   Sequence   11 AA;
 SQ   0  A; 0  R; 1  N; 0  D; 0  B; 0  C; 0  Q; 1  E; 0  Z; 1  G; 0  H;
 SQ   1  I; 0  L; 0  K; 0  M; 1  F; 0  P; 0  S; 3  T; 0  W; 0  Y; 3  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.70
Residue Identity =    66%  Matches          =      2  Mismatches   =     1
Gaps             =      0  Conservative Substitutions               =     0

       X X
    XCXNXI
       | |
       NGIVTVTFVTE
       X X     10
```

4. US-08-121-713B-1 (1-6)
   P80008 Synthetic peptide Sp-23 with residues 2-11 deduced

```
 ID   P80008 standard; protein; 11 AA.
 AC   P80008;
 DT   14-SEP-1990  (first entry)
```



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 DE   Synthetic peptide Sp-23 with residues 2-11 deduced from the gag sequence
 DE   of a human proviral locus endogenous retrovirus-1
 KW   Synthetic peptide Sp-23; endogenous retrovirus-1; tumour detection;
 KW   chromosome 18.
 OS   erv-1 provirus/Homo sapiens.
 PN   US4777127-A.
 PD   11-OCT-1988.
 PF   30-SEP-1985; 781478.
 PR   30-SEP-1985; US-781478.
 PA   (LABS-) Labsystem Oy.
 PI   Jukka S, Amtti V;
 DR   WPI; 88-307164/43.
 PT   Purified human retro-virus-related peptide prods. -
 PT   useful as speific reagents for detection and treatment of
 PT   tumours, such as renal cell adenocarcinoma and choriocarcinoma
 PS   ; Table 1, pages 3 and 4; 6pp; English.
 CC   A defective, endogenous provirus was isolated from a human recombinant
 CC   DNA library by using an endogenous chimpanzee retroviral pol fragment as
 CC   probe.  The structure of this fragment is highly related to that of BaEV
 CC   This genome, termed HC-20 (or endogenous retrovirus-1; erv-1), has been
 CC   assigned to human chromosome 18.  A decapeptide, deduced from the gag
 CC   portion of erv-1 has been isolated.  From this, an undecapeptide (Sp-23)
 CC   which contains the decapeptide as residues 2 through to 11 has been
 CC   synthesized.  A polyclonal antibody raised against the undecapeptide in
 CC   rabbits has detected a human retrovirus-related Mr75,00 protein which
 CC   contains the decapeptide.  Polyclonal antibodies have been raised against
 CC   the decapeptide, Sp-23 and the Mr 75,000 protein.  These antibodies are
 CC   used as specific reagents for the detection of tumours such as renal cel
 CC   adenocarcinoma and choriocarcinoma, among others, and the placental
 CC   disorders including blighted ova, hydatidform and destructive moles.  The
 CC   sequence of synthetic peptide (sp-23) fits 6 of 10 with the BaEV p30 and
 CC   7 of 10 with the Mo-MuLV p30 sequence.
 SQ   Sequence   11 AA;
 SQ   0 A;  1 R;  1 N;  0 D;  0 B;  1 C;  1 Q;  2 E;  0 Z;  0 G;  0 H;
 SQ   0 I;  1 L;  0 K;  0 M;  1 F;  1 P;  1 S;  0 T;  0 W;  1 Y;  0 V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.70
Residue Identity =    40%  Matches          =      2  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

     X   X
    XCXNXI
     | |
     CENPSQFYERL
     X   X   10
```

5. US-08-121-713B-1 (1-6)
   R03394 Fragment of pertussis toxin S1 subunit.

```
 ID   R03394 standard; protein; 11 AA.
 AC   R03394;
 DT   31-JUL-1990  (first entry)
 DE   Fragment of pertussis toxin S1 subunit.
 KW   Whooping chough; subunit S1; vaccine.
 OS   Bordetella pertussis.
 PN   WO9001494-A.
 PD   22-FEB-1990.
 PF   31-JUL-1989; 03298.
 PR   2-AUG-1988; US-227372.
```

```
PA   (STRD) Leland Stanford Jr Univ.
PI   Steinman L, Oksenberg JR, Schoolnik GK, Judd AK;
DR   WPI; 90-083479/11.
PT   Polypeptide(s) useful as Bordetella pertussis vaccines -
PT   comprise specified sequence(s) of S1 subunit.
PS   Disclosure; pp; English.
CC   Useful as a vaccine for whooping cough, free from the side effects
CC   associated with the intact S1 subunit.
SQ   Sequence   11 AA;
SQ   0 A;  1 R;  1 N;  0 D;  0 B;  0 C;  0 Q;  1 E;  0 Z;  2 G;  1 H;
SQ   1 I;  0 L;  0 K;  0 M;  0 F;  0 P;  0 S;  2 T;  0 W;  1 Y;  1 V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.70
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

     X    X
     XCXNXI
        | |
    RVYHNGITGET
     X    X 10
```

6. US-08-121-713B-1 (1-6)
   R05524 Tumour necrosis factor derived peptide.

```
ID   R05524 standard; protein; 12 AA.
AC   R05524;
DT   24-OCT-1990  (first entry)
DE   Tumour necrosis factor derived peptide.
KW   Tumour necrosis factor; TNF; neoplastic disease; autoimmune
KW   disease; infection; inflammation; transplant rejection.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Modified-site   4..4
FT   /label=Hcy
FT   Disulfide-bond  4..10
PN   DE3841768-A.
PD   13-JUN-1990.
PF   12-DEC-1988; 841768.
PR   12-DEC-1988; DE-841768.
PA   (BADI) BASF AG.
PI   Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;
DR   WPI; 90-186584/25.
PT   New tumour necrosis factor derived peptide(s) - for treating or
PT   preventing neoplastic and auto-immune diseases, infection, inflammation
PT   and transplant rejection reaction.
PS   Example 60; Page 10; 17pp; German.
CC   To residue N1 is attached Ac and to residue D12 NH2.
CC   This peptide is an example of a highly generic sequence of the
CC   formula       X-A-Gly-B-Y
CC   A= Asp, His or Asn;
CC   B= Val, Met or Phe;
CC   X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;
CC   Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z;
CC   G= H or an amino protecting group;
CC   Z= OH, NH2 or carboxy protecting group; or G and Z together are a
CC   covalent bond or the gp. CO(CH2)aNH; a=1-12;
CC   R, U, V and W= peptide chains of 1-4 naturally occuring alpha aminoacids;
CC   M and Q= H, isopropyl, sec-butyl, phenyl, 1-hydroxy-ethyl, 3-indolyl- or
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CC   4-imidazoly-methyl or (CH2)bT; b=1-6;
CC   T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd), mercapto,
CC   amino, carboxy, carbamoyl or quanidino; or
CC   M ans Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or
CC   (CH)2eNH CO(CH2)gNH CO(CH2) f; c and d=1-4; e and f=1-6; g=1-12.
CC   The peptide is a low mol. wt. deriv. of TNF.
CC   See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.
SQ   Sequence   12 AA;
SQ   2 A;  1 R;  2 N;  1 D;  0 B;  2 C;  0 Q;  1 E;  0 Z;  1 G;  0 H;
SQ   0 I;  1 L;  0 K;  0 M;  0 F;  0 P;  0 S;  0 T;  0 W;  0 Y;  1 V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.70
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

     X    X
     XCXNXI
      | |
   NALCANGVECRD
     X    10
```

7. US-08-121-713B-1 (1-6)
   P10340 Somatostatin deriv. A50.

```
ID   P10340 standard; peptide; 13 AA.
AC   P10340;
DT   15-DEC-1992  (first entry)
DE   Somatostatin deriv. A50.
KW   Growth Hormone secretion; GH; diabetes mellitus; angiopathy;
KW   acromegaly; diagnosis.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Modified_site   1
FT   /note= "(4Cl)Phe"
FT   Modified_site   3
FT   /label= Nle
FT   Misc_difference 14
FT   /note= "Cys-NH-(CH2)2-OH, Cys-NH-(CH2)3-OH or
FT   as amide formed with 3-amino-butyrolactone"
PN   CH-621770-A.
PD   27-FEB-1981.
PF   11-SEP-1980; 125375.
PR   23-FEB-1976; CH-002175.
PA   (SANO ) SANDOZ AG.
PI   Sandrin E, Bauer W;
DR   WPI; 81-21515D/13  (21515D).
PT   Somatostatin derivs. prodn. - useful for treating diabetes,
PT   acromegalia and angiopathia
PS   Example 1; Page 6-7; 8pp; German.
CC   This peptide is an example of a generic formula for somatostatin
CC   derivs. which inhibit secretion of growth hormone and are useful to
CC   treat diabetes mellitus, acromegaly, angiopathy and in diagnosis.
CC   See P10308-P10348.
SQ   Sequence   13 AA;
SQ   0  A; 0  R; 1  N; 0  D; 0  B; 2  C; 0  Q; 0  E; 0  Z; 0  G; 0  H;
SQ   0  I; 0  L; 1  K; 0  M; 4  F; 0  P; 1  S; 2  T; 1  W; 0  Y; 0  V;
SQ   1 Others;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.70
```

```
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions              =     0

    X    X
    XCXNXI
     |||
    FCXNFFWKTFTSC
    X    X  10
```

8. US-08-121-713B-1 (1-6)
   R06485 N-terminal of plasma protein which binds activated

```
 ID   R06485 standard; peptide; 13 AA.
 AC   R06485;
 DT   03-JAN-1991  (first entry)
 DE   N-terminal of plasma protein which binds activated C4.
 KW   Complement; 120 kDa protein.
 OS   Homo sapiens.
 PN   WO9008770-A.
 PD   09-AUG-1990.
 PF   02-FEB-1990; U00716.
 PR   02-FEB-1989; US-305458.
 PA   (USDC ) US SEC OF COMMERCE.
 PI   Hammer CH, Jacobs RM, Frank MM;
 DR   WPI; 90-260889/34.
 PT   New purified single-chain plasma protein - binds to activated C4
 PT   and C3 of the classical complement pathway.
 PS   Claim 2; Page 28; 40pp; English.
 CC   The new protein, of which this sequence is the N-terminal, is a
 CC   single chain plasma protein of 120 kD which inhibits lytic
 CC   functional activity of  the classical complement pathway.
 CC   Quantitive Manchini analysis has identified about 300 ul of the
 CC   protein in plasma and serum.  The molecule contains approx. equal
 CC   amts. of N- and O-linked CHO (14%).  It is cleaved by Kallikrein
 CC   into 85 and 35 kD fragments; the 85 kD fragment is subsequently
 CC   cleaved into fragments of 60 and 25 kD.  Studies show that a mixt.
 CC   of the fragments, but not the intact protein, has a potent vaso-
 CC   dilating acivity in guinea pigs.  The protein is believed to be
 CC   a new complement regulatory factor and shares several character-
 CC   istics with the C2 protein.
 SQ   Sequence   13 AA;
 SQ   0  A; 0  R; 1  N; 2  D; 0  B; 0  C; 0  Q; 1  E; 0  Z; 1  G; 0  H;
 SQ   2  I; 1  L; 1  K; 0  M; 0  F; 0  P; 1  S; 1  T; 0  W; 1  Y; 1  V;
```

```
Initial Score    =      4  Optimized Score  =      4  Significance =  3.70
Residue Identity =    40%  Matches          =      2  Mismatches   =     3
Gaps             =      0  Conservative Substitutions              =     0

    X   X
    XCXNXI
      | |
     EKNGIDIYSLTVD
     X   X   10
```

9. US-08-121-713B-1 (1-6)
   R41498 TNF inhibitory peptide X.

```
 ID   R41498 standard; peptide; 14 AA.
 AC   R41498;
 DT   23-FEB-1994  (first entry)
 DE   TNF inhibitory peptide X.
 KW   Tumour necrosis factor; TNF; inhibition; solid phase synthesis; ss.
 OS   Synthetic.
 FH   Key             Location/Qualifiers
 FT   Disulfide_bond  3..12
 FT   /note= "Optional di-sulphide bond"
 PN   J05194594-A.
 PD   03-AUG-1993.
 PF   21-JAN-1992; 029044.
 PR   21-JAN-1992; JP-029044.
 PA   (SAGA ) SAGAMI CHEM RES CENTRE.
 DR   WPI; 93-282916/36.
 PT   TNF inhibitory novel peptide(s) - include N-terminal amino Gp.
 PT   which is opt. modified with acetyl, T-butoxy-carbonyl or
 PT   benzyl-oxy-carbonyl Gp. and C-terminal carboxy Gp. is opt.
 PT   amidated
 PS   Claim 1; Page 6; 8pp; Japanese.
 CC   The sequences given in R41489-99 are tumour necrosis factor (TNF)
 CC   inhibitory peptides.  They may optionally be modified at the N-
 CC   terminal with an acetyl, t-butoxycarbonyl or benzyloxycarbonyl, and
 CC   at the C-terminal they are optionally amidated.  These peptides are
 CC   produced by solid phase synthesis methods and may be produced at low
 CC   cost.
 SQ   Sequence   14 AA;
 SQ   0  A; 0  R; 1  N; 0  D; 0  B; 2  C; 1  Q; 1  E; 0  Z; 1  G; 1  H;
 SQ   0  I; 3  L; 0  K; 0  M; 0  F; 0  P; 2  S; 1  T; 0  W; 0  Y; 1  V;
```

```
Initial Score    =      4  Optimized Score  =      4  Significance =  3.70
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions              =     0

    X    X
    XCXNXI
     | |
    SLCLNGTVHLSCQE
    X    X 10
```

10. US-08-121-713B-1 (1-6)
    R57135 Recombinant mature xenoxin-1 N-terminal sequence.

```
 ID   R57135 standard; Protein; 15 AA.
 AC   R57135;
 DT   22-FEB-1995  (first entry)
 DE   Recombinant mature xenoxin-1 N-terminal sequence.
 KW   Defensin A; pro-sequence; heterologous protein production;
 KW   fleshfly; yeast expression vector; yeast alpha-mating factor;
 KW   pre-BGL2; xenoxin-1; Xenopus laevis.
 OS   Synthetic.
 FH   Key             Location/Qualifiers
 FT   Misc_difference 3
 FT   /note= "not identified by sequencing method"
 FT   Misc_difference 14
 FT   /note= "not identified by sequencing method"
 PN   EP-607080-A.
 PD   20-JUL-1994.
 PF   11-JAN-1994; 400062.
 PR   11-JAN-1993; FR-000171.
```

```
PA   (TRGE ) TRANSGENE SA.
PI   Achstetter T;
DR   WPI; 94-226998/28.
PT   Cassette for expression and synthesis of mature heterologous
PT   protein in yeast - included pre sequence and pro sequence from an
PT   insect defensin precursor, also new expression vectors and
PT   transformed hosts
PS   Example 6; Page 30; 39pp; French.
CC   Expression vectors were constructed for recombinant expression of
CC   xenoxin-1 in transformed yeast hosts. The vectors comprised the
CC   sequence of pre BGL2, the pro sequence yeast alpha1-mating factor
CC   and the sequence coding for mature xenoxin-1, under the
CC   control of a modified alpha1-MF promoter. The construction
CC   procedure for preparing the vectors included PCR amplification of
CC   a sequence coding for mature xenoxin-1 (having the amino acid
CC   sequence R57134) using the primers Q69212 and Q69213. The amplified
CC   product had an EagI site at the 5'-end and a SalI site at the 3'-end.
CC   The N-terminus of the recombinantly produced protein was sequenced
CC   and was found to correspond to the expected N-terminal sequence for
CC   xenoxin-1 (see R57135).
SQ   Sequence   15 AA;
SQ   1  A; 0  R; 2  N; 0  D; 0  B; 0  C; 2  Q; 0  E; 0  Z; 1  G; 0  H;
SQ   1  I; 2  L; 2  K; 1  M; 0  F; 0  P; 0  S; 0  T; 0  W; 0  Y; 1  V;
SQ   2 Others;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.70
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

        X    X
        XCXNXI
          | |
    LKXVNLQANGIKMXQ
        X  10
```

11. US-08-121-713B-1 (1-6)
    R51437 Circumsporozoite protein region II+ peptide #11.

```
ID   R51437 standard; peptide; 15 AA.
AC   R51437;
DT   26-OCT-1994  (first entry)
DE   Circumsporozoite protein region II+ peptide #11.
KW   Region II+; circumsporozoite; CS; Plasmodium; inhibitor; binding;
KW   receptor; hepatocytes; malaria-susceptible; mammal; infection;
KW   antibody; liver; human hepatocyte cell line; HepG2.
OS   Plasmodium sp.
PN   WO9406464-A.
PD   31-MAR-1994.
PF   17-SEP-1993; U08800.
PR   17-SEP-1992; US-947033.
PA   (UYNY ) UNIV NEW YORK STATE.
PI   Cerami C,  Frevert U,  Nussenzweig V,  Sinnis P;
DR   WPI; 94-118161/14.
PT   Peptide(s) corresp. to Region II+ of circumsporozoite - are used
PT   for inhibiting hepatocyte invasion by malarial sporozoites for
PT   preventing malaria infection
PS   Claim 10; Page 33; 42pp; English.
CC   The sequences given in R51427-35 are peptide fragments derived from
CC   region II+ of the circumsporozoite (CS) protein derived from various
```



```
CC   Plasmodium species.  These peptides fragments may be used as an
CC   inhibitor for the binding of CS polypeptides to receptors of
CC   hepatocytes from malaria-susceptible mammals.  These peptides can be
CC   administered to malaria susceptible mammals to prevent infection,
CC   and they can be used to produce antibodies which can be used to
CC   prevent infection.  The peptides were tested for inhibition of CS
CC   binding to liver sections or to the human hepatocyte cell line HepG2.
SQ   Sequence   15 AA;
SQ   0  A; 1  R; 1  N; 0  D; 0  B; 2  C; 1  Q; 0  E; 0  Z; 2  G; 0  H;
SQ   2  I; 0  L; 1  K; 0  M; 0  F; 1  P; 1  S; 1  T; 0  W; 0  Y; 2  V;

Initial Score    =      4  Optimized Score  =      6  Significance =  3.70
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

        X    X
        XCXNXI
         | | |
   PCSVTCGNGIQVIRK
        X   10
```

12. US-08-121-713B-1 (1-6)
    R09375 Sequence of peptide TPI used to isolate onco-devel

```
ID   R09375 standard; Protein; 15 AA.
AC   R09375;
DT   26-MAR-1992  (first entry)
DE   Sequence of peptide TPI used to isolate onco-developmentally
DE   regulated alpha-N-acetylgalactosaminyltransferase (AGT).
KW   Tumour diagnosis; tumour cell; enzyme; fibronectin;
PN   EP-354652-A.
PD   14-FEB-1990.
PF   22-JUN-1989; 306283.
PR   12-AUG-1988; US-231576.
PA   (BIOM-) BIOMEMBRANE INST.
PA   (HUTC-) HUTCHINSON F CANCER RES.
PI   Hakomori SI;
DR   WPI; 90-046346/07.
PT   Onco-developmentally regulated n-acetyl
PT   galactosaminyl-transferase - isolated from onco-foetal tissue
PT   membrane fraction and used in detection of tumour cells
PS   Claim 3; Page 13; 16pp; English.
CC   The inventors claim a method for the isolation of AGT as a component
CC   of a particulate membrane fraction sepd. from cell and tissue
CC   homogenates. The prefd. method is by contacting onco foetal tissue
CC   with an immobilised polypeptide substrate comprising
CC   VTY (R09374); TPI (R09375); TPQ (R09376); or a normal fibronectin to
CC   form an affinity complex and then eluting the enzyme.
SQ   Sequence   15 AA;
SQ   0  A; 0  R; 1  N; 1  D; 0  B; 0  C; 0  Q; 0  E; 0  Z; 3  G; 1  H;
SQ   1  I; 0  L; 0  K; 0  M; 1  F; 2  P; 0  S; 3  T; 0  W; 1  Y; 1  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.70
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            XCXNXI
              | |
```

```
    TPFVTHPGYDTGNGI
            10    X
```

13. US-08-121-713B-1 (1-6)
    P91752 Antigenic N-terminal peptide of human fibrinogen g

```
 ID   P91752 standard; protein; 15 AA.
 AC   P91752;
 DT   17-MAY-1990  (first entry)
 DE   Antigenic N-terminal peptide of human fibrinogen gamma chain.
 KW   N-terminal; antigenic peptide; fibrinogen; human leukocyte elastase;
 OS   Homo sapiens.
 PN   EP-345906-A.
 PD   13-DEC-1989.
 PF   07-JUN-1989; 201460.
 PR   10-JUN-1988; US-205416.
 PR   10-JUN-1988; US-205417.
 PR   10-JUN-1988; US-205418.
 PA   (MERI) Merck and Co. Inc.
 PI   Dahlgren ME, Mumford RA, Boger JS, Davies DTP;
 DR   WPI; 89-365672/50.
 PT   New elastase-induced fibrinogen cleavage peptide(s) - for prodn. of
 PS   Disclosure; page 8; 33pp; English.
 CC   connective tissue disease; gamma chain;
 CC   new diagnostic antibodies.
 CC   The peptide represents residues 358-372 of human fibrinogen (hF) gamma
 CC   chain. Tyrosines at positions 12 and 15 below are a tentative
 CC   assignment. The human leukocyte elastase (hLE) cleavage prod.
 CC   (AAs 1-4 below) is claimed (no. 4) and is used to raise monoclonal
 CC   antibodies. These are useful for rapid detection of hLE-induced cleavage
 CC   of hF, eg in diagnosis of connective tissue destructive diseases such
 CC   as emphysema, chronic bronchitis, cystic fibrosis, arthritis, psoriasis,
 CC   or atherosclerosis.
 CC   See also P91744-P91751.
 SQ   Sequence   15 AA;
 SQ   1 A;  0 R;  2 N;  1 D;  0 B;  0 C;  0 Q;  0 E;  0 Z;  2 G;  0 H;
 SQ   2 I;  0 L;  0 K;  0 M;  0 F;  1 P;  1 S;  2 T;  0 W;  3 Y;  0 V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.70
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

       X    X
       XCXNXI
          | |
   STPNGYDNGIIYATY
       X   10
```

14. US-08-121-713B-1 (1-6)
    R32709 N terminal of haematopoietic stem cell multiplier.

```
 ID   R32709 standard; Protein; 16 AA.
 AC   R32709;
 DT   16-JUN-1993  (first entry)
 DE   N terminal of haematopoietic stem cell multiplier.
 KW   Bone marrow deficiencies; cancer therapy;  tumour; carcinoma;
 KW   bone marrow transplants.
 PN   WO9303061-A.
```



```
 PD   18-FEB-1993.
 PF   24-JUL-1992; J00949.
 PR   26-JUL-1991; JP-187470.
 PR   26-JUL-1991; JP-187481.
 PA   (TORA ) TORAY IND INC.
 PI   Kawano G,  Kojima K,  Komiyama A,  Kubo T,  Nakahata T;
 PI   Sano E,  Sudot,  Tanaka R;
 DR   WPI; 93-076441/09.
 PT   Haematopoietic stem cell multiplier comprising IL-3 and IL-7 -
 PT   used for treatment and prevention of bone marrow disorders e.g.
 PT   after cancer therapy or bone marrow transplants
 PS   Disclosure; Page 36; 90pp; Japanese.
 CC   This sequence is the N terminal sequence of a haematopoietic stem
 CC   cell multiplier. "X" = any amino acid.
 SQ   Sequence   16 AA;
 SQ   0  A; 0  R; 2  N; 0  D; 0  B; 0  C; 0  Q; 0  E; 0  Z; 2  G; 0  H;
 SQ   2  I; 0  L; 1  K; 1  M; 0  F; 1  P; 0  S; 2  T; 0  W; 0  Y; 3  V;
 SQ   2 Others;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.70
Residue Identity =    40%  Matches          =      2  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

     X   X
    XCXNXI
       | |
     VVNGIPTXTNIGXMV
     X   X   10
```

15. US-08-121-713B-1 (1-6)
    R47008 IFN-alpha receptor position 271-287.

```
 ID   R47008 standard; Protein; 17 AA.
 AC   R47008;
 DT   16-SEP-1994  (first entry)
 DE   IFN-alpha receptor position 271-287.
 KW   Naturally-occuring; immunomodulatory protein; human; therapy; class I;
 KW   major histocompatibility complex; class II; allotype; type I diabetes;
 KW   autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
 KW   mutiple sclerosis; transplant rejection; vaccine; MHC.
 OS   Homo sapiens.
 PN   WO9404171-A.
 PD   03-MAR-1994.
 PF   11-AUG-1993; U07545.
 PR   11-AUG-1992; US-925460.
 PR   15-JUN-1993; US-925460.
 PA   (HARD ) HARVARD COLLEGE.
 PI   Chicz RM,  Hedley ML,  Stern LJ,  Strominger JL,  Urban RG;
 PI   Vignali DA;
 DR   WPI; 94-082825/10.
 PT   Novel immunomodulatory peptide(s) and nucleic acids - useful for
 PT   treatment of auto:immune diseases, transplant rejection and for
 PT   vaccination
 PS   Disclosure; Page 48; 139pp; English.
 CC   The sequences given in R49291-505 and R46981-7038 represent peptide
 CC   fragments of naturally-occuring immunomodulatory proteins.  These
 CC   fragments are between 10-30 residues in length and bind to a human
 CC   major histocompatibility complex (MHC) class II allotype.  These
 CC   peptides may be used for therapy of autoimmune diseases, such as
```

```
CC   type I diabetes, rheumatoid arthritis and mutiple sclerosis, and to
CC   reduce transplant rejection.  They may also be used for vaccination
CC   providing an exclusively T-cell-mediated response, which can be
CC   class I or class-II based, or both, depending on the length and
CC   character of the immunogenic peptides.
SQ   Sequence   17 AA;
SQ   0  A; 0  R; 2  N; 1  D; 0  B; 1  C; 1  Q; 1  E; 0  Z; 1  G; 1  H;
SQ   1  I; 1  L; 3  K; 0  M; 0  F; 1  P; 0  S; 0  T; 1  W; 1  Y; 1  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.70
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             XCXNXI
              | |
    NHLYKWKQIPDCENVK
          10 X    X
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq1pir.res made by  on Fri 19 May 95 8:47:13-PDT.


Query sequence being compared:US-08-121-713B-1 (1-6)
Number of sequences searched:                75511
Number of scores above cutoff:                3753

     Results of the initial comparison of US-08-121-713B-1 (1-6) with:
   Data bank : PIR 43, all entries

100000-
      -
N     -                    *
U50000-
M     -
B     -
E     -
R     *
      -
O     -
F10000-
      -
S     -
E 5000-                                    *
Q     -
U     -
E     -
N     -
C     -
E     -
S 1000-
      -
      -
   500-
      -
```



```
      -
      -
      -
      -
    100-
      -
      -
     50-
      -
      -
      -
      -
      -
      -
      -
     10-
      -
      -
      5-                                                              *
      -
      -
      -
      -
      -
      -
      -
      0----------------------------------------------------------------------
       ||     |   |  |     ||     |    | |     ||     |     |     |
SCORE 0|     1   |  1     2|     3    | 3     4|     5     5     6
STDEV  0         1          2          3        4
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	1.03

Times:	CPU	Total Elapsed
	00:01:11.96	00:01:12.00

Number of residues:	22468834
Number of sequences searched:	75511
Number of scores above cutoff:	3753

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

4 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. NBMSH	complement factor H precursor	1234	6	6	4.85	0
2. S47464	methylaspartate mutase (EC 5.	483	6	6	4.85	0
3. S44573	hypothetical protein YKL609 -	259	6	6	4.85	0
4. S37984	probable purine nucleotide-bi	244	6	6	4.85	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 2 standard deviations above mean ****					
5. PS0249	porin - rice (strain Nihonbar	14	4	4	2.91	0
6. A40383	gene X protein - Escherichia	16	4	7350559	2.91	0
7. E60977	14-3-3 protein homolog, 15K -	19	4	4	2.91	0
8. S06487	ferredoxin, 15K, mitochondria	22	4	4	2.91	0
9. A54725	cecropin B - Chinese oak silk	35	4	4	2.91	0
10. S45125	hypothetical protein N2023 -	35	4	4	2.91	0
11. CKAOBP	cecropin B - Chinese oak silk	36	4	4	2.91	0
12. B31252	metallothionein II - yeast (C	37	4	4	2.91	0
13. A23617	conglutin delta-2 small chain	37	4	6	2.91	0
14. B32307	ribosomal protein L36 - Bacil	37	4	4	2.91	0
15. R5BS36	ribosomal protein L36 - Bacil	37	4	4	2.91	0
16. R5LV36	ribosomal protein L36 - liver	37	4	4	2.91	0
17. S11265	ribosomal protein YL43 - yeas	39	4	4	2.91	0
18. B18891	licheninase (EC 3.2.1.73) II	40	4	4	2.91	0
19. A18891	licheninase (EC 3.2.1.73) I -	40	4	4	2.91	0
20. PQ0752	beta-fructofuranosidase (EC 3	40	4	4	2.91	0
21. E22565	R-phycoerythrin beta-3 chain	40	4	4	2.91	0
22. A24553	cuticle protein SC1 - flesh f	43	4	4	2.91	0
23. W5WLEP	E5 protein - European elk pap	43	4	4	2.91	0
24. BXSA1	antibacterial protein 1 - Sta	44	4	4	2.91	0
25. A28167	arylamine N-acetyltransferase	46	4	4	2.91	0
26. A60443	thymidylate synthase (EC 2.1.	46	4	4	2.91	0
27. S10214	hexon-associated protein (VII	47	4	4	2.91	0
28. JQ0359	insulin - colubrid snake (Zao	51	4	4	2.91	0
29. INRS	insulin - western diamondback	51	4	4	2.91	0
30. INGS	insulin - goose	51	4	4	2.91	0
31. JC1197	metallothionein II - yeast (C	52	4	4	2.91	0
32. RUPF	rubredoxin - Pyrococcus furio	53	4	4	2.91	0
33. A05024	hypothetical protein 55 - liv	55	4	4	2.91	0
34. S01585	photosystem II protein psbK p	55	4	4	2.91	0
35. NTHNB2	neurotoxin B-II - ribbon worm	55	4	4	2.91	0
36. NTHNB4	neurotoxin B-IV - ribbon worm	55	4	4	2.91	0
37. TLBP54	tail fiber protein gp35 - pha	58	4	4	2.91	0
38. JN0750	Rz1 protein - phage lambda	60	4	4	2.91	0
39. QXBP7L	hypothetical protein C-60 (ni	60	4	4	2.91	0
40. S25992	hypothetical protein 61 - liv	61	4	6	2.91	0
41. C34123	depressant toxin BjIT2 - Egyp	61	4	4	2.91	0
42. D40667	neurotoxin - Naja naja	62	4	4	2.91	0
43. JK0221	short neurotoxin 1 - monocled	62	4	4	2.91	0
44. CKWKB	cecropin B precursor - cecrop	62	4	4	2.91	0

45. N1NJ1F short neurotoxin 1 - Chinese 62 4 4 2.91 0

1. US-08-121-713B-1 (1-6)
NBMSH complement factor H precursor - mouse

```
ENTRY            NBMSH      #type complete
TITLE            complement factor H precursor - mouse
ALTERNATE_NAMES  protein beta-1-H
ORGANISM         #formal_name Mus musculus #common_name house mouse
DATE             30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change
                   28-Oct-1994
ACCESSIONS       A26154
REFERENCE        A26154
   #authors      Kristensen, T.; Tack, B.F.
   #journal      Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3963-3967
   #title        Murine protein H is comprised of 20 repeating units, 61 amino
                   acids in length.
   #cross-references MUID:86233353
   #accession    A26154
      ##molecule_type mRNA
      ##residues      1-1234 ##label KRI
COMMENT     Two codominant alleles of factor H are present in mice.
COMMENT     Factor H functions as a cofactor in the inactivation of C3b by
              serine proteinase I and also increases the rate of dissociation
              of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5
              convertase) in the alternative complement pathway.
GENETICS
   #map_position 1
CLASSIFICATION   #superfamily complement factor H; complement factor H repeat
                   homology
KEYWORDS         complement; duplication; glycoprotein; plasma
FEATURE
   1-18              #domain signal sequence #status predicted #label SIG\
   19-1234           #product complement factor H #label MPT\
   21-80             #domain complement factor H repeat homology #label FH01\
   85-141            #domain complement factor H repeat homology #label FH02\
   146-205           #domain complement factor H repeat homology #label FH03\
   210-262           #domain complement factor H repeat homology #label FH04\
   267-320           #domain complement factor H repeat homology #label FH05\
   325-384           #domain complement factor H repeat homology #label FH06\
   389-442           #domain complement factor H repeat homology #label FH07\
   448-505           #domain complement factor H repeat homology #label FH08\
   509-564           #domain complement factor H repeat homology #label FH09\
   569-622           #domain complement factor H repeat homology #label FH10\
   629-683           #domain complement factor H repeat homology #label FH11\
   690-743           #domain complement factor H repeat homology #label FH12\
   752-802           #domain complement factor H repeat homology #label FH13\
   808-861           #domain complement factor H repeat homology #label FH14\
   867-931           #domain complement factor H repeat homology #label FH15\
   936-989           #domain complement factor H repeat homology #label FH16\
   994-1048          #domain complement factor H repeat homology #label FH17\
   1053-1107         #domain complement factor H repeat homology #label FH18\
   1114-1168         #domain complement factor H repeat homology #label FH19\
   1172-1233         #domain complement factor H repeat homology #label FH20\
   21-66,52-80,85-129,
   114-141,146-192,
   178-205,210-251,
   237-262,267-309,
   294-320,325-374,
```

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     357-385,389-431,
     416-442,448-494,
     477-505,509-553,
     536-564,569-610,
     597-622,629-672,
     658-683,690-732,
     718-743,752-791,
     780-802,808-850,
     836-861,867-920,
     906-931,936-978,
     964-989,994-1037,
     1023-1048,
     1053-1096,
     1082-1107,
     1114-1157,
     1143-1168,
     1172-1223,
     1206-1233          #disulfide_bonds #status predicted\
     676,721,773,801,
     1030,1061,1225     #binding_site carbohydrate (Asn) (covalent) #status
                          predicted
  SUMMARY           #length 1234  #molecular-weight 139081  #checksum 3676
  SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.85
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

              X    X
              XCXNXI
               | | |
    PLELFGQVEVMCENGIWTEKPKCRDS
      1090    X 1100      1110


2. US-08-121-713B-1 (1-6)
   S47464       methylaspartate mutase (EC 5.4.99.1) - Clostridium

  ENTRY             S47464     #type complete
  TITLE             methylaspartate mutase (EC 5.4.99.1) - Clostridium
                      cochlearium
  ORGANISM          #formal_name Clostridium cochlearium
  DATE              23-Nov-1994; #sequence_revision 23-Nov-1994; #text_change
                      23-Nov-1994
  ACCESSIONS        S47464
  REFERENCE         S47461
     #authors       Zelder, O.
     #submission    submitted to the EMBL Data Library, August 1994
     #accession     S47464
        ##status        preliminary
        ##residues      1-483 ##label ZEL
        ##cross-references EMBL:X80997
  SUMMARY           #length 483  #molecular-weight 53574  #checksum 4915
  SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.85
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

              X    X
```



```
              XCXNXI
               | | |
    DAYTRQNRYDECENGIKESEKAGRSL
      100     X 110       120


3. US-08-121-713B-1 (1-6)
   S44573       hypothetical protein YKL609 - yeast (Saccharomyces

  ENTRY             S44573     #type complete
  TITLE             hypothetical protein YKL609 - yeast (Saccharomyces
                      cerevisiae)
  ORGANISM          #formal_name Saccharomyces cerevisiae
  DATE              28-Sep-1994; #sequence_revision 28-Sep-1994; #text_change
                      28-Sep-1994
  ACCESSIONS        S44573
  REFERENCE         S44563
     #authors       Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger,
                      F.
     #journal       Yeast (1994) 10:35-40
     #title         DNA sequencing of a 36.2 kb fragment located between the FAS1
                      and LAP4 loci of chromosome XI of Saccharomyces cerevisiae.
     #accession     S44573
        ##status        preliminary
        ##residues      1-259 ##label VAN
        ##cross-references EMBL:Z26877
  SUMMARY           #length 259  #molecular-weight 28620  #checksum 3202
  SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.85
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

              X    X
              XCXNXI
               | | |
    LVDILSITESSCENGIDILIACNKSE
     150       160 X     170


4. US-08-121-713B-1 (1-6)
   S37984       probable purine nucleotide-binding protein YKL154w

  ENTRY             S37984     #type complete
  TITLE             probable purine nucleotide-binding protein YKL154w - yeast
                      (Saccharomyces cerevisiae)
  ORGANISM          #formal_name Saccharomyces cerevisiae
  DATE              03-May-1994 #sequence_revision 03-May-1994 #text_change
                      08-Dec-1994
  ACCESSIONS        S37984; S37796
  REFERENCE         S37976
     #authors       Vandenbol, M.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger,
                      F.
     #submission    submitted to the Protein Sequence Database, March 1994
     #accession     S37984
        ##molecule_type DNA
        ##residues      1-244 ##label VAN
        ##cross-references EMBL:Z28154
  REFERENCE         S37786
     #authors       Vandenbol, M.; Bolle, P.; Dion, C.; Portetelle, D.; Hilger,
```

```
                  F.
   #submission    submitted to the EMBL Data Library, September 1993
   #description   DNA sequencing of a 36.2 kb fragment located between the FAS1
                    and LAP4 loci of chromosome XI of S. cerevisiae.
   #accession     S37796
      ##molecule_type DNA
      ##residues       'TLPLLFISIIAHGIR',1-244 ##label VA2
      ##cross-references EMBL:Z26877
GENETICS
   #map_position 11L
KEYWORDS          P-loop; purine nucleotide binding
FEATURE
   45-52               #region purine nucleotide-binding motif A (P-loop)\
   51                  #binding_site ATP/GTP (Lys) #status predicted
SUMMARY           #length 244  #molecular-weight 26974  #checksum 2448
SEQUENCE

Initial Score     =      6  Optimized Score  =      6  Significance =  4.85
Residue Identity  =    50%  Matches          =      3  Mismatches   =     3
Gaps              =      0  Conservative Substitutions               =     0

            X    X
            XCXNXI
             | | |
   LVDILSITESSCENGIDILIACNKSE
        140 X     150


5. US-08-121-713B-1 (1-6)
   PS0249       porin - rice (strain Nihonbare) (fragment)

ENTRY             PS0249     #type fragment
TITLE             porin - rice (strain Nihonbare) (fragment)
ORGANISM          #formal_name Oryza sativa #common_name rice
DATE              03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
                    03-Feb-1994
ACCESSIONS        PS0249
REFERENCE         PS0206
   #authors       Tsugita, A.
   #submission    submitted to JIPID, April 1993
   #contents      callus
   #accession     PS0249
      ##molecule_type protein
      ##residues       1-14 ##label TSU
SUMMARY           #length 14  #checksum 7764
SEQUENCE

Initial Score     =      4  Optimized Score  =      4  Significance =  2.91
Residue Identity  =    33%  Matches          =      2  Mismatches   =     4
Gaps              =      0  Conservative Substitutions               =     0

          X    X
          XCXNXI
            | |
   AVTFTDDHTANGIK
           10  X


6. US-08-121-713B-1 (1-6)
   A40383       gene X protein - Escherichia coli plasmid R100 (fr
```



```
ENTRY             A40383     #type fragment
TITLE             gene X protein - Escherichia coli plasmid R100 (fragment)
ORGANISM          #formal_name Escherichia coli
DATE              27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change
                    18-Jun-1993
ACCESSIONS        A40383
REFERENCE         A40383
   #authors       Inamoto, S.; Yoshioka, Y.; Ohtsubo, E.
   #journal       J. Biol. Chem. (1991) 266:10086-10092
   #title         Site- and strand-specific nicking in Vitro at oriT by the
                    TraY-TraI endonuclease of plasmid R100.
   #cross-references MUID:91244768
   #accession     A40383
      ##status         preliminary
      ##molecule_type DNA
      ##residues       1-16 ##label INA
      ##note           sequence not compared to nucleotide translation
GENETICS
   #genome        plasmid
SUMMARY           #length 16  #checksum 4
SEQUENCE

Initial Score     =      4  Optimized Score  =      4  Significance =  2.91
Residue Identity  =    33%  Matches          =      2  Mismatches   =     4
Gaps              =      0  Conservative Substitutions               =     0

          X    X
          XCXNXI
           |   |
   MKKWMLAICLMFINGI
           10  X


7. US-08-121-713B-1 (1-6)
   E60977       14-3-3 protein homolog, 15K - California sea hare

ENTRY             E60977     #type fragment
TITLE             14-3-3 protein homolog, 15K - California sea hare (fragment)
ORGANISM          #formal_name Aplysia californica #common_name California sea
                    hare
DATE              31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                    03-Feb-1994
ACCESSIONS        E60977
REFERENCE         A60977
   #authors       Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz,
                    M.A.; Barzilai, A.; Karl, K.A.; Kandel, E.R.
   #journal       Electrophoresis (1989) 10:152-157
   #title         Development of a database of amino acid sequences for
                    proteins identified and isolated on two-dimensional
                    polyacrylamide gels.
   #accession     E60977
      ##molecule_type protein
      ##residues       1-19 ##label SWE
SUMMARY           #length 19  #checksum 4274
SEQUENCE

Initial Score     =      4  Optimized Score  =      4  Significance =  2.91
Residue Identity  =    33%  Matches          =      2  Mismatches   =     4
Gaps              =      0  Conservative Substitutions               =     0
```

```
            X    X
            XCXNXI
              | |
    ITKDYRKQIEKELNGI
        10  X    X
```

8. US-08-121-713B-1 (1-6)
   S06487 ferredoxin, 15K, mitochondrial - pig (fragment)

```
 ENTRY            S06487     #type fragment
 TITLE            ferredoxin, 15K, mitochondrial - pig (fragment)
 ORGANISM         #formal_name Sus scrofa domestica #common_name domestic pig
 DATE             30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
                    26-May-1994
 ACCESSIONS       S06487
 REFERENCE        S06485
    #authors      Driscoll, W.J.; Omdahl, J.L.
    #journal      Eur. J. Biochem. (1989) 185:181-187
    #title        Characterization and N-terminal amino acid sequence of
                    multiple ferredoxins in kidney and adrenal mitochondria.
    #cross-references MUID:90032674
    #accession    S06487
       ##molecule_type protein
       ##residues      1-22 ##label DRI
 CLASSIFICATION   #superfamily glycine cleavage system protein H
 KEYWORDS         electron transfer; mitochondrion
 SUMMARY          #length 22  #checksum 9488
 SEQUENCE

Initial Score    =      4  Optimized Score  =      4  Significance =  2.91
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            XCXNXI
              | |
    SKFTDKVEWITTENGIGTVG
          10  X    20
```

9. US-08-121-713B-1 (1-6)
   A54725 cecropin B - Chinese oak silkmoth

```
 ENTRY            A54725     #type complete
 TITLE            cecropin B - Chinese oak silkmoth
 ORGANISM         #formal_name Antheraea pernyi #common_name Chinese oak
                    silkmoth
 DATE             11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change
                    11-Nov-1994
 ACCESSIONS       A54725
 REFERENCE        A54725
    #authors      Craig, A.G.; Engstroem, A.; Bennich, H.; Kamensky, I.
    #journal      Biomed. Environ. Mass Spectrom. (1987) 14:669-673
    #title        Plasma desorption mass spectrometry coupled with conventional
                    peptide sequencing techniques.
    #accession    A54725
       ##status       preliminary
       ##molecule_type protein
```



```
       ##residues      1-35 ##label CRA
 KEYWORDS         amidation
 SUMMARY          #length 35  #molecular-weight 3818  #checksum 6340
 SEQUENCE

Initial Score    =      4  Optimized Score  =      4  Significance =  2.91
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            XCXNXI
              | |
    IFKKIEKVGRNIRNGIIKAGPAVAVL
        10  X    20
```

10. US-08-121-713B-1 (1-6)
    S45125 hypothetical protein N2023 - yeast (Saccharomyces

```
 ENTRY            S45125     #type complete
 TITLE            hypothetical protein N2023 - yeast (Saccharomyces cerevisiae)
 ORGANISM         #formal_name Saccharomyces cerevisiae
 DATE             03-May-1994 #sequence_revision 02-Aug-1994 #text_change
                    02-Aug-1994
 ACCESSIONS       S45125
 REFERENCE        S45118
    #authors      Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.
    #submission   submitted to the EMBL Data Library, January 1994
    #description  Twelve open reading frames revealed on the 23.6 kbp segment
                    flanking the centromere on the Saccharomyces cerevisiae
                    chromosome XIV right arm.
    #accession    S45125
       ##molecule_type DNA
       ##residues      1-35 ##label VER
       ##cross-references EMBL:X77395
 GENETICS
    #map_position 14
 SUMMARY          #length 35  #molecular-weight 3966  #checksum 7961
 SEQUENCE

Initial Score    =      4  Optimized Score  =      4  Significance =  2.91
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            XCXNXI
              | |
    SIFCIPNIIAFFNNGIPTIISKIT
          20 X    X 30
```

11. US-08-121-713B-1 (1-6)
    CKAOBP cecropin B - Chinese oak silkmoth

```
 ENTRY            CKAOBP     #type complete
 TITLE            cecropin B - Chinese oak silkmoth
 ORGANISM         #formal_name Antheraea pernyi #common_name Chinese oak
                    silkmoth
 DATE             17-Dec-1982 #sequence_revision 30-Sep-1988 #text_change
                    30-Sep-1993
```

```
ACCESSIONS       A01771
REFERENCE        A91122
   #authors      Qu, X.; Steiner, H.; Engstrom, A.; Bennich, H.; Boman, H.G.
   #journal      Eur. J. Biochem. (1982) 127:219-224
   #title        Insect immunity: isolation and structure of cecropins B and D
                   from pupae of the Chinese oak silk moth, Antheraea pernyi.
   #cross-references MUID:83053368
   #accession    A01771
      ##molecule_type protein
      ##residues      1-36 ##label QUX
      ##note          the carboxyl end is blocked
CLASSIFICATION   #superfamily cecropin
SUMMARY          #length 36  #molecular-weight 3905  #checksum 9328
SEQUENCE

Initial Score    =      4  Optimized Score  =      4  Significance =  2.91
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            XCXNXI
              | |
   IFKKIEKVGRNIRNGIIKAGPAVAVL
        10   X    20
```

12. US-08-121-713B-1 (1-6)
    B31252 metallothionein II - yeast (Candida glabrata) (fra

```
ENTRY            B31252     #type fragments
TITLE            metallothionein II - yeast (Candida glabrata) (fragments)
ORGANISM         #formal_name Candida glabrata
DATE             31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
                   30-Sep-1993
ACCESSIONS       B31252
REFERENCE        A94212
   #authors      Mehra, R.K.; Tarbet, E.B.; Gray, W.R.; Winge, D.R.
   #journal      Proc. Natl. Acad. Sci. U.S.A. (1988) 85:8815-8819
   #title        Metal-specific synthesis of two metallothioneins and
                   gamma-glutamyl peptides in Candida glabrata.
   #cross-references MUID:89057829
   #accession    B31252
      ##molecule_type protein
      ##residues      1-37 ##label MEH
SUMMARY          #length 37  #checksum 1778
SEQUENCE

Initial Score    =      4  Optimized Score  =      4  Significance =  2.91
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            XCXNXI
              | |
   CQYDCHCANCACENSASNECSCQTCK
      10     X  20        30
```

13. US-08-121-713B-1 (1-6)
    A23617 conglutin delta-2 small chain - narrow-leaved blue


```
ENTRY            A23617     #type complete
TITLE            conglutin delta-2 small chain - narrow-leaved blue lupine
ORGANISM         #formal_name Lupinus angustifolius #common_name narrow-leaved
                   blue lupine
DATE             31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
                   18-Jun-1993
ACCESSIONS       A23617
REFERENCE        A91358
   #authors      Lilley, G.G.; Inglis, A.S.
   #journal      FEBS Lett. (1986) 195:235-241
   #title        Amino acid sequence of conglutin delta, a sulfur-rich seed
                   protein of Lupinus angustifolius L. Sequence homology with
                   the C-III alpha-amylase inhibitor from wheat.
   #accession    A23617
      ##molecule_type protein
      ##residues      1-37 ##label LIL
SUMMARY          #length 37  #molecular-weight 4598  #checksum 2819
SEQUENCE

Initial Score    =      4  Optimized Score  =      6  Significance =  2.91
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            XCXNXI
              | | |
   KRQLQQVNLRHCENHIDQRIQQQQEE
   10       20   X    30
```

14. US-08-121-713B-1 (1-6)
    B32307 ribosomal protein L36 - Bacillus subtilis

```
ENTRY            B32307     #type complete
TITLE            ribosomal protein L36 - Bacillus subtilis
ALTERNATE_NAMES  ribosomal protein B
ORGANISM         #formal_name Bacillus subtilis
DATE             31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
                   18-Jun-1993
ACCESSIONS       A32307; B32307
REFERENCE        A32307
   #authors      Boylan, S.A.; Suh, J.W.; Thomas, S.M.; Price, C.W.
   #journal      J. Bacteriol. (1989) 171:2553-2562
   #title        Gene encoding the alpha core subunit of Bacillus subtilis RNA
                   polymerase is cotranscribed with the genes for initiation
                   factor 1 and ribosomal proteins B, S13, S11, and L17.
   #cross-references MUID:89213940
   #accession    A32307
      ##molecule_type DNA
      ##residues      1-37 ##label BOY
      ##note          sequence not compared to nucleotide translation
CLASSIFICATION   #superfamily Escherichia coli ribosomal protein L36
KEYWORDS         protein biosynthesis; ribosome
SUMMARY          #length 37  #molecular-weight 4305  #checksum 3561
SEQUENCE

Initial Score    =      4  Optimized Score  =      4  Significance =  2.91
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0
```

```
            X    X
            XCXNXI
             | |
    VIRRKGKVMVICENPKHKQKQG
       20     X  30


15. US-08-121-713B-1 (1-6)
    R5BS36       ribosomal protein L36 - Bacillus stearothermophilu

 ENTRY            R5BS36     #type complete
 TITLE            ribosomal protein L36 - Bacillus stearothermophilus
 ALTERNATE_NAMES  ribosomal protein BL38; ribosomal protein II
 ORGANISM         #formal_name Bacillus stearothermophilus
 DATE             31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change
                    30-Jun-1993
 ACCESSIONS       S08566
 REFERENCE        S07236
    #authors      Tanaka, I.; Kimura, M.; Kimura, J.; Dijk, J.
    #journal      FEBS Lett. (1984) 166:343-346
    #title        The amino acid sequence of two small ribosomal proteins from
                    Bacillus stearothermophilus.
    #cross-references MUID:84108949
    #accession    S08566
       ##molecule_type protein
       ##residues      1-37 ##label TAN
 CLASSIFICATION   #superfamily Escherichia coli ribosomal protein L36
 KEYWORDS         protein biosynthesis; ribosome
 SUMMARY          #length 37  #molecular-weight 4361  #checksum 3946
 SEQUENCE

Initial Score    =      4  Optimized Score  =      4  Significance =  2.91
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            XCXNXI
             | |
    VIRRRGKVMVICENPKHKQRQG
       20     X  30
> O <
O| |O  IntelliGenetics
> O <

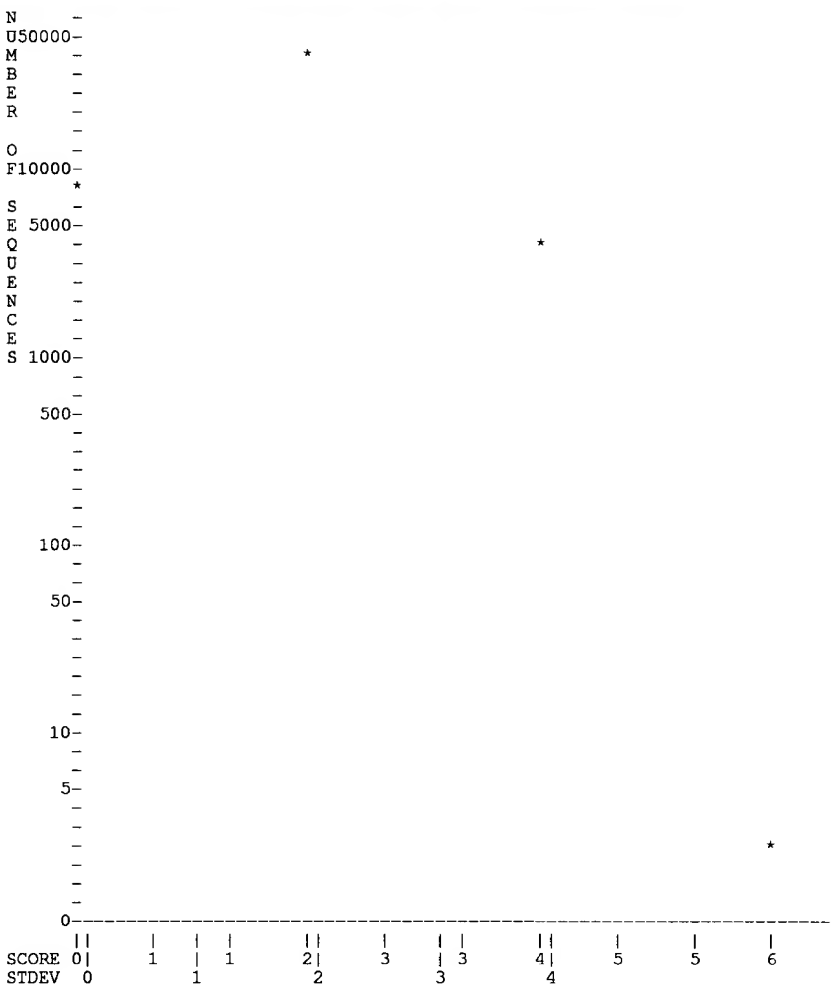
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq1spt.res made by  on Fri 19 May 95 8:51:45-PDT.


Query sequence being compared:US-08-121-713B-1 (1-6)
Number of sequences searched:                43470
Number of scores above cutoff:                3752

     Results of the initial comparison of US-08-121-713B-1 (1-6) with:
   Data bank : Swiss-Prot 31, all entries

100000-
      -
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		

Cutoff score 0
Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	0.93

Times:	CPU	Total Elapsed
	00:00:43.02	00:00:43.00

Number of residues: 15335248
Number of sequences searched: 43470
Number of scores above cutoff: 3752

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

2 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. CFAH_MOUSE	COMPLEMENT FACTOR H PRECURSOR	1234	6	6	5.36	0
2. YKP4_YEAST	HYPOTHETICAL 27.0 KD PROTEIN	244	6	6	5.36	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 3 standard deviations above mean ****					
3. UKA4_HUMAN	UNKNOWN PROTEIN FROM 2D-PAGE	16	4	4	3.22	0
4. COXJ_ONCMY	CYTOCHROME C OXIDASE POLYPEPT	23	4	4	3.22	0
5. CECB_ANTPE	CECROPIN B.	35	4	4	3.22	0
6. RL36_THETH	50S RIBOSOMAL PROTEIN L36 (RI	37	4	4	3.22	0
7. RL36_MARPO	50S RIBOSOMAL PROTEIN L36.	37	4	4	3.22	0
8. RL36_BACSU	50S RIBOSOMAL PROTEIN L36 (RI	37	4	4	3.22	0
9. RL36_BACST	50S RIBOSOMAL PROTEIN L36 (RI	37	4	4	3.22	0
10. CG2S_LUPAN	CONGLUTIN DELTA-2 SMALL CHAIN	37	4	6	3.22	0
11. RL43_YEAST	60S RIBOSOMAL PROTEIN YL43 (F	39	4	4	3.22	0
12. ORN3_PLAOR	ORNATIN A3.	41	4	4	3.22	0
13. VE5_PAPVE	E5 PROTEIN.	43	4	4	3.22	0
14. CUP1_SARBU	LARVAL CUTICLE PROTEIN SC1 (F	43	4	4	3.22	0
15. GGI1_STAHA	ANTIBACTERIAL PROTEIN 1 (GONO	44	4	4	3.22	0
16. HEX8_ADE40	HEXON-ASSOCIATED PROTEIN PREC	47	4	4	3.22	0
17. RB12_MOUSE	RAS-RELATED PROTEIN RAB-12 (F	49	4	4	3.22	0
18. MT2_CANGA	METALLOTHIONEIN-II.	51	4	4	3.22	0
19. INS_ZAODH	INSULIN.	51	4	4	3.22	0
20. INS_CROAT	INSULIN.	51	4	4	3.22	0
21. INS_ANSAN	INSULIN.	51	4	4	3.22	0

22.	TCTP_ARATH	TRANSLATIONALLY CONTROLLED TU	53	4	4	3.22	0
23.	RUBR_PYRFU	RUBREDOXIN (RD).	53	4	4	3.22	0
24.	PSBK_MARPO	PHOTOSYSTEM II 4 KD REACTION	55	4	4	3.22	0
25.	NXB4_CERLA	NEUROTOXIN B-IV.	55	4	4	3.22	0
26.	NXB2_CERLA	NEUROTOXIN B-II.	55	4	4	3.22	0
27.	Y60_LAMBD	HYPOTHETICAL NIN REGION PROTE	60	4	4	3.22	0
28.	NXS1_NAJKA	SHORT NEUROTOXIN 1 (TOXIN C-6	62	4	4	3.22	0
29.	NXS1_NAJAT	SHORT NEUROTOXIN 1 (COBROTOXI	62	4	4	3.22	0
30.	CECB_HYACE	CECROPIN B PRECURSOR (IMMUNE	62	4	4	3.22	0
31.	IMAP_DROFU	MALE ACCESSORY GLAND SERINE-P	63	4	4	3.22	0
32.	UREI_BACSB	UREASE ACCESSORY PROTEIN UREI	65	4	4	3.22	0
33.	MALX_KLEPN	MALX PROTEIN (FRAGMENT).	65	4	4	3.22	0
34.	XEN2_XENLA	XENOXIN-2.	66	4	4	3.22	0
35.	RL21_HALMA	50S RIBOSOMAL PROTEIN HL21/HL	66	4	4	3.22	0
36.	IGF2_CHICK	INSULIN-LIKE GROWTH FACTOR II	66	4	4	3.22	0
37.	RNH_MYCSM	RIBONUCLEASE H (EC 3.1.26.4)	67	4	4	3.22	0
38.	NUSG_CGDAB	TRANSCRIPTION ANTITERMINATION	70	4	4	3.22	0
39.	VTB2_XENLA	VITELLOGENIN B2 PRECURSOR (VT	71	4	4	3.22	0
40.	VTB1_XENLA	VITELLOGENIN B1 PRECURSOR (VT	71	4	4	3.22	0
41.	HPI1_ECTHA	HIGH POTENTIAL IRON-SULFUR PR	71	4	4	3.22	0
42.	DISI_AGKPI	DISINTEGRIN APPLAGIN (PLATELE	71	4	4	3.22	0
43.	DISI_AGKHA	DISINTEGRIN HALYSIN (PLATELET	71	4	4	3.22	0
44.	D230_PEA	DISEASE RESISTANCE RESPONSE P	72	4	4	3.22	0
45.	DISG_TRIGA	DISINTEGRIN TRIGRAMIN GAMMA (	73	4	4	3.22	0

1. US-08-121-713B-1 (1-6)
CFAH_MOUSE COMPLEMENT FACTOR H PRECURSOR (PROTEIN BETA-1-H).

```
ID   CFAH_MOUSE     STANDARD;      PRT;  1234 AA.
AC   P06909;
DT   01-JAN-1988 (REL. 06, CREATED)
DT   01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   COMPLEMENT FACTOR H PRECURSOR (PROTEIN BETA-1-H).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   86233353
RA   KRISTENSEN T., TACK B.F.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 83:3963-3967(1986).
CC   -!- FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION OF
CC       C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF THE
CC       C3BBB COMPLEX (C3 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5
CC       CONVERTASE) IN THE ALTERNATIVE COMPLEMENT PATHWAY.
CC   -!- POLYMORPHISM: TWO CODOMINANT ALLELES OF FACTOR H ARE PRESENT IN
CC       MICE.
CC   -!- SIMILARITY: CONTAINS 20 SUSHI (SCR) REPEATS.
DR   EMBL; M12660; MMH.
DR   PIR; A26154; NBMSH.
DR   HSSP; P08603; 1HFI.
KW   COMPLEMENT ALTERNATE PATHWAY; PLASMA; GLYCOPROTEIN; REPEAT; SUSHI;
KW   SIGNAL.
FT   SIGNAL        1     18       BY SIMILARITY.
FT   CHAIN        19   1234       COMPLEMENT FACTOR H.
FT   DOMAIN       20   1224       20 X SUSHI (SCR) REPEATS.
FT   REPEAT       20     81       SUSHI 1.
FT   REPEAT       84    142       SUSHI 2.
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FT   REPEAT      145    206       SUSHI 3.
FT   REPEAT      209    263       SUSHI 4.
FT   REPEAT      266    321       SUSHI 5.
FT   REPEAT      324    386       SUSHI 6.
FT   REPEAT      388    443       SUSHI 7.
FT   REPEAT      447    506       SUSHI 8.
FT   REPEAT      508    565       SUSHI 9.
FT   REPEAT      568    623       SUSHI 10.
FT   REPEAT      628    684       SUSHI 11.
FT   REPEAT      689    744       SUSHI 12.
FT   REPEAT      751    803       SUSHI 13.
FT   REPEAT      807    862       SUSHI 14.
FT   REPEAT      866    932       SUSHI 15.
FT   REPEAT      935    990       SUSHI 16.
FT   REPEAT      993   1049       SUSHI 17.
FT   REPEAT     1052   1108       SUSHI 18.
FT   REPEAT     1113   1169       SUSHI 19.
FT   REPEAT     1171   1234       SUSHI 20.
FT   DISULFID     21     66       BY SIMILARITY.
FT   DISULFID     52     80       BY SIMILARITY.
FT   DISULFID     85    129       BY SIMILARITY.
FT   DISULFID    114    141       BY SIMILARITY.
FT   DISULFID    146    192       BY SIMILARITY.
FT   DISULFID    178    205       BY SIMILARITY.
FT   DISULFID    210    251       BY SIMILARITY.
FT   DISULFID    237    262       BY SIMILARITY.
FT   DISULFID    267    309       BY SIMILARITY.
FT   DISULFID    294    320       BY SIMILARITY.
FT   DISULFID    325    374       BY SIMILARITY.
FT   DISULFID    357    385       BY SIMILARITY.
FT   DISULFID    389    431       BY SIMILARITY.
FT   DISULFID    416    442       BY SIMILARITY.
FT   DISULFID    448    494       BY SIMILARITY.
FT   DISULFID    477    505       BY SIMILARITY.
FT   DISULFID    509    553       BY SIMILARITY.
FT   DISULFID    536    564       BY SIMILARITY.
FT   DISULFID    569    610       BY SIMILARITY.
FT   DISULFID    597    622       BY SIMILARITY.
FT   DISULFID    629    672       BY SIMILARITY.
FT   DISULFID    658    683       BY SIMILARITY.
FT   DISULFID    690    732       BY SIMILARITY.
FT   DISULFID    718    743       BY SIMILARITY.
FT   DISULFID    752    791       BY SIMILARITY.
FT   DISULFID    780    802       BY SIMILARITY.
FT   DISULFID    808    850       BY SIMILARITY.
FT   DISULFID    836    861       BY SIMILARITY.
FT   DISULFID    867    920       BY SIMILARITY.
FT   DISULFID    906    931       BY SIMILARITY.
FT   DISULFID    936    978       BY SIMILARITY.
FT   DISULFID    964    989       BY SIMILARITY.
FT   DISULFID    994   1037       BY SIMILARITY.
FT   DISULFID   1023   1048       BY SIMILARITY.
FT   DISULFID   1053   1096       BY SIMILARITY.
FT   DISULFID   1082   1107       BY SIMILARITY.
FT   DISULFID   1114   1157       BY SIMILARITY.
FT   DISULFID   1143   1168       BY SIMILARITY.
FT   DISULFID   1172   1223       BY SIMILARITY.
FT   DISULFID   1206   1233       BY SIMILARITY.
FT   CARBOHYD    676    676       POTENTIAL.
FT   CARBOHYD    721    721       POTENTIAL.
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FT   CARBOHYD    773    773       POTENTIAL.
FT   CARBOHYD    801    801       POTENTIAL.
FT   CARBOHYD   1030   1030       POTENTIAL.
FT   CARBOHYD   1061   1061       POTENTIAL.
FT   CARBOHYD   1225   1225       POTENTIAL.
SQ   SEQUENCE   1234 AA;  139082 MW;  8347878 CN;

Initial Score    =      6  Optimized Score  =      6  Significance =  5.36
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             XCXNXI
              | | |
    PLELFGQVEVMCENGIWTEKPKCRDS
      1090    X 1100      1110


2. US-08-121-713B-1 (1-6)
   YKP4_YEAST   HYPOTHETICAL 27.0 KD PROTEIN IN APE2-GPM1 INTERGEN

ID   YKP4_YEAST     STANDARD;      PRT;   244 AA.
AC   P36057;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 27.0 KD PROTEIN IN APE2-GPM1 INTERGENIC REGION.
GN   YKL154W OR YKL609.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C;
RM   94378720
RA   VANDENBOL M., BOLLE P.-A., DION C., PORTETELLE D., HILGER F.;
RL   YEAST 10:S35-S40(1994).
CC   -!- SIMILARITY: DISTANTLY RELATED TO RAS SUPERFAMILY.
DR   EMBL; Z26877; SCDCHR11.
DR   EMBL; Z28154; SCYKL154W.
DR   PIR; S37984; S37984.
KW   HYPOTHETICAL PROTEIN; GTP-BINDING.
FT   NP_BIND      45     52       GTP (POTENTIAL).
FT   NP_BIND      87     91       GTP (POTENTIAL).
FT   NP_BIND     154    157       GTP (POTENTIAL).
SQ   SEQUENCE   244 AA;  26974 MW;  308102 CN;

Initial Score    =      6  Optimized Score  =      6  Significance =  5.36
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             XCXNXI
              | | |
    LVDILSITESSCENGIDILIACNKSE
         140 X     150


3. US-08-121-713B-1 (1-6)
   UKA4_HUMAN   UNKNOWN PROTEIN FROM 2D-PAGE OF EPIDERMAL KERATINO
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ID   UKA4_HUMAN      STANDARD;      PRT;    16 AA.
AC   P31145;
DT   01-JUL-1993 (REL. 26, CREATED)
DT   01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   UNKNOWN PROTEIN FROM 2D-PAGE OF EPIDERMAL KERATINOCYTES (SPOT 2120)
DE   (FRAGMENTS).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=KERATINOCYTES;
RM   93162043
RA   RASMUSSEN H.H., VAN DAMME J., PUYPE M., GESSER B., CELIS J.E.,
RA   VANDEKERCKHOVE J.;
RL   ELECTROPHORESIS 13:960-969(1992).
CC   -!- ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.74,
CC       ITS MW IS: 21.2 KD.
DR   AARHUS/GHENT-2DPAGE; 2120; IEF.
FT   NON_TER       1      1
FT   UNSURE        4      5
FT   UNSURE        7      7
FT   NON_CONS      9     10
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1809 MW;  1385 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.22
Residue Identity =    66%  Matches          =      2  Mismatches   =     1
Gaps             =      0  Conservative Substitutions               =     0

      X X
    XCXNXI
      | |
      NGIHDLDNIFILN
      X X     10
```

4. US-08-121-713B-1 (1-6)
   COXJ_ONCMY CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER (EC 1.

```
ID   COXJ_ONCMY      STANDARD;      PRT;    23 AA.
AC   P80333;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER (EC 1.9.3.1) (VIIIC)
DE   (FRAGMENT).
OS   ONCORHYNCHUS MYKISS (RAINBOW TROUT) (SALMO GAIRDNERI).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC   OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=LIVER;
RM   94237150
RA   FREUND R., KADENBACH B.;
RL   EUR. J. BIOCHEM. 221:1111-1116(1994).
CC   -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC       CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC       MITOCHONDRIAL ELECTRON TRANSPORT.
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CC   -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
CC       4 FERRICYTOCHROME C.
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
DR   PIR; S43632; S43632.
KW   OXIDOREDUCTASE; INNER MEMBRANE; MITOCHONDRION.
FT   NON_TER      23     23
SQ   SEQUENCE   23 AA;  2635 MW;  3126 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.22
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            XCXNXI
              || |
   NMVPEKQKLFQAXNGIPVHLF
        10  X     20
```

5. US-08-121-713B-1 (1-6)
   CECB_ANTPE CECROPIN B.

```
ID   CECB_ANTPE      STANDARD;      PRT;    35 AA.
AC   P01509;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
DE   CECROPIN B.
OS   ANTHERAEA PERNYI (CHINESE OAK SILK MOTH).
OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; LEPIDOPTERA.
RN   [1]
RP   PARTIAL SEQUENCE.
RM   83053368
RA   QU X.-M., STEINER H., ENGSTROM A., BENNICH H., BOMAN H.G.;
RL   EUR. J. BIOCHEM. 127:219-224(1982).
RN   [2]
RP   SEQUENCE.
RM   88108273
RA   CRAIG A.G., ENGSTROM A., BENNICH H., KAMENSKY I.;
RL   BIOMED. ENVIRON. MASS SPECTROM. 14:669-673(1987).
CC   -!- FUNCTION: CECROPINS HAVE LYTIC AND ANTIBACTERIAL ACTIVITY AGAINST
CC       SEVERAL GRAM-POSITIVE & GRAM-NEGATIVE BACTERIA.
DR   PIR; A01771; CKAOBP.
DR   PIR; A54725; A54725.
DR   PROSITE; PS00268; CECROPIN.
KW   INSECT IMMUNITY; ANTIBIOTIC; HEMOLYMPH; AMIDATION; MULTIGENE FAMILY.
FT   MOD_RES      35     35       AMIDATION.
SQ   SEQUENCE   35 AA;  3818 MW;  5337 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.22
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            XCXNXI
              | |
   IFKKIEKVGRNIRNGIIKAGPAVAVL
       10   X    20
```

6. US-08-121-713B-1 (1-6)
RL36_THETH 50S RIBOSOMAL PROTEIN L36 (RIBOSOMAL PROTEIN B).

```
ID   RL36_THETH     STANDARD;      PRT;    37 AA.
AC   P80256;
DT   01-OCT-1993 (REL. 27, CREATED)
DT   01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   50S RIBOSOMAL PROTEIN L36 (RIBOSOMAL PROTEIN B).
GN   RPMJ OR RPL36.
OS   THERMUS AQUATICUS (SUBSP. THERMOPHILUS).
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC   UNCERTAIN.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=HB8;
RA   BOYSEN R.I., SCHROEDER W., ERDMANN V.A.;
RL   SUBMITTED (SEP-1993) TO THE SWISS-PROT DATA BANK.
CC   -!- SIMILARITY: BELONGS TO THE L36P FAMILY OF RIBOSOMAL PROTEINS.
DR   PROSITE; PS00828; RIBOSOMAL_L36.
KW   RIBOSOMAL PROTEIN.
SQ   SEQUENCE   37 AA;  4421 MW;  6411 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.22
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions              =     0

            X    X
            XCXNXI
             | |
   VIRRHGRVYVICENPKHKQRQG
      20     X  30
```

7. US-08-121-713B-1 (1-6)
RL36_MARPO 50S RIBOSOMAL PROTEIN L36.

```
ID   RL36_MARPO     STANDARD;      PRT;    37 AA.
AC   P12142;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE   50S RIBOSOMAL PROTEIN L36.
GN   RPL36 OR SECX.
OS   MARCHANTIA POLYMORPHA (LIVERWORT).
OG   CHLOROPLAST.
OC   EUKARYOTA; PLANTA; EMBRYOPHYTA; BRYOPHYTA; HEPATICOPSIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   89068687
RA   FUKUZAWA H., KOHCHI T., SANO T., SHIRAI H., UMESONO K., INOKUCHI H.,
RA   OZEKI H., OHYAMA K.;
RL   J. MOL. BIOL. 203:333-351(1988).
RN   [2]
RP   COMPLETE GENOME.
RA   OHYAMA K., FUKUZAWA H., KOHCHI T., SHIRAI H., SANO T., SANO S.,
RA   UMESONO K., SHIKI Y., TAKEUCHI M., CHANG Z., AOTA S., INOKUCHI H.,
RA   OZEKI H.;
RL   NATURE 322:572-574(1986).
CC   -!- SIMILARITY: BELONGS TO THE L36P FAMILY OF RIBOSOMAL PROTEINS.
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DR   EMBL; X04465; CHMPXX.
DR   PIR; A05060; R5LV36.
DR   PROSITE; PS00828; RIBOSOMAL_L36.
KW   RIBOSOMAL PROTEIN; CHLOROPLAST.
SQ   SEQUENCE   37 AA;  4521 MW;  5888 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.22
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions              =     0

            X    X
            XCXNXI
             | |
   MKIRASVRKICENCRLIRRRRRIMV
           10    X   20
```

8. US-08-121-713B-1 (1-6)
RL36_BACSU 50S RIBOSOMAL PROTEIN L36 (RIBOSOMAL PROTEIN II) (

```
ID   RL36_BACSU     STANDARD;      PRT;    37 AA.
AC   P20278;
DT   01-FEB-1991 (REL. 17, CREATED)
DT   01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   50S RIBOSOMAL PROTEIN L36 (RIBOSOMAL PROTEIN II) (RIBOSOMAL PROTEIN B)
DE   (BL38).
GN   RPMJ.
OS   BACILLUS SUBTILIS.
OC   PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   89213940
RA   BOYLAN S.A., SUH J.-W., THOMAS S.M., PRICE C.W.;
RL   J. BACTERIOL. 171:2553-2562(1989).
CC   -!- SIMILARITY: BELONGS TO THE L36P FAMILY OF RIBOSOMAL PROTEINS.
DR   EMBL; M26414; M26414.
DR   PIR; B32307; B32307.
DR   SUBTILIST; BG11042; RPMJ.
DR   PROSITE; PS00828; RIBOSOMAL_L36.
KW   RIBOSOMAL PROTEIN.
SQ   SEQUENCE   37 AA;  4305 MW;  7120 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.22
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions              =     0

            X    X
            XCXNXI
             | |
   VIRRKGKVMVICENPKHKQKQG
      20     X  30
```

9. US-08-121-713B-1 (1-6)
RL36_BACST 50S RIBOSOMAL PROTEIN L36 (RIBOSOMAL PROTEIN II) (

```
ID   RL36_BACST     STANDARD;      PRT;    37 AA.
AC   P07841;
DT   01-AUG-1988 (REL. 08, CREATED)
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DT   01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
DT   01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE   50S RIBOSOMAL PROTEIN L36 (RIBOSOMAL PROTEIN II) (RIBOSOMAL PROTEIN B)
DE   (BL38).
GN   RPMJ.
OS   BACILLUS STEAROTHERMOPHILUS.
OC   PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN   [1]
RP   SEQUENCE.
RM   84108949
RA   TANAKA I., KIMURA M., KIMURA J., DIJK J.;
RL   FEBS LETT. 166:343-346(1984).
CC   -!- SIMILARITY: BELONGS TO THE L36P FAMILY OF RIBOSOMAL PROTEINS.
DR   PIR; S08566; R5BS36.
DR   PROSITE; PS00828; RIBOSOMAL_L36.
KW   RIBOSOMAL PROTEIN.
SQ   SEQUENCE   37 AA;  4361 MW;  6570 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.22
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions              =     0

             X    X
             XCXNXI
              | |
   VIRRRGKVMVICENPKHKQRQG
      20     X  30
```

10. US-08-121-713B-1 (1-6)
    CG2S_LUPAN CONGLUTIN DELTA-2 SMALL CHAIN.

```
ID   CG2S_LUPAN     STANDARD;      PRT;    37 AA.
AC   P09930;
DT   01-MAR-1989 (REL. 10, CREATED)
DT   01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT   01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
DE   CONGLUTIN DELTA-2 SMALL CHAIN.
OS   LUPINUS ANGUSTIFOLIUS (NARROW-LEAVED BLUE LUPINE).
OC   EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
OC   FABACEAE.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=CV. WHITE;
RA   LILLEY G.G., INGLIS A.S.;
RL   FEBS LETT. 195:235-241(1986).
CC   -!- SUBUNIT: DIMER OF A SMALL CHAIN AND A LARGE CHAIN LINKED BY TWO
CC       DISULFIDE BONDS.
DR   PIR; A23617; A23617.
KW   SEED.
FT   DISULFID      8      8       INTERCHAIN (WITH C-29 OF LARGE CHAIN).
FT   DISULFID     20     20       INTERCHAIN (WITH C-17 OR C-18 OF LARGE
FT                                CHAIN).
FT   DOMAIN       29     37       GLU/GLN-RICH.
SQ   SEQUENCE   37 AA;  4598 MW;  4779 CN;

Initial Score    =      4  Optimized Score  =      6  Significance =  3.22
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions              =     0
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```
             X    X
             XCXNXI
              | | |
   KRQLQQVNLRHCENHIDQRIQQQQEE
   10        20   X    30
```

11. US-08-121-713B-1 (1-6)
    RL43_YEAST 60S RIBOSOMAL PROTEIN YL43 (FRAGMENT).

```
ID   RL43_YEAST     STANDARD;      PRT;    39 AA.
AC   P05747;
DT   01-NOV-1988 (REL. 09, CREATED)
DT   01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   60S RIBOSOMAL PROTEIN YL43 (FRAGMENT).
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE.
RA   OKATA E., HIGO K.-I., ITOH T.;
RL   MOL. GEN. GENET. 195:544-546(1984).
CC   -!- SIMILARITY: BELONGS TO THE L29E FAMILY OF RIBOSOMAL PROTEINS.
DR   PIR; S11265; S11265.
KW   RIBOSOMAL PROTEIN.
FT   NON_TER       39     39
SQ   SEQUENCE   39 AA;  4532 MW;  8733 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.22
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions              =     0

             X    X
             XCXNXI
              | |
   NHTAHNQTRKAHRNGIKKPKTYKYPS
       10    X   20         30
```

12. US-08-121-713B-1 (1-6)
    ORN3_PLAOR ORNATIN A3.

```
ID   ORN3_PLAOR     STANDARD;      PRT;    41 AA.
AC   P25510;
DT   01-MAY-1992 (REL. 22, CREATED)
DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT   01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
DE   ORNATIN A3.
OS   PLACOBDELLA ORNATA (TURTLE LEECH).
OC   EUKARYOTA; METAZOA; ANNELIDA; HIRUDINEA.
RN   [1]
RP   SEQUENCE.
RM   92111479
RA   MAZUR P., HENZEL W.J., SEYMOUR J.L., LAZARUS R.A.;
RL   EUR. J. BIOCHEM. 202:1073-1082(1991).
CC   -!- FUNCTION: POTENT INHIBITOR OF FIBRINOGEN INTERACTION WITH PLATELET
CC       RECEPTORS EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. MAY PREVENT
CC       BLOOD FROM CLOTTING DURING EITHER FEEDING AND/OR STORAGE OF
CC       INGESTED BLOOD.
CC   -!- SIMILARITY: HIGH, TO THE OTHER P.ORNATA ORNATINS, AND TO  M.DECORA
```

```
CC       DECORSIN.
CC   -!- SIMILARITY: SMALL, TO THE SNAKE FAMILY OF DISINTEGRINS.
DR   PIR; S19621; S19621.
KW   BLOOD COAGULATION; PLATELET; CELL ADHESION.
FT   SITE         33     35       CELL ATTACHMENT SITE.
SQ   SEQUENCE   41 AA;  4386 MW;  7138 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.22
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             XCXNXI
                | |
    IKESGQPNDKCRCNGITCTVGKCKIG
      10      X 20 X      30
```

13. US-08-121-713B-1 (1-6)
    VE5_PAPVE E5 PROTEIN.

```
ID   VE5_PAPVE      STANDARD;      PRT;    43 AA.
AC   P11330;
DT   01-JUL-1989 (REL. 11, CREATED)
DT   01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT   01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
DE   E5 PROTEIN.
OS   EUROPEAN ELK PAPILLOMAVIRUS (EEPV).
OC   VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   87219878
RA   AHOLA H., BERGMAN P., STROEM A.C., MORENO-LOPEZ J., PETTERSON U.;
RL   GENE 50:195-205(1986).
DR   EMBL; M15953; PAPPPECG.
DR   PIR; E29499; W5WLEP.
KW   EARLY PROTEIN.
SQ   SEQUENCE   43 AA;  5182 MW;  9855 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.22
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             XCXNXI
              | |
    FLVWWDQFGCRCENMQL
      30      X 40 X
```

14. US-08-121-713B-1 (1-6)
    CUP1_SARBU LARVAL CUTICLE PROTEIN SC1 (FRAGMENT).

```
ID   CUP1_SARBU     STANDARD;      PRT;    43 AA.
AC   P14485;
DT   01-JAN-1990 (REL. 13, CREATED)
DT   01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT   01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)
DE   LARVAL CUTICLE PROTEIN SC1 (FRAGMENT).
OS   SARCOPHAGA BULLATA (FLESH FLY).
```



```
OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN   [1]
RP   SEQUENCE.
RM   86037264
RA   HENZEL W.J., MOLE J.E., MULLIGAN K., LIPKE H.;
RL   J. MOL. EVOL. 22:39-45(1985).
CC   -!- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF FLESH FLY.
CC   -!- SIMILARITY: WITH OTHER INSECT LARVAL CUTICLE PROTEINS.
DR   PIR; A24553; A24553.
DR   PROSITE; PS00233; CUTICLE_FLEXIBLE.
KW   STRUCTURAL PROTEIN; CUTICLE.
FT   SIMILAR      23    >43       CUTICULAR "CONSENSUS SEQUENCE".
FT   NON_TER      43     43
SQ   SEQUENCE   43 AA;  4556 MW;  9428 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.22
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

      X    X
      XCXNXI
         | |
   ALETSNGIHFVAIGGDEH
     X     10
```

15. US-08-121-713B-1 (1-6)
    GGI1_STAHA ANTIBACTERIAL PROTEIN 1 (GONOCOCCAL GROWTH INHIBIT

```
ID   GGI1_STAHA     STANDARD;      PRT;    44 AA.
AC   P11697;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)
DE   ANTIBACTERIAL PROTEIN 1 (GONOCOCCAL GROWTH INHIBITOR 1).
OS   STAPHYLOCOCCUS HAEMOLYTICUS.
OC   PROKARYOTA; FIRMICUTES; COCCI; MICROCOCCACEAE.
RN   [1]
RP   SEQUENCE.
RM   88339821
RA   WATSON D.C., YAGUCHI M., BISAILLON J.G., BEAUDET R., MOROSOLI R.;
RL   BIOCHEM. J. 252:87-93(1988).
CC   -!- THIS PROTEIN IS POSSIBLY THE SIGNAL SEQUENCE OF A SECRETED OR
CC       MEMBRANE ASSOCIATED PROTEIN.
CC   -!- SIMILARITY: HIGH, TO ANTIBACTERIAL PROTEINS 2 AND 3.
DR   PIR; S00599; BXSA1.
KW   ANTIBIOTIC; SIGNAL; FORMYLATION.
FT   MOD_RES       1      1       FORMYLATION (POTENTIAL).
SQ   SEQUENCE   44 AA;  4523 MW;  10878 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.22
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             XCXNXI
                | |
   WGKMGTSIVGIVENGITVLGKIFGF
 20        30    X   40
```

maryh@stic **stdin**

NeWSprinter20

Fri May 19 10:53:29 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

```
> O <
O| |O  IntelliGenetics
> O <
```

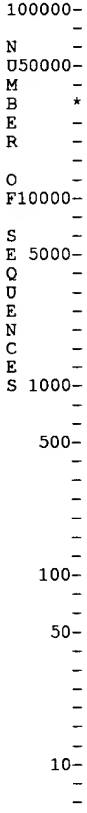
SEQ 2

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

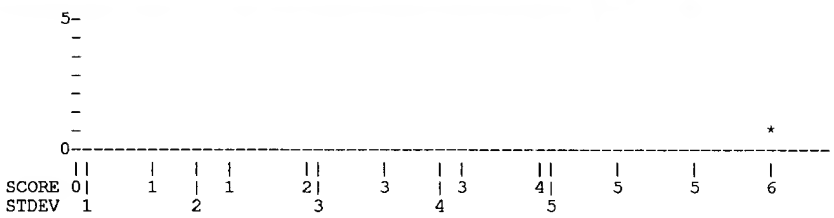
Results file sq2asq.res made by on Fri 19 May 95 8:38:38-PDT.

Query sequence being compared:US-08-121-713B-2 (1-6)
Number of sequences searched: 53402
Number of scores above cutoff: 4688

Results of the initial comparison of US-08-121-713B-2 (1-6) with:
Data bank : A-GeneSeq 18, all entries



Data data 121713



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	0	1	1.10

Times:	CPU	Total Elapsed
	00:00:34.99	00:00:35.00

Number of residues: 6354270
Number of sequences searched: 53402
Number of scores above cutoff: 4688

Cut-off raised to 2.
Cut-off raised to 3.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% similar sequence to the query sequence was found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. R05222	Antigen GX5401FL encoded by E	2189	6	6	5.47	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 3 standard deviations above mean ****					
2. R37844	Sequence of tryptic peptide 2	8	4	4	3.65	0
3. R37843	Sequence of tryptic peptide 2	8	4	4	3.65	0
4. R35986	Hepatitis C virus (HCV) epito	8	4	4	3.65	0

5.	R07930	Tryptic fragment T22 (a) of r	9	4	4	3.65	0
6.	R46721	Rabies virus major antigenic	11	4	4	3.65	0
7.	R51694	B.thuringiensis serovar Japon	13	4	4	3.65	0
8.	P10343	Somatostatin deriv. A57.	13	4	4	3.65	0
9.	R41498	TNF inhibitory peptide X.	14	4	4	3.65	0
10.	P10114	Somatostatin analogue.	14	4	4	3.65	0
11.	R48995	Blastogenesis inducing peptid	15	4	4	3.65	0
12.	R48238	S1033 from N.meningitidis IM2	17	4	4	3.65	0
13.	R55149	Transglutaminase peptide.	18	4	4	3.65	0
14.	R53567	Birch pollen major allergen "	18	4	4	3.65	0
15.	P50732	Sequence of peptide having ep	18	4	4	3.65	0
16.	R33359	Sequence of tryptic peptide d	19	4	4	3.65	0
17.	R60258	Mouse NF-ATp DNA splice site.	20	4	4	3.65	0
18.	R51825	Der f II derived peptide, DF	20	4	4	3.65	0
19.	R36477	DFII-1(1-20), a Dermatophagoi	20	4	4	3.65	0
20.	R27605	Endothelin antagonist #12 (Dp	21	4	4	3.65	0
21.	R27604	Endothelin antagonist #11 (Dp	21	4	4	3.65	0
22.	R27603	Endothelin antagonist #10 (Dp	21	4	4	3.65	0
23.	R27602	Endothelin antagonist #9 (Dpr	21	4	4	3.65	0
24.	R12780	Saraphotoxin Ac-s6c.	21	4	4	3.65	0
25.	R12779	Saraphotoxin 6Hse-s6c.	21	4	4	3.65	0
26.	R07484	Blood pressure regulating pep	21	4	4	3.65	0
27.	R07482	Blood pressure regulating pep	21	4	4	3.65	0
28.	P60550	Fragment of UK rotavirus majo	22	4	4	3.65	0
29.	R34153	CDR2 domain of human V beta 2	23	4	4	3.65	0
30.	R28971	Selectin based anti-adhesion	23	4	4	3.65	0
31.	R20801	uPA/GF domain-alpha1AT-P fusi	24	4	4	3.65	0
32.	R20799	PRB1-uPA/GF domain fusion jun	24	4	4	3.65	0
33.	R36478	DFII-2(11-35), a Dermatophago	25	4	4	3.65	0
34.	R51826	Der f II derived peptide, DF	26	4	4	3.65	0
35.	R24867	Sequence of peptide fragment	26	4	4	3.65	0
36.	P81308	Atrial natriuretic polypeptid	26	4	4	3.65	0
37.	R32877	N-terminal of Rat alpha-amida	28	4	4	3.65	0
38.	P20197	Sequence of [D-Trp22]-somatos	28	4	4	3.65	0
39.	P93340	Amino terminus sequence of an	28	4	4	3.65	0
40.	R15584	Immunopeptide #3 derived from	29	4	4	3.65	0
41.	R15583	Immunopeptide #2 derived from	30	4	4	3.65	0
42.	P81726	Sequence of novel serine prot	30	4	4	3.65	0
43.	P80977	Sequence of novel serine prot	30	4	4	3.65	0
44.	P81730	Sequence of novel serine prot	30	4	4	3.65	0
45.	P81734	Sequence of novel serine prot	30	4	4	3.65	0

1. US-08-121-713B-2 (1-6)
R05222 Antigen GX5401FL encoded by Eimeria tenella genomi

ID R05222 standard; protein; 2189 AA.
AC R05222;
DT 02-AUG-1990 (first entry)
DE Antigen GX5401FL encoded by Eimeria tenella genomic DNA
KW Eimeria tenella; antigen GX5401FL; antigen GX5401; avian coccidiosis.
OS Eimeria tenella.
PN WO9000403-A.
PD 25-JAN-1990.
PF 05-JUL-1989; U02918.
PR 05-JUL-1988; US-215162.
PA (GENE-) Genex Corp.
PI Anderson DM, McCandliss RJ, Strausberg SL, Strausberg RL;
DR WPI; 90-051586/07.
DR N-PSDB; Q03324.

PT Cloned gene or fragment encoding antigenic protein -
PT which binds with antibodies against avian coccidia, and
PT transformed cells used in vaccine
PS Claim 10; Page 93; Fig 14; 134pp; English.
CC It is encoded by an open reading frame contained within the sequence of
CC clone 533 which was derived from an E. tenella genomic library screened
CC with radioactively labelled cDNA encoding the GX5401 antigen. It is of
CC about 250 Kd. It carries several repeated peptide sequences and
CC is rich in cysteine residues. The open reading frame also encodes a
CC potential signal sequence for protein secretion. Also new are an
CC expression vector contg. cloned gene, and host cells transformed with
CC the vector. The transformed cells are used in a vaccine to immunise
CC birds against avian coccidiosis. By labelling the peptides, they can be
CC used as a type-specific probe. May also be used in an assay to detect
CC Ab against the coccidia. The Abs are used to identify transformed cells
CC contg. the DNA.
SQ Sequence 2189 AA;
SQ 202 A; 40 R; 103 N; 148 D; 0 B; 236 C; 50 Q; 242 E; 0 Z;317 G; 54 H;
SQ 47 I; 51 L; 66 K; 12 M; 55 F; 85 P; 165 S; 168 T; 17 W; 36 Y; 95 V;

Initial Score = 6 Optimized Score = 6 Significance = 5.47
Residue Identity = 50% Matches = 3 Mismatches = 3
Gaps = 0 Conservative Substitutions = 0

```
            X   X
            CXNXIX
            | | |
   EASPCGANTHCLNTIGSYECECKDGY
     440    X 450       460
```

2. US-08-121-713B-2 (1-6)
R37844 Sequence of tryptic peptide 2 of rat natural kille

ID R37844 standard; peptide; 8 AA.
AC R37844;
DT 01-OCT-1993 (first entry)
DE Sequence of tryptic peptide 2 of rat natural killer protease
DE (RNKP-1).
KW DNA fragmentation; fragmentin; lymphocyte serine granule protease;
KW apoptosis; therapy.
OS Rattus rattus.
PN WO9311246-A.
PD 10-JUN-1993.
PF 25-NOV-1992; CA0515.
PR 25-NOV-1991; GB-024986.
PA (UYMA-) UNIV MANITOBA.
PI Greenberg AH;
DR WPI; 93-197064/24.
PT Lymphocyte serine granule protease and its DNA - effects DNA
PT fragmentation and induces apoptosis, used for treating tumours
PS Claim 6; Table 2, page 28; 57pp; English.
CC Fragmentin 2 is a lymphocyte serine granule protease having DNA
CC fragmenting and apoptosis-inducing activity. It has a non-reduced
CC apparent mol. wt. of 31 kD and a reduced apparent mol. wt. of 32 kD.
CC It is prepd. from rat natural killer tumour cell line RNK-16. Four
CC tryptic peptides of fragmentin 2 were prepared and sequenced. The AA
CC sequence is illustrated in Table 2 and compared to the deduced AA
CC sequences of three granule proteases; the rat natural killer cell
CC protease RNKP-1 which was cloned from the same RNK-16 tumour used to

```
CC   purify fragmentin, the murine T cell granule proteases CCPI/Granzyme
CC   B and Hanukah Factor (HF)/granzyme A. Fragmentin was highly
CC   homologous to RNKP-1 differing in only two of forty-one
CC   identifiable AAs. CCPI/Granzyme B was also closely related as it
CC   differed in seven amino acids, while 21 amino acids did not match
CC   the corresponding HF/Granzyme A sequence.
SQ   Sequence   8 AA;
SQ   2  A; 0  R; 1  N; 1  D; 0  B; 1  C; 0  Q; 1  E; 0  Z; 1  G; 0  H;
SQ   1  I; 0  L; 0  K; 0  M; 0  F; 0  P; 0  S; 0  T; 0  W; 0  Y; 0  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =    40%  Matches          =      2  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

     X   X
    CXNXIX
      | |
     ANEICAGD
     X   X
```

3. US-08-121-713B-2 (1-6)
   R37843 Sequence of tryptic peptide 2 of fragmentin 2.

```
ID   R37843 standard; peptide; 8 AA.
AC   R37843;
DT   01-OCT-1993  (first entry)
DE   Sequence of tryptic peptide 2 of fragmentin 2.
KW   DNA fragmentation; fragmentin; lymphocyte serine granule protease;
KW   apoptosis; therapy.
OS   Rattus rattus.
PN   WO9311246-A.
PD   10-JUN-1993.
PF   25-NOV-1992; CA0515.
PR   25-NOV-1991; GB-024986.
PA   (UYMA-) UNIV MANITOBA.
PI   Greenberg AH;
DR   WPI; 93-197064/24.
PT   Lymphocyte serine granule protease and its DNA - effects DNA
PT   fragmentation and induces apoptosis, used for treating tumours
PS   Claim 6; Table 2, page 28; 57pp; English.
CC   Fragmentin 2 is a lymphocyte serine granule protease having DNA
CC   fragmenting and apoptosis-inducing activity. It has a non-reduced
CC   apparent mol. wt. of 31 kD and a reduced apparent mol. wt. of 32 kD.
CC   It is prepd. from rat natural killer tumour cell line RNK-16. Four
CC   tryptic peptides of fragmentin 2 were prepared and sequenced. The AA
CC   sequence is illustrated in Table 2 and compared to the deduced AA
CC   sequences of three granule proteases; the rat natural killer cell
CC   protease RNKP-1 which was cloned from the same RNK-16 tumour used to
CC   purify fragmentin, the murine T cell granule proteases CCPI/Granzyme
CC   B and Hanukah Factor (HF)/granzyme A. Fragmentin was highly
CC   homologous to RNKP-1 differing in only two of forty-one
CC   identifiable AAs. CCPI/Granzyme B was also closely related as it
CC   differed in seven amino acids, while 21 amino acids did not match
CC   the corresponding HF/Granzyme A sequence.
SQ   Sequence   8 AA;
SQ   2  A; 0  R; 1  N; 1  D; 0  B; 0  C; 0  Q; 1  E; 0  Z; 1  G; 0  H;
SQ   1  I; 0  L; 0  K; 0  M; 0  F; 0  P; 0  S; 0  T; 0  W; 0  Y; 0  V;
SQ   1 Others;
```



```
Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =    60%  Matches          =      3  Mismatches   =     2
Gaps             =      0  Conservative Substitutions               =     0

     X   X
    CXNXIX
      | ||
     ANEIXAGD
     X   X
```

4. US-08-121-713B-2 (1-6)
   R35986 Hepatitis C virus (HCV) epitope.

```
ID   R35986 standard; protein; 8 AA.
AC   R35986;
DT   24-MAY-1993  (first entry)
DE   Hepatitis C virus (HCV) epitope.
KW   Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
KW   immobilised reagent; immunoassay; diagnosis; detection; treatment;
KW   infection.
OS   Hepatitis C virus type 1.
PN   WO9300365-A.
PD   07-JAN-1993.
PF   24-JUN-1992; U05388.
PR   24-JUN-1991; US-722489.
PA   (CHIR ) CHIRON CORP.
PI   Chien DY,  Rutter W;
DR   WPI; 93-036334/04.
PT   Polypeptide(s) comprising truncated hepatitis C virus sequences -
PT   for detection, prevention and treatment of hepatitis C infection
PS   Example A; Page 37; 80pp; English.
CC   This octamer was found to be immunoreactive with anti-HCV anti-sera.
CC   In the epitope mapping experiment three different samples of anti-sera
CC   were reacted with the peptide octamer, and then incubated with
CC   HRP-labelled goat anti-human Ig antisera, to enable detection of
CC   binding. This epitope starts from amino acid 1762 of the HCV
CC   polyprotein.
SQ   Sequence   8 AA;
SQ   1  A; 0  R; 1  N; 0  D; 0  B; 0  C; 0  Q; 1  E; 0  Z; 0  G; 0  H;
SQ   1  I; 1  L; 1  K; 1  M; 0  F; 0  P; 0  S; 0  T; 1  W; 0  Y; 0  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =    40%  Matches          =      2  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

      X   X
      CXNXIX
        | |
    AKLMWNEI
      X   X
```

5. US-08-121-713B-2 (1-6)
   R07930 Tryptic fragment T22 (a) of rat phospholipase A2 i

```
ID   R07930 standard; protein; 9 AA.
AC   R07930;
DT   14-JAN-1991  (first entry)
DE   Tryptic fragment T22 (a) of rat phospholipase A2 inhibitor.
```

```
KW   Human N-lipocortin; placenta; inflammation reduction; arthritis;
KW   rat phospholipase A2 inhibitor; tryptic fragment T22 (a).
OS   Homo sapiens.
PN   US4950646-A.
PD   21-AUG-1990.
PF   10-JAN-1986; 929199.
PR   10-JAN-1985; US-690146.
PR   15-MAR-1985; US-712376.
PR   14-AUG-1985; US-765877.
PR   05-SEP-1985; US-772892.
PR   10-JAN-1986; US-929199.
PA   (BIOJ ) BIOGEN NV.
PI   Wallner BP, Pepinsky RB, Garwin JL, Schindler DG, Huang KS;
DR   WPI; 90-274549/36.
PT   Pure fragment of human lipocortin - useful for reducing
PT   inflammation or for treating arthritis, etc.
PS   Disclosure; Fig 2; 51pp; English.
CC   Rat phospholipase A2 inhibitor protein was isolated from the
CC   extracellular supernatant of rat peritoneal exudate cells.
CC   For tryptic fragment T22 (b) see R07931.
CC   The protein was isolated and sequenced to produce oligonucleotide
CC   probes in order to identify human lipocortin and N-lipocortin.
CC   See also Q05805-25, Q06581, R07926-37 and R07956-66.
SQ   Sequence   9 AA;
SQ   0  A; 0  R; 1  N; 1  D; 0  B; 0  C; 0  Q; 2  E; 0  Z; 0  G; 0  H;
SQ   2  I; 0  L; 1  K; 1  M; 0  F; 0  P; 1  S; 0  T; 0  W; 0  Y; 0  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =     33%  Matches         =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

       X    X
       CXNXIX
         | |
     SEIDMNEIK
       X    X
```

6. US-08-121-713B-2 (1-6)
   R46721 Rabies virus major antigenic site III R333E mutant

```
ID   R46721 standard; protein; 11 AA.
AC   R46721;
DT   26-SEP-1994  (first entry)
DE   Rabies virus major antigenic site III R333E mutant.
KW   Rabies virus; avirulent; double mutant; SAD Berne strain; SAG2;
KW   live vaccine; Control Virus Standard strain; CVS; glycoprotein G505;
KW   antigen; immunogen.
OS   Rabies Virus.
FH   Key             Location/Qualifiers
FT   Peptide         1..11
FT   /label= antigenic_site_III
FT   /note= "amino acids 330-340 of the CVS strain
FT   (identical to site III from SAD Berne
FT   strain)"
FT   Misc_difference 4
FT   /note= "wild-type Arg333 is substd. by Glu"
PN   FR2693655-A.
PD   21-JAN-1994.
PF   20-JUL-1992; 008947.
```



```
PR   20-JUL-1992; FR-008947.
PA   (VIRB-) VIRBAC SA.
PI   Benejean J, Coulon P, Flamand A, Lefay F, Tuffereau M;
DR   WPI; 94-058963/08.
PT   Avirulent anti-rabies vaccine with double mutation in position
PT   333 of glyco-protein - of SAD strain, esp. having Glutamic acid
PT   instead of Arginine, stable against reversion and with good
PT   protective activity
PS   Claim 6; ; 16pp; French.
CC   An antirabies vaccine comprises a double mutant form of the external
CC   glycoprotein. In the mutant strain the codon at position 333 differs
CC   by at least 2 nucleotides from the wild-type Arg codon. The pref.
CC   mutation (specifically claimed) is from Arg to Glu. The mutation is
CC   stable to reversion and results in an attenuated virus for use in
CC   live vaccines. The specification does not include any sequence
CC   listings; R46721 is major antigenic site III (i.e. amino acids 330-
CC   340) of the CVS strain (see Geneseq P40082 for the full-length
CC   glycoprotein sequence) modified as described in the claims.
SQ   Sequence   11 AA;
SQ   0  A; 0  R; 1  N; 0  D; 0  B; 0  C; 0  Q; 2  E; 0  Z; 0  G; 0  H;
SQ   2  I; 0  L; 1  K; 0  M; 0  F; 1  P; 1  S; 1  T; 1  W; 0  Y; 1  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =     33%  Matches         =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

       X    X
       CXNXIX
         | |
    KSVETWNEIIP
       X   10
```

7. US-08-121-713B-2 (1-6)
   R51694 B.thuringiensis serovar Japonensis insecticidal pr

```
ID   R51694 standard; peptide; 13 AA.
AC   R51694;
DT   04-NOV-1994  (first entry)
DE   B.thuringiensis serovar Japonensis insecticidal protein N-terminal.
KW   insecticidal protein; Coleoptera larvae; Buibui fungus;
KW   Bacillus thuringiensis; serovar Japonensis.
OS   Bacillus thuringiensis (serovar Japonensis, strain Buibui).
FH   Key             Location/Qualifiers
FT   Misc_difference 1..2
FT   /note= "undefined"
PN   J06065292-A.
PD   08-MAR-1994.
PF   11-AUG-1992; 213886.
PR   11-AUG-1992; JP-213886.
PA   (KUBI ) KUBOTA CORP.
DR   WPI; 94-121220/15.
PT   Insecticidal protein and DNA from Bacillus thuringiensis serovar
PT   Japonensis strain Buibui - useful in insecticides against
PT   Coleoptera insects
PS   Disclosure; Page 4; 18pp; Japanese.
CC   An insecticidal protein with activity against Coleopteran
CC   insect larvae has been isolated from Bacillus thuringiensis serovar
CC   japonensis strain Buibui. The N-terminal amino acid sequence was
CC   determined and used for the design of a probe to clone DNA coding
```

```
CC   for the insecticidal protein.
SQ   Sequence   13 AA;
SQ   1  A; 0  R; 3  N; 1  D; 0  B; 0  C; 1  Q; 1  E; 0  Z; 0  G; 0  H;
SQ   2  I; 1  L; 0  K; 0  M; 0  F; 1  P; 0  S; 0  T; 0  W; 0  Y; 0  V;
SQ   2 Others;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

       X    X
       CXNXIX
         | |
   XXPNNQNEIIDAL
       X   10
```

8. US-08-121-713B-2 (1-6)
P10343 Somatostatin deriv. A57.

```
ID   P10343 standard; Protein; 13 AA.
AC   P10343;
DT   15-DEC-1992  (first entry)
DE   Somatostatin deriv. A57.
KW   Growth Hormone secretion; GH; diabetes mellitus; angiopathy;
KW   acromegaly; diagnosis.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Modified_site   1
FT   /note= "(4Cl)Phe"
FT   Modified_site   3
FT   /label= Nle
FT   Misc_difference 13
FT   /note= "Cys-NH-CH(CH2OH)2,
FT   Cys-NH-CH(CH2OH)CH2CH2OH,
FT   Cys-NH-CH(CH2OH)CH2CH2CH2OH or
FT   as amide formed with 4-amino-pentanoic
FT   acid lactone"
PN   CH-621770-A.
PD   27-FEB-1981.
PF   11-SEP-1980; 125375.
PR   23-FEB-1976; CH-002175.
PA   (SANO ) SANDOZ AG.
PI   Sandrin E, Bauer W;
DR   WPI; 81-21515D/13  (21515D).
PT   Somatostatin derivs. prodn. - useful for treating diabetes,
PT   acromegalia and angiopathy
PS   Example 1; Page 7; 8pp; German.
CC   This peptide is an example of a generic formula for somatostatin
CC   derivs. which inhibit secretion of growth hormone and are useful to
CC   treat diabetes mellitus, acromegaly, angiopathy and in diagnosis.
CC   See P10308-P10348.
SQ   Sequence   13 AA;
SQ   0  A; 0  R; 1  N; 0  D; 0  B; 2  C; 0  Q; 0  E; 0  Z; 0  G; 0  H;
SQ   0  I; 0  L; 1  K; 0  M; 4  F; 0  P; 1  S; 2  T; 1  W; 0  Y; 0  V;
SQ   1 Others;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0
```



```
       X    X
       CXNXIX
       | | |
     FCXNFFWKTFTSC
       X    X 10
```

9. US-08-121-713B-2 (1-6)
R41498 TNF inhibitory peptide X.

```
ID   R41498 standard; peptide; 14 AA.
AC   R41498;
DT   23-FEB-1994  (first entry)
DE   TNF inhibitory peptide X.
KW   Tumour necrosis factor; TNF; inhibition; solid phase synthesis; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Disulfide_bond  3..12
FT   /note= "Optional di-sulphide bond"
PN   J05194594-A.
PD   03-AUG-1993.
PF   21-JAN-1992; 029044.
PR   21-JAN-1992; JP-029044.
PA   (SAGA ) SAGAMI CHEM RES CENTRE.
DR   WPI; 93-282916/36.
PT   TNF inhibitory novel peptide(s) - include N-terminal amino Gp.
PT   which is opt. modified with acetyl, T-butoxy-carbonyl or
PT   benzyl-oxy-carbonyl Gp. and C-terminal carboxy Gp. is opt.
PT   amidated
PS   Claim 1; Page 6; 8pp; Japanese.
CC   The sequences given in R41489-99 are tumour necrosis factor (TNF)
CC   inhibitory peptides.  They may optionally be modified at the N-
CC   terminal with an acetyl, t-butoxycarbonyl or benzyloxycarbonyl, and
CC   at the C-terminal they are optionally amidated.  These peptides are
CC   produced by solid phase synthesis methods and may be produced at low
CC   cost.
SQ   Sequence   14 AA;
SQ   0  A; 0  R; 1  N; 0  D; 0  B; 2  C; 1  Q; 1  E; 0  Z; 1  G; 1  H;
SQ   0  I; 3  L; 0  K; 0  M; 0  F; 0  P; 2  S; 1  T; 0  W; 0  Y; 1  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

       X    X
       CXNXIX
       | |
     SLCLNGTVHLSCQE
       X     10
```

10. US-08-121-713B-2 (1-6)
P10114 Somatostatin analogue.

```
ID   P10114 standard; peptide; 14 AA.
AC   P10114;
DT   15-DEC-1992  (first entry)
DE   Somatostatin analogue.
KW   Deprotection; selenocysteine; Sec.
```

```
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Modified_site   3
FT   /label= Cys, OTHER
FT   /note= "selenocysteine (Sec)"
FT   Modified_site   14
FT   /label= Cys, OTHER
FT   /note= "selenocysteine (Sec)"
FT   Disulfide_bond  3..14
FT   Misc_difference 8
FT   /note= "D- or L- form residue"
PN   DD-146289-A.
PD   04-FEB-1981.
PF   27-SEP-1979; 215859.
PR   27-SEP-1979; DD-215859.
PA   (HART/) HARTRODT B.
PI   Hartrodt B, Neubert K, Jakubke HD, Krabiell U;
DR   WPI; 81-30862D/18  (30862D).
PT   Somatostatin and analogues prodn. from oligopeptide fragments -
PT   useful for treating acromegalia, angiopathy and diabetes
PS   Claim 1; Page 33; 36pp; German.
CC   The prodn. of the somatostatin analogue having the formula given
CC   below is claimed.  The process is relatively simple, esp. it avoids
CC   acidolytic deprotection of Trp-8 (needed in known processes) which
CC   can cause side reactions.  The oligopeptide starting materials can
CC   be made by the active ester method which requires only minimal side-
CC   chain protection.  The method is esp. applied to produce a cpd.
CC   where amino acids 3 and 14 are Sec and Trp-8 is in D-form, which
CC   cannot be made by other methods.  The prod. is useful in treating
CC   acromegalia, angiopathy and diabetes mellitus, and as diagnostic
CC   agents.
SQ   Sequence   14 AA;
SQ   1  A; 0  R; 1  N; 0  D; 0  B; 2  C; 0  Q; 0  E; 0  Z; 1  G; 0  H;
SQ   0  I; 1  L; 1  K; 0  M; 3  F; 0  P; 1  S; 2  T; 1  W; 0  Y; 0  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

      X    X
      CXNXIX
      | |
    AGCLNFFWKTFTSC
      X     10
```

11. US-08-121-713B-2 (1-6)
    R48995 Blastogenesis inducing peptide #1.

```
ID   R48995 standard; peptide; 15 AA.
AC   R48995;
DT   14-SEP-1994  (first entry)
DE   Blastogenesis inducing peptide #1.
KW   Blastogenesis; mite-sensitised; lymphocyte; homodimer; heterodimer;
KW   solid phase synthesis; diagnosis; mite allergy; disulphide bond.
OS   Synthetic.
PN   WO9404572-A.
PD   03-MAR-1994.
PF   10-AUG-1993; J01127.
PR   14-AUG-1992; JP-216955.
```



```
PA   (ASAK ) ASAHI BREWERIES LTD.
PA   (TORI ) TORII & CO LTD.
PI   Ando T,  Ikeda S,  Okumura Y;
DR   WPI; 94-083115/10.
PT   Peptides which cause blastogenesis of mite-sensitised lymphocyles
PT   - as diagnostic agents for mite allery.
PS   Claim 2; Page 26; 33pp; Japanese.
CC   The sequences given in R48995-96 are peptides which cause
CC   blastogenesis in mite-sensitised lymphocytes.  These peptides may be
CC   used as individual peptides, homo- or heterodimers.  These peptides
CC   were produced by standard methods of solid phase synthesis and may
CC   be used as diagnostic agents for the diagnosis of mite allergy.  The
CC   dimeric peptides are formed by disulphide bonds between Cys8 or Cys5
CC   respectively.
SQ   Sequence   15 AA;
SQ   1  A; 0  R; 2  N; 3  D; 0  B; 1  C; 1  Q; 1  E; 0  Z; 0  G; 0  H;
SQ   1  I; 0  L; 3  K; 0  M; 0  F; 0  P; 0  S; 0  T; 0  W; 0  Y; 2  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

         X    X
         CXNXIX
         | |
   DQVDVKDCANNEIKK
          10  X
```

12. US-08-121-713B-2 (1-6)
    R48238 S1033 from N.meningitidis IM2169 transferrin recep

```
ID   R48238 standard; peptide; 17 AA.
AC   R48238;
DT   15-JUL-1994  (first entry)
DE   S1033 from N.meningitidis IM2169 transferrin receptor Tbp1 subunit.
KW   Transferrin receptor; Tbp1 subunit; strain IM2169; meningitis vaccine;
KW   iron transport protein; iron chelator; internal tryptic peptide.
OS   Neisseria meningitidis (strain IM2169).
FH   Key             Location/Qualifiers
FT   Misc_difference 16
FT   /note= "undetermined amino acid"
FT   Misc_difference 17
FT   /note= "undetermined amino acid"
PN   FR2692592-A.
PD   24-DEC-1993.
PF   19-JUN-1992; 007493.
PR   19-JUN-1992; FR-007493.
PA   (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
PA   (TRGE ) TRANSGENE SA.
PI   Bloch M,  Bouchon-Theisen B,  Jacobs E,  Legrain M;
PI   Mazarin V, Shryvers AB, Schryvers AB;
DR   WPI; 94-028254/04.
PT   DNA coding for Neisseria meningitidis proteins - namely
PT   transferrin receptor subunits
PS   Example 2; Page 22; 60pp; French.
CC   The transferrin receptor was isolated from a lysate of Neisseria
CC   meningitidis strain IM2169. The subunits Tbp1 and Tbp2 were separated
CC   and subjected to microsequencing at the N-terminal end. The Tbp1
CC   subunit was subjected to trypsin digestion in order to obtain
```

```
CC   internal peptides. See R48236-R48239 for tryptic peptide sequences.
SQ   Sequence   17 AA;
SQ   2  A; 0  R; 2  N; 0  D; 0  B; 0  C; 0  Q; 3  E; 0  Z; 2  G; 0  H;
SQ   2  I; 0  L; 0  K; 0  M; 0  F; 0  P; 2  S; 1  T; 0  W; 1  Y; 0  V;
SQ   2 Others;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

         X    X
         CXNXIX
           | |
   TAGSSGAINEIEYENXX
         X 10 X
```

13. US-08-121-713B-2 (1-6)
    R55149 Transglutaminase peptide.

```
ID   R55149 standard; peptide; 18 AA.
AC   R55149;
DT   16-DEC-1994  (first entry)
DE   Transglutaminase peptide.
KW   Transglutaminase; TGase; fish; liver; Teragra chalcogramma;
KW   Pagrus major; enzyme; acyl transfer; gamma-carboxyamide;
KW   glutamine.
OS   Pagrus major.
PN   J06113844-A.
PD   26-APR-1994.
PF   15-DEC-1992; 334224.
PR   19-AUG-1992; JP-220296.
PA   (AJIN ) AJINOMOTO KK.
DR   WPI; 94-172742/21.
PT   Compsn. contg. trans-glutaminase derived from fish liver - useful
PT   for prepn. of protein-gelled prod., esp. food prod.
PS   Disclosure; Page 11; 26pp; Japanese.
CC   A compsn. contains at least 0.5 units per mg protein of a novel
CC   transglutaminase (TGase).  The TGase is derived from fish liver
CC   (esp. Teragra chalcogramma and Pagrus major) and catalyses the
CC   acyl tranfer reaction between the gamma-carboxyamide gp. of the
CC   glutamine residue of a peptide chain and various prim. amines.
CC   TGase is useful for prepn. of protein-gelled prods., esp. food.
SQ   Sequence   18 AA;
SQ   2  A; 3  R; 1  N; 0  D; 0  B; 0  C; 1  Q; 3  E; 0  Z; 2  G; 0  H;
SQ   1  I; 1  L; 0  K; 0  M; 0  F; 1  P; 1  S; 1  T; 0  W; 0  Y; 1  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

          X    X
          CXNXIX
            | |
    AGRRVTEPSNEIAEQGRL
           10  X
```

14. US-08-121-713B-2 (1-6)
    R53567 Birch pollen major allergen "Bet v I" amino acids


```
ID   R53567 standard; peptide; 18 AA.
AC   R53567;
DT   29-NOV-1994  (first entry)
DE   Birch pollen major allergen "Bet v I" amino acids 93-110.
KW   Order Fagales; tree pollen; birch; hazel; alder; major allergen;
KW   allergy; T-cell epitope; Bet v I; Cor a I; Aln g I; tolerance.
OS   Synthetic.
PN   WO9410194-A.
PD   11-MAY-1994.
PF   25-OCT-1993; AT0163.
PR   27-OCT-1992; AT-002125.
PR   14-JAN-1993; AT-000043.
PA   (BIOM-) BIOMAY PRODN & HANDELSGES MBH.
PI   Breitenbach M,  Ebner C,  Ferreira F,  Kraft D,  Rumpold H;
PI   Scheiner O,  Schenk S,  Szepfalusi Z,  Valenta R;
DR   WPI; 94-167383/20.
PT   New peptide(s) derived from tree pollen allergens - able to
PT   induce T cell tolerance, useful in diagnoses and therapy of
PT   allergies
PS   Claim 1; Page 10; 12pp; German.
CC   The 17kD major allergens from trees of the Order Fagales (esp.
CC   birches, hazels and alders) are highly homologous. Peptides derived
CC   from the T-cell epitopes of these allergens, partic. from the birch
CC   Bet v I allergen are useful for diagnosing tree pollen allergy and
CC   for stimulating or blocking T-cells of allergic patients in an
CC   allergen-specific manner. The peptides can also be used to provoke
CC   tolerance to the allergen-specific T-cells. The peptides have one
CC   of the sequences R53560-R53569.
SQ   Sequence   18 AA;
SQ   1  A; 0  R; 1  N; 2  D; 0  B; 0  C; 0  Q; 2  E; 0  Z; 1  G; 0  H;
SQ   3  I; 1  L; 2  K; 0  M; 0  F; 1  P; 1  S; 2  T; 0  W; 0  Y; 1  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

         X    X
         CXNXIX
           | |
   DTLEKISNEIKIVATPDG
         X  10
```

15. US-08-121-713B-2 (1-6)
    P50732 Sequence of peptide having epidermal growth factor

```
ID   P50732 standard; peptide; 18 AA.
AC   P50732;
DT   29-NOV-1991  (first entry)
DE   Sequence of peptide having epidermal growth factor (EGF)-like
DE   activity.
KW   De-fleecing agent; autophosphorylation inducer; antiulcer agent.
PN   WO8501284-A.
PD   28-MAR-1985.
PF   14-SEP-1984; U01459.
PR   14-SEP-1983; IL-069719.
PA   (KOMO/) KOMORIYA A.
PI   Komoriya A, Meyers CA, Schlessinger J;
DR   WPI; 85-087027/14.
```

```
  PT   Polypeptide(s) with epidermal growth factor-like activity - also
  PT   useful for de-fleecing sheep
  PS   Claim 6; Page 10; 16pp; English.
  CC   The peptides of the invention contain a 10 AA residue SQ of the
  CC   natural EGF-like hormone corresp. to the SQ between Cys(20) and
  CC   Cys(31). They activate EGF-sensitive kinase and induce
  CC   autophosphorylation of the EGF receptors and other endogenous
  CC   membrane proteins. They also stimulate thymidine incorporation into
  CC   human foreskin fibroblasts. Dose is sufficient to give at least
  CC   50 micro m  blood concn.
  SQ   Sequence   18 AA;
  SQ   0  A; 0  R; 1  N; 1  D; 0  B; 3  C; 0  Q; 1  E; 0  Z; 2  G; 1  H;
  SQ   1  I; 2  L; 0  K; 1  M; 0  F; 0  P; 2  S; 1  T; 0  W; 1  Y; 1  V;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.65
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions              =     0

    X    X
    CXNXIX
    | |
    CLNGGVCMHIESLDSY
    X    X  10
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq2pir.res made by  on Fri 19 May 95 8:48:10-PDT.


Query sequence being compared:US-08-121-713B-2 (1-6)
Number of sequences searched:                75511
Number of scores above cutoff:                3756

     Results of the initial comparison of US-08-121-713B-2 (1-6) with:
   Data bank : PIR 43, all entries

100000-
      -
N     -                    *
U50000-
M     -
B     -
E     -                                                    :
R     *
      -
O     -
F10000-
      -                                                   *
S     -
E 5000-
Q     -
U     -
E     -
N     -
C     -
E     -
```



```
S 1000-
      -
      -
   500-
      -
      -
      -
      -
      -
      -
      -
   100-
      -
      -
    50-
      -
      -
      -
      -
      -                                                          *
      -
    10-
      -
      -
     5-
      -
      -
      -
      -
      -
      -
      -
     0-----------------------------------------------------------------------
       ||     |   | |     ||     |    | |     ||     |     |     |
SCORE 0|     1   | 1     2|     3    | 3     4|     5     5     6
STDEV  0         1         2          3        4
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	1.02

Times:	CPU	Total Elapsed
	00:01:07.11	00:01:08.00

Number of residues:	22468834
Number of sequences searched:	75511
Number of scores above cutoff:	3756

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

15 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. RNEGB	DNA-directed RNA polymerase (	1082	6	6	4.90	0
2. JC1469	beta-adrenergic-receptor kina	688	6	6	4.90	0
3. A39336	beta-adrenergic-receptor kina	688	6	6	4.90	0
4. S21296	mating-type locus protein b6	410	6	6	4.90	0
5. S21295	mating-type locus protein b5	410	6	6	4.90	0
6. B32696	mating-type locus protein b2	410	6	6	4.90	0
7. A36671	mating-type locus protein b1	410	6	6	4.90	0
8. D32696	b3 protein - smut fungus (Ust	410	6	6	4.90	0
9. A32696	b1 protein - smut fungus (Ust	410	6	6	4.90	0
10. E36671	mating-type locus protein b6	410	6	6	4.90	0
11. D36671	mating-type locus protein b5	410	6	6	4.90	0
12. C36671	mating-type locus protein b3	410	6	6	4.90	0
13. A49915	GutQ homolog - Escherichia co	317	6	6	4.90	0
14. W6WL58	E6 protein - human papillomav	149	6	6	4.90	0
15. S28743	NADH dehydrogenase (ubiquinon	81	6	6	4.90	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 2 standard deviations above mean ****					
16. S01763	gene X protein - Escherichia	12	4	4	2.94	0
17. A28514	dihydrolipoamide dehydrogenas	16	4	4	2.94	0
18. A49245	clustered asparagine-rich pro	17	4	4	2.94	0
19. F27393	spore coat protein, 34K - Bac	20	4	4	2.94	0
20. A28070	mutT protein - Escherichia co	20	4	4	2.94	0
21. C26944	cytotoxic T-lymphocyte protei	20	4	4	2.94	0
22. B48186	ATP synthase beta 2 subunit -	23	4	4	2.94	0
23. B27393	spore coat protein, 59K - Bac	23	4	4	2.94	0
24. S24279	hypothetical protein 3 - porc	23	4	4	2.94	0
25. B44560	terephthalate 1,2-dioxygenase	25	4	4	2.94	0
26. S26754	ribosomal protein YmL3, mitoc	28	4	4	2.94	0
27. S03947	hydrogen dehydrogenase (EC 1.	29	4	4	2.94	0
28. A22977	delta-endotoxin - Bacillus th	30	4	4	2.94	0
29. JS0339	hypothetical 4.4K protein - L	35	4	4	2.94	0
30. JU0109	S-carboxymethylcysteine synth	36	4	4	2.94	0
31. A33852	N5-(carboxyethyl)ornithine sy	37	4	4	2.94	0
32. A48368	N5,N10-methenyltetrahydrometh	38	4	4	2.94	0
33. A30010	cytochrome-c oxidase (EC 1.9.	42	4	4	2.94	0
34. A26929	sacQ protein - Bacillus liche	46	4	4	2.94	0
35. EGRT	epidermal growth factor - rat	48	4	4	2.94	0
36. VDBPHK	kil protein - phage HK022	50	4	4	2.94	0
37. A45352	41K fiber protein - human ade	51	4	4	2.94	0
38. S08288	epidermal growth factor, low	51	4	4	2.94	0
39. E31439	ovomucoid, third domain - ele	51	4	4	2.94	0

40. LNLDAT	lectin alpha chain - Tangier	54	4	4	2.94	0
41. A36141	Cop protein - Bacillus subtil	55	4	4	2.94	0
42. ERAD65	early E1A 6K protein - human	55	4	4	2.94	0
43. JN0740	hypothetical 6.7K protein - p	57	4	4	2.94	0
44. JN0739	hypothetical 6.4K protein - p	57	4	4	2.94	0
45. S15871	neurotoxin 5 - Indian cobra	62	4	4	2.94	0

1. US-08-121-713B-2 (1-6)
RNEGB DNA-directed RNA polymerase (EC 2.7.7.6) beta chai

ENTRY RNEGB #type complete
TITLE DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Euglena gracilis chloroplast
ORGANISM #formal_name chloroplast Euglena gracilis
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Mar-1993
ACCESSIONS S09210
REFERENCE S09210
#authors Yepiz-Plascencia, G.M.; Radebaugh, C.A.; Hallick, R.B.
#journal Nucleic Acids Res. (1990) 18:1869-1878
#title The Euglena gracilis chloroplast rpoB gene. Novel gene organization and transcription of the RNA polymerase subunit operon.
#cross-references MUID:90245579
#accession S09210
##molecule_type DNA
##residues 1-1082 ##label YEP
##cross-references EMBL:X17191
##note the authors translated the codon CGT for residue 132 as Gly
GENETICS
#gene rpoB
#genome chloroplast
#introns 13/3; 89/2; 117/1; 154/3; 227/3; 241/1; 288/2; 732/3
CLASSIFICATION #superfamily DNA-directed RNA polymerase beta chain
KEYWORDS chloroplast; nucleotidyltransferase; transcription
SUMMARY #length 1082 #molecular-weight 124531 #checksum 6067
SEQUENCE

Initial Score = 6 Optimized Score = 6 Significance = 4.90
Residue Identity = 50% Matches = 3 Mismatches = 3
Gaps = 0 Conservative Substitutions = 0

```
            X   X
            CXNXIX
            | | |
   KNYSFFNLLGCLNEISQKNFKLIKKV
     610    X 620       630
```

2. US-08-121-713B-2 (1-6)
JC1469 beta-adrenergic-receptor kinase (EC 2.7.1.126) 2 -

ENTRY JC1469 #type complete
TITLE beta-adrenergic-receptor kinase (EC 2.7.1.126) 2 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
ACCESSIONS JC1469

```
  REFERENCE        JC1469
     #authors      Parruti, G.; Ambrosini, G.; Sallese, M.; De Blasi, A.
     #journal      Biochem. Biophys. Res. Commun. (1993) 190:475-481
     #title        Molecular cloning, functional expression and mRNA analysis of
                     human beta-adrenergic receptor kinase 2.
     #accession    JC1469
        ##molecule_type mRNA
        ##residues      1-688 ##label PAR
        ##note          the nucleotide sequence is not given in this paper
  COMMENT    This enzyme plays a role in the regulation of receptor-mediated
               immune functions.
  KEYWORDS         phosphotransferase
  SUMMARY          #length 688  #molecular-weight 79601  #checksum 6536
  SEQUENCE

 Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
 Residue Identity =    50%  Matches          =      3  Mismatches   =     3
 Gaps             =      0  Conservative Substitutions               =     0

              X    X
              CXNXIX
              | | |
     KIGFLLFKDFCLNEINEAVPQVKFYE
           70 X    X 80


3. US-08-121-713B-2 (1-6)
   A39336       beta-adrenergic-receptor kinase (EC 2.7.1.126) - b

  ENTRY            A39336     #type complete
  TITLE            beta-adrenergic-receptor kinase (EC 2.7.1.126) - bovine
  ORGANISM         #formal_name Bos primigenius taurus #common_name cattle
  DATE             03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change
                     23-Jun-1993
  ACCESSIONS       A39336
  REFERENCE        A39336
     #authors      Benovic, J.L.; Onorato, J.J.; Arriza, J.L.; Stone, W.C.;
                     Lohse, M.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.;
                     Caron, M.G.; Lefkowitz, R.J.
     #journal      J. Biol. Chem. (1991) 266:14939-14946
     #title        Cloning, expression, and chromosomal localization of
                     beta-adrenergic receptor kinase 2. A new member of the
                     receptor kinase family.
     #cross-references MUID:91332005
     #accession    A39336
        ##status        preliminary
        ##molecule_type mRNA
        ##residues      1-688 ##label BEN
        ##cross-references GB:M73216
  KEYWORDS         phosphotransferase
  SUMMARY          #length 688  #molecular-weight 79803  #checksum 9052
  SEQUENCE

 Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
 Residue Identity =    50%  Matches          =      3  Mismatches   =     3
 Gaps             =      0  Conservative Substitutions               =     0

              X    X
              CXNXIX
              | | |
```



```
     RIGFLLFKDFCLNEINEAVPQVKFYE
           70 X    X 80


4. US-08-121-713B-2 (1-6)
   S21296       mating-type locus protein b6 - smut fungus (Ustila

  ENTRY            S21296     #type complete
  TITLE            mating-type locus protein b6 - smut fungus (Ustilago maydis)
  ORGANISM         #formal_name Ustilago maydis #common_name corn smut
  DATE             19-Feb-1994; #sequence_revision 19-Feb-1994; #text_change
                     19-Feb-1994
  ACCESSIONS       S21296
  REFERENCE        S21295
     #authors      Kronstad, J.W.; Leong, S.A.
     #submission   submitted to the EMBL Data Library, July 1990
     #accession    S21296
        ##status        preliminary
        ##residues      1-410 ##label KRO
        ##cross-references EMBL:X53902
  SUMMARY          #length 410  #molecular-weight 46517  #checksum 7490
  SEQUENCE

 Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
 Residue Identity =    50%  Matches          =      3  Mismatches   =     3
 Gaps             =      0  Conservative Substitutions               =     0

              X    X
              CXNXIX
              | | |
     PKLSLSKFLECLNEIEHEFLRDKVEH
         10    X   20        30


5. US-08-121-713B-2 (1-6)
   S21295       mating-type locus protein b5 - smut fungus (Ustila

  ENTRY            S21295     #type complete
  TITLE            mating-type locus protein b5 - smut fungus (Ustilago maydis)
  ORGANISM         #formal_name Ustilago maydis #common_name corn smut
  DATE             19-Feb-1994; #sequence_revision 19-Feb-1994; #text_change
                     19-Feb-1994
  ACCESSIONS       S21295
  REFERENCE        S21295
     #authors      Kronstad, J.W.; Leong, S.A.
     #submission   submitted to the EMBL Data Library, July 1990
     #accession    S21295
        ##status        preliminary
        ##residues      1-410 ##label KRO
        ##cross-references EMBL:X53901
  SUMMARY          #length 410  #molecular-weight 46304  #checksum 6080
  SEQUENCE

 Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
 Residue Identity =    50%  Matches          =      3  Mismatches   =     3
 Gaps             =      0  Conservative Substitutions               =     0

              X    X
              CXNXIX
              | | |
```

```
      PNFSLTSFLECLNEIEHEFLRDKEEN
          10    X   20        30
```

6. US-08-121-713B-2 (1-6)
   B32696 mating-type locus protein b2 - smut fungus (Ustila

```
 ENTRY            B32696     #type complete
 TITLE            mating-type locus protein b2 - smut fungus (Ustilago maydis)
 ORGANISM         #formal_name Ustilago maydis #common_name corn smut
 DATE             22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change
                    14-Jul-1994
 ACCESSIONS       B36671; B32696
 REFERENCE        A36671
    #authors      Kronstad, J.W.; Leong, S.A.
    #journal      Genes Dev. (1990) 4:1384-1395
    #title        The b mating-type locus of Ustilago maydis contains variable
                    and constant regions.
    #cross-references MUID:91032990
    #accession    B36671
       ##status        preliminary
       ##molecule_type DNA
       ##residues      1-410 ##label KRO
       ##note          sequence not compared to nucleotide translation
       ##note          the nucleotide sequence is not given in this paper
 REFERENCE        A32696
    #authors      Schulz, B.; Banuett, F.; Dahl, M.; Schlesinger, R.; Schaefer,
                    W.; Martin, T.; Herskowitz, I.; Kahmann, R.
    #journal      Cell (1990) 60:295-306
    #title        The b alleles of U. maydis, whose combinations program
                    pathogenic development, code for polypeptides containing a
                    homeodomain-related motif.
    #cross-references MUID:90124638
    #accession    B32696
       ##status        preliminary
       ##molecule_type DNA
       ##residues      1-410 ##label SCH
       ##cross-references GB:M58554
 CLASSIFICATION   #superfamily mating-type locus protein b1
 SUMMARY          #length 410  #molecular-weight 45957  #checksum 5041
 SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             CXNXIX
             | | |
    PNFSLTSFVECLNEIEHEFLRDKLEN
        10    X   20        30
```

7. US-08-121-713B-2 (1-6)
   A36671 mating-type locus protein b1 - smut fungus (Ustila

```
 ENTRY            A36671     #type complete
 TITLE            mating-type locus protein b1 - smut fungus (Ustilago maydis)
 ORGANISM         #formal_name Ustilago maydis #common_name corn smut
 DATE             12-Apr-1991 #sequence_revision 03-Apr-1992 #text_change
```



```
                    30-Sep-1993
 ACCESSIONS       A36671
 REFERENCE        A36671
    #authors      Kronstad, J.W.; Leong, S.A.
    #journal      Genes Dev. (1990) 4:1384-1395
    #title        The b mating-type locus of Ustilago maydis contains variable
                    and constant regions.
    #cross-references MUID:91032990
    #accession    A36671
       ##status        preliminary
       ##molecule_type DNA
       ##residues      1-410 ##label KRO
       ##note          the authors translated the codon GAG for residue 100 as
                        Asp
 CLASSIFICATION   #superfamily mating-type locus protein b1
 SUMMARY          #length 410  #molecular-weight 46197  #checksum 7183
 SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             CXNXIX
             | | |
    PNFSLISFLECLNEIEHEFLRDKGEN
        10    X   20        30
```

8. US-08-121-713B-2 (1-6)
   D32696 b3 protein - smut fungus (Ustilago maydis)

```
 ENTRY            D32696     #type complete
 TITLE            b3 protein - smut fungus (Ustilago maydis)
 ORGANISM         #formal_name Ustilago maydis #common_name corn smut
 DATE             22-Jun-1990 #sequence_revision 28-Aug-1992 #text_change
                    30-Sep-1993
 ACCESSIONS       D32696
 REFERENCE        A32696
    #authors      Schulz, B.; Banuett, F.; Dahl, M.; Schlesinger, R.; Schaefer,
                    W.; Martin, T.; Herskowitz, I.; Kahmann, R.
    #journal      Cell (1990) 60:295-306
    #title        The b alleles of U. maydis, whose combinations program
                    pathogenic development, code for polypeptides containing a
                    homeodomain-related motif.
    #cross-references MUID:90124638
    #accession    D32696
       ##status        preliminary
       ##molecule_type DNA
       ##residues      1-410 ##label SCH
       ##cross-references GB:M58555
       ##note          the authors translated the codon CCG for residue 194 as
                        Arg
 CLASSIFICATION   #superfamily mating-type locus protein b1
 SUMMARY          #length 410  #molecular-weight 46323  #checksum 3467
 SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0
```

```
              X    X
              CXNXIX
              | | |
    PKLSLSKFLECLNEIEHEFLRDKVEH
        10    X   20        30
```

9. US-08-121-713B-2 (1-6)
   A32696 b1 protein - smut fungus (Ustilago maydis)

```
 ENTRY            A32696     #type complete
 TITLE            b1 protein - smut fungus (Ustilago maydis)
 ORGANISM         #formal_name Ustilago maydis #common_name corn smut
 DATE             22-Jun-1990 #sequence_revision 28-Aug-1992 #text_change
                    30-Sep-1993
 ACCESSIONS       A32696
 REFERENCE        A32696
    #authors      Schulz, B.; Banuett, F.; Dahl, M.; Schlesinger, R.; Schaefer,
                    W.; Martin, T.; Herskowitz, I.; Kahmann, R.
    #journal      Cell (1990) 60:295-306
    #title        The b alleles of U. maydis, whose combinations program
                    pathogenic development, code for polypeptides containing a
                    homeodomain-related motif.
    #cross-references MUID:90124638
    #accession    A32696
       ##status        preliminary
       ##molecule_type DNA
       ##residues      1-410 ##label SCH
       ##cross-references GB:M58553
 CLASSIFICATION   #superfamily mating-type locus protein b1
 SUMMARY          #length 410  #molecular-weight 46254  #checksum 7550
 SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

              X    X
              CXNXIX
              | | |
    PNFSLISFLECLNEIEHEFLRDKGEN
        10    X   20        30
```

10. US-08-121-713B-2 (1-6)
    E36671 mating-type locus protein b6 - smut fungus (Ustila

```
 ENTRY            E36671     #type complete
 TITLE            mating-type locus protein b6 - smut fungus (Ustilago maydis)
 ORGANISM         #formal_name Ustilago maydis #common_name corn smut
 DATE             12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change
                    30-Sep-1993
 ACCESSIONS       E36671
 REFERENCE        A36671
    #authors      Kronstad, J.W.; Leong, S.A.
    #journal      Genes Dev. (1990) 4:1384-1395
    #title        The b mating-type locus of Ustilago maydis contains variable
                    and constant regions.
    #cross-references MUID:91032990
```



```
    #accession    E36671
       ##status        preliminary
       ##molecule_type DNA
       ##residues      1-410 ##label KRO
       ##cross-references GB:X54071
 CLASSIFICATION   #superfamily mating-type locus protein b1
 SUMMARY          #length 410  #molecular-weight 46517  #checksum 7490
 SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

              X    X
              CXNXIX
              | | |
    PKLSLSKFLECLNEIEHEFLRDKVEH
        10    X   20        30
```

11. US-08-121-713B-2 (1-6)
    D36671 mating-type locus protein b5 - smut fungus (Ustila

```
 ENTRY            D36671     #type complete
 TITLE            mating-type locus protein b5 - smut fungus (Ustilago maydis)
 ORGANISM         #formal_name Ustilago maydis #common_name corn smut
 DATE             12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change
                    30-Sep-1993
 ACCESSIONS       D36671
 REFERENCE        A36671
    #authors      Kronstad, J.W.; Leong, S.A.
    #journal      Genes Dev. (1990) 4:1384-1395
    #title        The b mating-type locus of Ustilago maydis contains variable
                    and constant regions.
    #cross-references MUID:91032990
    #accession    D36671
       ##status        preliminary
       ##molecule_type DNA
       ##residues      1-410 ##label KRO
       ##cross-references EMBL:X54069
 CLASSIFICATION   #superfamily mating-type locus protein b1
 SUMMARY          #length 410  #molecular-weight 46304  #checksum 6080
 SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

              X    X
              CXNXIX
              | | |
    PNFSLTSFLECLNEIEHEFLRDKEEN
        10    X   20        30
```

12. US-08-121-713B-2 (1-6)
    C36671 mating-type locus protein b3 - smut fungus (Ustila

```
 ENTRY            C36671     #type complete
 TITLE            mating-type locus protein b3 - smut fungus (Ustilago maydis)
```

```
  ORGANISM          #formal_name Ustilago maydis #common_name corn smut
  DATE              12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change
                      17-Feb-1994
  ACCESSIONS        C36671
  REFERENCE         A36671
     #authors       Kronstad, J.W.; Leong, S.A.
     #journal       Genes Dev. (1990) 4:1384-1395
     #title         The b mating-type locus of Ustilago maydis contains variable
                      and constant regions.
     #cross-references MUID:91032990
     #accession     C36671
        ##status         preliminary
        ##molecule_type DNA
        ##residues       1-410 ##label KRO
        ##note           sequence not compared to nucleotide translation
        ##note           the nucleotide sequence is not given in this paper
  CLASSIFICATION    #superfamily mating-type locus protein b1
  SUMMARY           #length 410  #molecular-weight 46382  #checksum 3513
  SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             CXNXIX
             | | |
    PKLSLSKFLECLNEIEHEFLRDKVEH
        10    X   20        30


13. US-08-121-713B-2 (1-6)
    A49915       GutQ homolog - Escherichia coli

  ENTRY             A49915     #type complete
  TITLE             GutQ homolog - Escherichia coli
  ORGANISM          #formal_name Escherichia coli
  DATE              07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change
                      18-Nov-1994
  ACCESSIONS        A49915
  REFERENCE         A49915
     #authors       Cieslewicz, M.J.; Steenbergen, S.M.; Vimr, E.R.
     #journal       J. Bacteriol. (1993) 175:8018-8023
     #title         Cloning, sequencing, expression, and complementation analysis
                      of the Escherichia coli K1 kps region 1 gene, kpsE, and
                      identification of an upstream open reading frame encoding a
                      protein with homology to GutQ.
     #cross-references MUID:94075243
     #contents      K1
     #accession     A49915
        ##status         preliminary
        ##molecule_type DNA
        ##residues       1-317 ##label CIE
        ##cross-references NCBIN:140654; NCBIP:140655
        ##note           sequence inconsistent with nucleotide translation
        ##note           sequence extracted from NCBI backbone
  SUMMARY           #length 317  #molecular-weight 34434  #checksum 5610
  SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
```



```
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             CXNXIX
             | | |
    EAEEKMQKDKCLNVIGDQQGK
     300       310 X


14. US-08-121-713B-2 (1-6)
    W6WL58       E6 protein - human papillomavirus type 58

  ENTRY             W6WL58     #type complete
  TITLE             E6 protein - human papillomavirus type 58
  ORGANISM          #formal_name human papillomavirus type 58
     #note          host Homo sapiens (man)
  DATE              31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
                      24-Feb-1994
  ACCESSIONS        E36779
  REFERENCE         A36779
     #authors       Kirii, Y.; Iwamoto, S.; Matsukura, T.
     #journal       Virology (1991) 185:424-427
     #title         Human papillomavirus type 58 DNA sequence.
     #cross-references MUID:92024102
     #accession     E36779
        ##molecule_type DNA
        ##residues       1-149 ##label KIR
        ##cross-references GB:D90400
        ##note          the translation of the nucleotide sequence is not given
                         in this paper
  CLASSIFICATION    #superfamily papillomavirus E6 protein
  KEYWORDS          early protein; zinc finger
  SUMMARY           #length 149  #molecular-weight 17794  #checksum 1553
  SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             CXNXIX
             | | |
    GDTLEQTLKKCLNEILIRCIICQRPL
        90    X  100       110


15. US-08-121-713B-2 (1-6)
    S28743       NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain

  ENTRY             S28743     #type complete
  TITLE             NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - blue
                      mussel mitochondrion (SGC4)
  ORGANISM          #formal_name mitochondrion Mytilus edulis #common_name blue
                      mussel
  DATE              22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                      22-Nov-1993
  ACCESSIONS        S28743
  REFERENCE         S28743
     #authors       Hoffmann, R.J.; Boore, J.L.; Brown, W.M.
```

```
      #journal      Genetics (1992) 131:397-412
      #title        A novel mitochondrial genome organization for the blue
                      mussel, Mytilus edulis.
      #accession    S28743
         ##status        preliminary
         ##residues      1-81 ##label HOF
         ##cross-references EMBL:M83756
   SUMMARY          #length 81  #molecular-weight 8952  #checksum 8800
   SEQUENCE

Initial Score    =      6  Optimized Score  =      6  Significance =  4.90
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

              X    X
              CXNXIX
              | | |
     GVHAGLGQFSCLNEIVQKNYFTYQLV
    40        50    X   60
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq2spt.res made by  on Fri 19 May 95 8:53:47-PDT.


Query sequence being compared:US-08-121-713B-2 (1-6)
Number of sequences searched:                43470
Number of scores above cutoff:                3751

      Results of the initial comparison of US-08-121-713B-2 (1-6) with:
   Data bank : Swiss-Prot 31, all entries

100000-
      -
N     -
U50000-
M     -                    *
B     -
E     -
R     -
      -
O     -
F10000-
      -
S     *
E 5000-                                          *
Q     -
U     -
E     -
N     -
C     -
E     -
S 1000-
      -
      -
   500-
```



```
      -
      -
      -
      -
      -
      -
    100-
      -
      -
     50-
      -
      -
      -
      -
      -
      -
      -
      -
     10-                                                              *
      -
      -
      5-
      -
      -
      -
      -
      -
      -
      -
      0-------------------------------------------------------------------
       ||     |   |  |      ||     |   | |     ||     |     |     |
SCORE 0|     1   |  1      2|     3   | 3     4|     5     5     6
STDEV  0         1          2          3        4


                              PARAMETERS

Similarity matrix      Unitary      K-tuple                      2
Mismatch penalty             1      Joining penalty             20
Gap penalty               1.00      Window size                  6
Gap size penalty          0.05
Cutoff score                 0
Randomization group          0

Initial scores to save      45      Alignments to save          15
Optimized scores to save     0      Display context             10

                          SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                              1            3          0.91

Times:                      CPU                   Total Elapsed
                      00:00:43.98                 00:00:44.00

Number of residues:              15335248
Number of sequences searched:       43470
Number of scores above cutoff:       3751

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

10 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. RPOB_EUGGR	DNA-DIRECTED RNA POLYMERASE B	1082	6	6	5.47	0
2. ARK2_HUMAN	BETA-ADRENERGIC RECEPTOR KINA	688	6	6	5.47	0
3. ARK2_BOVIN	BETA-ADRENERGIC RECEPTOR KINA	688	6	6	5.47	0
4. ARK2_RAT	BETA-ADRENERGIC RECEPTOR KINA	688	6	6	5.47	0
5. B3_USTMA	MATING-TYPE LOCUS ALLELE B3 P	410	6	6	5.47	0
6. B6_USTMA	MATING-TYPE LOCUS ALLELE B6 P	410	6	6	5.47	0
7. B5_USTMA	MATING-TYPE LOCUS ALLELE B5 P	410	6	6	5.47	0
8. B2_USTMA	MATING-TYPE LOCUS ALLELE B2 P	410	6	6	5.47	0
9. B1_USTMA	MATING-TYPE LOCUS ALLELE B1 P	410	6	6	5.47	0
10. VE6_HPV58	E6 PROTEIN.	149	6	6	5.47	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 3 standard deviations above mean ****					
11. COTB_BACSU	SPORE COAT PROTEIN B (FRAGMEN	23	4	4	3.28	0
12. RM03_YEAST	MITOCHONDRIAL 60S RIBOSOMAL P	28	4	4	3.28	0
13. HOXY_NOCOP	NAD-REDUCING HYDROGENASE HOXS	29	4	4	3.28	0
14. ITR2_CUCSA	TRYPSIN INHIBITOR IIB (CSTI-I	32	4	4	3.28	0
15. SG2_RANRI	SECRETOGRANIN II (FRAGMENT).	33	4	4	3.28	0
16. DEF7_RABIT	CORTICOSTATIN VI (CS-VI) (NEU	34	4	4	3.28	0
17. DHCO_LACLA	N5-(L-1-CARBOXYETHYL)-L-ORNIT	37	4	4	3.28	0
18. CU47_LACCU	BACTERIOCIN CURVATICIN FS47 (	38	4	4	3.28	0
19. FUC3_RAT	FUCTININ 3 (FUCOSYLTRANSFERAS	39	4	4	3.28	0
20. PRE_BACLI	REGULATORY PROTEIN.	40	4	4	3.28	0
21. LPW_VIBPA	TRP OPERON LEADER PEPTIDE.	41	4	4	3.28	0
22. REPE_ECOLI	REP PROTEIN (E PROTEIN) (F4 P	43	4	6	3.28	0
23. CRTC_RHOSH	HYDROXYNEUROSPORENE DEHYDROGE	44	4	4	3.28	0
24. DEGQ_BACLI	DEGRADATION ENZYME REGULATION	46	4	4	3.28	0
25. EGF_RAT	EPIDERMAL GROWTH FACTOR (EGF)	48	4	4	3.28	0
26. C555_BACAZ	CYTOCHROME C555 (FRAGMENTS).	50	4	4	3.28	0
27. ATP8_PODAN	ATP SYNTHASE PROTEIN 8 (EC 3.	50	4	4	3.28	0
28. IOVO_EUDEL	OVOMUCOID (FRAGMENT).	51	4	4	3.28	0
29. LECA_LATTI	LECTIN ALPHA CHAIN.	54	4	4	3.28	0
30. ATP8_NEUCR	ATP SYNTHASE PROTEIN 8 (EC 3.	54	4	4	3.28	0
31. E1A6_ADE05	EARLY E1A 6 KD PROTEIN.	55	4	4	3.28	0
32. E1A6_ADE02	EARLY E1A 6 KD PROTEIN.	55	4	4	3.28	0
33. COP6_STAAU	COP-6 PROTEIN.	55	4	4	3.28	0
34. PSBK_TOBAC	PHOTOSYSTEM II 4 KD REACTION	61	4	4	3.28	0
35. TXW5_NAJNA	WEAK NEUROTOXIN 5.	62	4	4	3.28	0
36. RS16_ORYSA	30S RIBOSOMAL PROTEIN S16.	62	4	4	3.28	0
37. CXH2_ASPSC	CYTOTOXIN HOMOLOG S3C2.	63	4	4	3.28	0
38. TXW9_NAJKA	WEAK TOXIN CM-9A.	64	4	4	3.28	0
39. NXS1_BUNFA	SHORT NEUROTOXIN 1 (TOXIN V-I	64	4	4	3.28	0
40. TXW8_NAJNA	WEAK NEUROTOXIN 8.	65	4	4	3.28	0
41. TXW7_NAJNA	WEAK NEUROTOXIN 7.	65	4	4	3.28	0
42. TXW6_NAJNA	WEAK NEUROTOXIN 6.	65	4	4	3.28	0
43. TXW0_NAJNI	WEAK TOXIN CM-10.	65	4	4	3.28	0

44. RL33_MAIZE	50S RIBOSOMAL PROTEIN L33.	65	4	4	3.28	0
45. RL29_BACSU	50S RIBOSOMAL PROTEIN L29.	66	4	4	3.28	0

1. US-08-121-713B-2 (1-6)
RPOB_EUGGR DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6

```
ID   RPOB_EUGGR     STANDARD;      PRT;  1082 AA.
AC   P23579;
DT   01-NOV-1991 (REL. 20, CREATED)
DT   01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6).
GN   RPOB.
OS   EUGLENA GRACILIS.
OG   CHLOROPLAST.
OC   EUKARYOTA; PLANTA; PHYCOPHYTA; EUGLENOPHYTA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PRINGSHEIM Z;
RM   90245579
RA   YEPIZ-PLASCENCIA G.M., RADEBAUGH C.A., HALLICK R.B.;
RL   NUCLEIC ACIDS RES. 18:1869-1878(1990).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES.
CC   -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
CC       RNA(N).
CC   -!- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC       SUBUNITS: ALPHA, BETA, BETA', AND BETA".
DR   EMBL; X17191; CHEGRPO.
DR   PIR; S09210; RNEGB.
KW   TRANSCRIPTION; DNA-DIRECTED RNA POLYMERASE; CHLOROPLAST.
SQ   SEQUENCE   1082 AA;  124531 MW;  6191111 CN;

Initial Score    =      6  Optimized Score  =      6  Significance =  5.47
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions              =     0

             X    X
             CXNXIX
             | | |
    KNYSFFNLLGCLNEISQKNFKLIKKV
      610     X 620       630
```

2. US-08-121-713B-2 (1-6)
ARK2_HUMAN BETA-ADRENERGIC RECEPTOR KINASE 2 (EC 2.7.1.126) (

```
ID   ARK2_HUMAN     STANDARD;      PRT;   688 AA.
AC   P35626;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   BETA-ADRENERGIC RECEPTOR KINASE 2 (EC 2.7.1.126) (BETA-ARK-2).
GN   ADRBK2 OR BARK2.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
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```
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RM   93151831
RA   PARRUTI G., AMBROSINI G., SALLESE M., DE BLASI A.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 190:475-481(1993).
CC   -!- FUNCTION: SPECIFICALLY PHOSPHORYLATES THE AGONIST-OCCUPIED FORM
CC       OF THE BETA-ADRENERGIC AND CLOSELY RELATED RECEPTORS.
CC   -!- CATALYTIC ACTIVITY: ATP + [BETA-ADRENERGIC RECEPTOR] = ADP +
CC       [BETA-ADRENERGIC RECEPTOR] PHOSPHATE.
CC   -!- SIMILARITY: TO THE CATALYTIC DOMAINS OF OTHER SERINE/THREONINE
CC       KINASES. STRONG, TO OTHER KINASES THAT PHOSPHORYLATES G-COUPLED
CC       RECEPTORS.
DR   EMBL; X69117; HSBADRK2.
DR   HSSP; P05132; 1CTP.
DR   MIM; 109636; 11TH EDITION.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST.
KW   TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING.
FT   DOMAIN        1    196       N-TERMINAL.
FT   DOMAIN      197    436       CATALYTIC.
FT   DOMAIN      437    688       C-TERMINAL.
FT   NP_BIND     197    205       ATP (BY SIMILARITY).
FT   BINDING     220    220       ATP (BY SIMILARITY).
FT   ACT_SITE    317    317       BY SIMILARITY.
SQ   SEQUENCE   688 AA;  79677 MW;  2386685 CN;

Initial Score    =      6  Optimized Score  =      6  Significance =  5.47
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             CXNXIX
             | | |
    KIGFLLFKDFCLNEINEAVPQVKFYE
          70 X    X 80
```

3. US-08-121-713B-2 (1-6)
ARK2_BOVIN BETA-ADRENERGIC RECEPTOR KINASE 2 (EC 2.7.1.126) (

```
ID   ARK2_BOVIN     STANDARD;      PRT;   688 AA.
AC   P26818;
DT   01-AUG-1992 (REL. 23, CREATED)
DT   01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT   01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE   BETA-ADRENERGIC RECEPTOR KINASE 2 (EC 2.7.1.126) (BETA-ARK-2).
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RM   91332005
RA   BENOVIC J.L., ONORATO J.J., ARRIZA J.L., STONE W.C., LOHSE M.,
RA   JENKINS N.A., GILBERT D.J., COPELAND N.G., CARON M.G.,
RA   LEFKOWITZ R.J.;
RL   J. BIOL. CHEM. 266:14939-14946(1991).
CC   -!- FUNCTION: SPECIFICALLY PHOSPHORYLATES THE AGONIST-OCCUPIED FORM
CC       OF THE BETA-ADRENERGIC AND CLOSELY RELATED RECEPTORS, PROBABLY
CC       INDUCING A DESENSITIZATION OF THEM.
```



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CC   -!- CATALYTIC ACTIVITY: ATP + [BETA-ADRENERGIC RECEPTOR] = ADP +
CC       [BETA-ADRENERGIC RECEPTOR] PHOSPHATE.
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS; BRAIN, SPLEEN > HEART, LUNG >
CC       KIDNEY.
CC   -!- SIMILARITY: TO THE CATALYTIC DOMAINS OF OTHER SERINE/THREONINE
CC       KINASES. STRONG, TO OTHER KINASES THAT PHOSPHORYLATES G-COUPLED
CC       RECEPTORS.
DR   EMBL; M73216; BTBARK.
DR   PIR; A39336; A39336.
DR   HSSP; P05132; 1CTP.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST.
KW   TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
KW   MULTIGENE FAMILY.
FT   DOMAIN        1    196       N-TERMINAL.
FT   DOMAIN      197    436       CATALYTIC.
FT   DOMAIN      437    688       C-TERMINAL.
FT   NP_BIND     197    205       ATP (BY SIMILARITY).
FT   BINDING     220    220       ATP (BY SIMILARITY).
FT   ACT_SITE    317    317       BY SIMILARITY.
SQ   SEQUENCE   688 AA;  79803 MW;  2384837 CN;

Initial Score    =      6  Optimized Score  =      6  Significance =  5.47
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             CXNXIX
             | | |
    RIGFLLFKDFCLNEINEAVPQVKFYE
          70 X    X 80
```

4. US-08-121-713B-2 (1-6)
ARK2_RAT BETA-ADRENERGIC RECEPTOR KINASE 2 (EC 2.7.1.126) (

```
ID   ARK2_RAT       STANDARD;      PRT;   688 AA.
AC   P26819;
DT   01-AUG-1992 (REL. 23, CREATED)
DT   01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   BETA-ADRENERGIC RECEPTOR KINASE 2 (EC 2.7.1.126) (BETA-ARK-2).
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RM   93019546
RA   ARRIZA J.L., DAWSON T.M., SIMERLY R.B., MARTIN L.J., CARON M.G.,
RA   SNYDER S.H., LEFKOWITZ R.J.;
RL   J. NEUROSCI. 12:4045-4055(1992).
CC   -!- FUNCTION: SPECIFICALLY PHOSPHORYLATES THE AGONIST-OCCUPIED FORM
CC       OF THE BETA-ADRENERGIC AND CLOSELY RELATED RECEPTORS.
CC   -!- CATALYTIC ACTIVITY: ATP + [BETA-ADRENERGIC RECEPTOR] = ADP +
CC       [BETA-ADRENERGIC RECEPTOR] PHOSPHATE.
CC   -!- SIMILARITY: TO THE CATALYTIC DOMAINS OF OTHER SERINE/THREONINE
CC       KINASES. STRONG, TO OTHER KINASES THAT PHOSPHORYLATES G-COUPLED
CC       RECEPTORS.
DR   EMBL; M87855; RNBARK2.
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DR   HSSP; P05132; 1CTP.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST.
KW   TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING.
FT   DOMAIN        1    196       N-TERMINAL.
FT   DOMAIN      197    436       CATALYTIC.
FT   DOMAIN      437    688       C-TERMINAL.
FT   NP_BIND     197    205       ATP (BY SIMILARITY).
FT   BINDING     220    220       ATP (BY SIMILARITY).
FT   ACT_SITE    317    317       BY SIMILARITY.
SQ   SEQUENCE   688 AA;  79887 MW;  2345374 CN;

Initial Score    =      6  Optimized Score  =      6  Significance =  5.47
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             CXNXIX
             | | |
   KIGFLLFKDFCLNEIGEAVPQVKFYE
         70 X    X 80
```

5. US-08-121-713B-2 (1-6)
   B3_USTMA MATING-TYPE LOCUS ALLELE B3 PROTEIN.

```
ID   B3_USTMA       STANDARD;      PRT;   410 AA.
AC   P22017;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE   MATING-TYPE LOCUS ALLELE B3 PROTEIN.
OS   USTILAGO MAYDIS (SMUT FUNGUS).
OC   EUKARYOTA; FUNGI; BASIDIOMYCOTINA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RK32;
RM   90124638
RA   SCHULZ B., BANUETT F., DAHL M., SCHLESINGER R., SCHAEFER W.,
RA   MARTIN T., HERSKOWITZ I., KAHMANN R.;
RL   CELL 60:295-306(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 18604;
RM   91032990
RA   KRONSTAD J.W., LEONG S.A.;
RL   GENES DEV. 4:1384-1395(1990).
CC   -!- FUNCTION: THE B LOCUS HAS AT LEAST 25 ALLELES, AND ANY COMBINATION
CC       OF TWO DIFFERENT B ALLELES YIELDS A MULTIMERIC REGULATORY PROTEIN,
CC       THAT ACTIVATES GENES RESPONSIBLE FOR THE PATHOGENICITY AND FOR THE
CC       SEXUAL DEVELOPMENT OF THE FUNGUS WITHIN THE CORN PLANT.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
DR   EMBL; M58555; UMB3.
DR   PIR; D32696; D32696.
DR   PIR; C36671; C36671.
KW   DEVELOPMENTAL PROTEIN; DNA-BINDING; HOMEOBOX; NUCLEAR PROTEIN.
FT   DOMAIN        1    110       VARIABLE DOMAIN BETWEEN B ALLELES.
FT   DOMAIN      111    410       HIGHLY CONSERVED BETWEEN B ALLELES.
FT   DOMAIN      276    308       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DOMAIN      333    410       NOT ESSENTIAL FOR B3 FUNCTION.
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```
FT   DNA_BIND    134    179       HOMEOBOX-LIKE.
SQ   SEQUENCE   410 AA;  46323 MW;  894255 CN;

Initial Score    =      6  Optimized Score  =      6  Significance =  5.47
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             CXNXIX
             | | |
   PKLSLSKFLECLNEIEHEFLRDKVEH
       10    X   20        30
```

6. US-08-121-713B-2 (1-6)
   B6_USTMA MATING-TYPE LOCUS ALLELE B6 PROTEIN.

```
ID   B6_USTMA       STANDARD;      PRT;   410 AA.
AC   P22020;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE   MATING-TYPE LOCUS ALLELE B6 PROTEIN.
OS   USTILAGO MAYDIS (SMUT FUNGUS).
OC   EUKARYOTA; FUNGI; BASIDIOMYCOTINA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 22505;
RM   91032990
RA   KRONSTAD J.W., LEONG S.A.;
RL   GENES DEV. 4:1384-1395(1990).
CC   -!- FUNCTION: THE B LOCUS HAS AT LEAST 25 ALLELES, AND ANY COMBINATION
CC       OF TWO DIFFERENT B ALLELES YIELDS A MULTIMERIC REGULATORY PROTEIN,
CC       THAT ACTIVATES GENES RESPONSIBLE FOR THE PATHOGENICITY AND FOR THE
CC       SEXUAL DEVELOPMENT OF THE FUNGUS WITHIN THE CORN PLANT.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
DR   EMBL; X54071; UMMTB6.
DR   PIR; E36671; E36671.
DR   PIR; S21296; S21296.
KW   DEVELOPMENTAL PROTEIN; DNA-BINDING; HOMEOBOX; NUCLEAR PROTEIN.
FT   DOMAIN        1    110       VARIABLE DOMAIN BETWEEN B ALLELES.
FT   DOMAIN      111    410       HIGHLY CONSERVED BETWEEN B ALLELES.
FT   DOMAIN      276    308       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DOMAIN      333    410       NOT ESSENTIAL FOR B6 FUNCTION.
FT   DNA_BIND    134    179       HOMEOBOX-LIKE.
SQ   SEQUENCE   410 AA;  46517 MW;  901339 CN;

Initial Score    =      6  Optimized Score  =      6  Significance =  5.47
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             CXNXIX
             | | |
   PKLSLSKFLECLNEIEHEFLRDKVEH
       10    X   20        30
```

7. US-08-121-713B-2 (1-6)
   B5_USTMA MATING-TYPE LOCUS ALLELE B5 PROTEIN.

```
ID   B5_USTMA       STANDARD;      PRT;   410 AA.
AC   P22019;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE   MATING-TYPE LOCUS ALLELE B5 PROTEIN.
OS   USTILAGO MAYDIS (SMUT FUNGUS).
OC   EUKARYOTA; FUNGI; BASIDIOMYCOTINA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 22907;
RM   91032990
RA   KRONSTAD J.W., LEONG S.A.;
RL   GENES DEV. 4:1384-1395(1990).
CC   -!- FUNCTION: THE B LOCUS HAS AT LEAST 25 ALLELES, AND ANY COMBINATION
CC       OF TWO DIFFERENT B ALLELES YIELDS A MULTIMERIC REGULATORY PROTEIN,
CC       THAT ACTIVATES GENES RESPONSIBLE FOR THE PATHOGENICITY AND FOR THE
CC       SEXUAL DEVELOPMENT OF THE FUNGUS WITHIN THE CORN PLANT.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
DR   EMBL; X54069; UMMTB5.
DR   PIR; D36671; D36671.
DR   PIR; S21295; S21295.
KW   DEVELOPMENTAL PROTEIN; DNA-BINDING; HOMEOBOX; NUCLEAR PROTEIN.
FT   DOMAIN        1    110       VARIABLE DOMAIN BETWEEN B ALLELES.
FT   DOMAIN      111    410       HIGHLY CONSERVED BETWEEN B ALLELES.
FT   DOMAIN      276    308       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DOMAIN      333    410       NOT ESSENTIAL FOR B5 FUNCTION.
FT   DNA_BIND    134    179       HOMEOBOX-LIKE.
SQ   SEQUENCE   410 AA;  46304 MW;  903769 CN;

Initial Score    =      6  Optimized Score  =      6  Significance =  5.47
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             CXNXIX
             | | |
   PNFSLTSFLECLNEIEHEFLRDKEEN
      10    X   20        30
```

8. US-08-121-713B-2 (1-6)
   B2_USTMA MATING-TYPE LOCUS ALLELE B2 PROTEIN.

```
ID   B2_USTMA       STANDARD;      PRT;   410 AA.
AC   P22016;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE   MATING-TYPE LOCUS ALLELE B2 PROTEIN.
OS   USTILAGO MAYDIS (SMUT FUNGUS).
OC   EUKARYOTA; FUNGI; BASIDIOMYCOTINA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=518;
RM   90124638
RA   SCHULZ B., BANUETT F., DAHL M., SCHLESINGER R., SCHAEFER W.,
RA   MARTIN T., HERSKOWITZ I., KAHMANN R.;
RL   CELL 60:295-306(1990).
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```
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=518;
RM   91032990
RA   KRONSTAD J.W., LEONG S.A.;
RL   GENES DEV. 4:1384-1395(1990).
CC   -!- FUNCTION: THE B LOCUS HAS AT LEAST 25 ALLELES, AND ANY COMBINATION
CC       OF TWO DIFFERENT B ALLELES YIELDS A MULTIMERIC REGULATORY PROTEIN,
CC       THAT ACTIVATES GENES RESPONSIBLE FOR THE PATHOGENICITY AND FOR THE
CC       SEXUAL DEVELOPMENT OF THE FUNGUS WITHIN THE CORN PLANT.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
DR   EMBL; M58554; UMB2.
DR   PIR; B32696; B32696.
DR   PIR; B36671; B36671.
KW   DEVELOPMENTAL PROTEIN; DNA-BINDING; HOMEOBOX; NUCLEAR PROTEIN.
FT   DOMAIN        1    110       VARIABLE DOMAIN BETWEEN B ALLELES.
FT   DOMAIN      111    410       HIGHLY CONSERVED BETWEEN B ALLELES.
FT   DOMAIN      276    308       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DOMAIN      333    410       NOT ESSENTIAL FOR B2 FUNCTION.
FT   DNA_BIND    134    179       HOMEOBOX-LIKE.
SQ   SEQUENCE   410 AA;  45957 MW;  899890 CN;

Initial Score    =      6  Optimized Score  =      6  Significance =  5.47
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             CXNXIX
             | | |
   PNFSLTSFVECLNEIEHEFLRDKLEN
      10    X   20        30
```

9. US-08-121-713B-2 (1-6)
   B1_USTMA MATING-TYPE LOCUS ALLELE B1 PROTEIN.

```
ID   B1_USTMA       STANDARD;      PRT;   410 AA.
AC   P22015;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE   MATING-TYPE LOCUS ALLELE B1 PROTEIN.
OS   USTILAGO MAYDIS (SMUT FUNGUS).
OC   EUKARYOTA; FUNGI; BASIDIOMYCOTINA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=521;
RM   90124638
RA   SCHULZ B., BANUETT F., DAHL M., SCHLESINGER R., SCHAEFER W.,
RA   MARTIN T., HERSKOWITZ I., KAHMANN R.;
RL   CELL 60:295-306(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=521;
RM   91032990
RA   KRONSTAD J.W., LEONG S.A.;
RL   GENES DEV. 4:1384-1395(1990).
CC   -!- FUNCTION: THE B LOCUS HAS AT LEAST 25 ALLELES, AND ANY COMBINATION
CC       OF TWO DIFFERENT B ALLELES YIELDS A MULTIMERIC REGULATORY PROTEIN,
CC       THAT ACTIVATES GENES RESPONSIBLE FOR THE PATHOGENICITY AND FOR THE
```

```
CC       SEXUAL DEVELOPMENT OF THE FUNGUS WITHIN THE CORN PLANT.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
DR   EMBL; M58553; UMB1.
DR   EMBL; X61305; UMBMTLORF.
DR   PIR; A32696; A32696.
DR   PIR; A36671; A36671.
KW   DEVELOPMENTAL PROTEIN; DNA-BINDING; HOMEOBOX; NUCLEAR PROTEIN.
FT   DOMAIN        1    110       VARIABLE DOMAIN BETWEEN B ALLELES.
FT   DOMAIN      111    410       HIGHLY CONSERVED BETWEEN B ALLELES.
FT   DOMAIN      276    308       NUCLEAR LOCALIZATION SIGNAL
FT                                (POTENTIAL).
FT   DOMAIN      333    410       NOT ESSENTIAL FOR B1 FUNCTION.
FT   DNA_BIND    134    179       HOMEOBOX-LIKE.
FT   CONFLICT    168    169       HV -> QL (IN REF. 2).
FT   CONFLICT    218    218       Y -> S (IN REF. 2).
FT   CONFLICT    292    292       N -> K (IN REF. 2).
SQ   SEQUENCE   410 AA;  46254 MW;  904704 CN;

Initial Score    =      6  Optimized Score  =      6  Significance =  5.47
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            CXNXIX
            | | |
   PNFSLISFLECLNEIEHEFLRDKGEN
       10    X   20        30
```

10. US-08-121-713B-2 (1-6)
    VE6_HPV58   E6 PROTEIN.

```
ID   VE6_HPV58      STANDARD;      PRT;   149 AA.
AC   P26555;
DT   01-AUG-1992 (REL. 23, CREATED)
DT   01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   E6 PROTEIN.
GN   E6.
OS   HUMAN PAPILLOMAVIRUS TYPE 58.
OC   VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92024102
RA   KIRII Y., IWAMOTO S., MATSUKURA T.;
RL   VIROLOGY 185:424-427(1991).
CC   -!- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC       STRANDED DNA (IN VITRO).
CC   -!- SUBCELLULAR LOCATION: NUCLEAR MATRIX-ASSOCIATED.
DR   EMBL; D90400; PAPPPH58.
DR   PIR; E36779; W6WL58.
KW   EARLY PROTEIN; DNA-BINDING; NUCLEAR PROTEIN; ZINC-FINGER.
FT   ZN_FING      30     66       POTENTIAL.
FT   ZN_FING     103    139       POTENTIAL.
SQ   SEQUENCE   149 AA;  17794 MW;  106368 CN;

Initial Score    =      6  Optimized Score  =      6  Significance =  5.47
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0
```



```
            X    X
            CXNXIX
            | | |
   GDTLEQTLKKCLNEILIRCIICQRPL
       90    X  100       110
```

11. US-08-121-713B-2 (1-6)
    COTB_BACSU   SPORE COAT PROTEIN B (FRAGMENT).

```
ID   COTB_BACSU     STANDARD;      PRT;    23 AA.
AC   P07789;
DT   01-AUG-1988 (REL. 08, CREATED)
DT   01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   SPORE COAT PROTEIN B (FRAGMENT).
GN   COTB.
OS   BACILLUS SUBTILIS.
OC   PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   88011308
RA   DONOVAN W., ZHENG L., SANDMAN K., LOSICK R.;
RL   J. MOL. BIOL. 196:1-10(1987).
DR   EMBL; X05679; BSCOTBG.
DR   PIR; B27393; B27393.
DR   SUBTILIST; BG10491; COTB.
KW   SPORULATION.
FT   NON_TER      23     23
SQ   SEQUENCE   23 AA;  2937 MW;  3201 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.28
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            CXNXIX
              | |
   MSKRRMKYHSNNEISYYNFLHSM
           10    X   20
```

12. US-08-121-713B-2 (1-6)
    RM03_YEAST   MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (YML3) (FRA

```
ID   RM03_YEAST     STANDARD;      PRT;    28 AA.
AC   P36516;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (YML3) (FRAGMENT).
GN   MRPL3.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE.
RM   89078618
RA   GRAACK H.-R., GROHMANN L., CHOLI T.;
RL   FEBS LETT. 242:4-8(1988).
DR   PIR; S26754; S26754.
```

```
KW   RIBOSOMAL PROTEIN; MITOCHONDRION.
FT   NON_TER      28     28
SQ   SEQUENCE   28 AA;  3387 MW;  4768 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.28
Residue Identity =    40%  Matches          =      2  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

            X   X
            CXNXIX
              | |
    YKEYYQGLKSTVNEI
         20   X   X
```

13. US-08-121-713B-2 (1-6)
    HOXY_NOCOP NAD-REDUCING HYDROGENASE HOXS DELTA SUBUNIT (EC 1.

```
ID   HOXY_NOCOP     STANDARD;      PRT;    29 AA.
AC   P22660;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE   NAD-REDUCING HYDROGENASE HOXS DELTA SUBUNIT (EC 1.12.1.2) (FRAGMENT).
GN   HOXY.
OS   NOCARDIA OPACA.
OG   PLASMID.
OC   PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; NOCARDIOFORM.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=1B;
RM   89231684
RA   ZABOROSCH C., SCHNEIDER K., SCHLEGEL H.G., KRATZIN H.;
RL   EUR. J. BIOCHEM. 181:175-180(1989).
CC   -!- CATALYTIC ACTIVITY: H(2) + NAD(+) = H(+) + NADH.
CC   -!- COFACTOR: FMN, NICKEL, TWO 4FE-4S, A 3FE-4S, AND A 2FE-2S
CC       CLUSTER.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- SUBUNIT: TETRAMER OF AN ALPHA AND A GAMMA SUBUNITS (FLAVIN-
CC       CONTAINING DIMER), AND A DELTA AND A NICKEL-CONTAINING BETA
CC       SUBUNITS (HYDROGENASE DIMER).
CC   -!- SIMILARITY: TO OTHER [NIFE] OR [NIFESE] HYDROGENASES SMALL
CC       SUBUNIT.
DR   PIR; S03947; S03947.
KW   OXIDOREDUCTASE; IRON-SULFUR; 3FE-4S; PLASMID.
FT   NON_TER      29     29
SQ   SEQUENCE   29 AA;  3159 MW;  4265 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.28
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

        X    X
        CXNXIX
          | |
    MKHSEKNEIASHELPTTPLD
        X   10        20
```

14. US-08-121-713B-2 (1-6)

    ITR2_CUCSA TRYPSIN INHIBITOR IIB (CSTI-IIB).

```
ID   ITR2_CUCSA     STANDARD;      PRT;    32 AA.
AC   P10291;
DT   01-MAR-1989 (REL. 10, CREATED)
DT   01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT   01-MAR-1989 (REL. 10, LAST ANNOTATION UPDATE)
DE   TRYPSIN INHIBITOR IIB (CSTI-IIB).
OS   CUCUMIS SATIVUS (CUCUMBER).
OC   EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC   VIOLALES; CUCURBITACEAE.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SEED;
RM   85149300
RA   WIECZOREK M., OTLEWSKI J., COOK J., PARKS K., LELUK J.,
RA   WILIMOWSKA-PELC A., POLANOWSKI A., WILUSZ T., LASKOWSKI M. JR.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 126:646-652(1985).
CC   -!- SIMILARITY: BELONGS TO THE SQUASH FAMILY OF SERINE PROTEASE
CC       INHIBITORS.
DR   HSSP; P01074; 1CTI.
DR   PROSITE; PS00286; SQUASH_INHIBITOR.
KW   SERINE PROTEASE INHIBITOR.
FT   ACT_SITE      5      6       REACTIVE BOND.
FT   DISULFID      3     20       BY SIMILARITY.
FT   DISULFID     10     22       BY SIMILARITY.
FT   DISULFID     16     29       BY SIMILARITY.
SQ   SEQUENCE   32 AA;  3535 MW;  5380 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.28
Residue Identity =    33%  Matches          =      2  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            CXNXIX
            |    |
    HDSDCLLDCVCLEDIGYCGVS
          20 X    X 30
```

15. US-08-121-713B-2 (1-6)
    SG2_RANRI SECRETOGRANIN II (FRAGMENT).

```
ID   SG2_RANRI      STANDARD;      PRT;    33 AA.
AC   P30945;
DT   01-JUL-1993 (REL. 26, CREATED)
DT   01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   SECRETOGRANIN II (FRAGMENT).
OS   RANA RIDIBUNDA (LAUGHING FROG) (MARSH FROG).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=BRAIN;
RM   91285100
RA   VAUDRY H., CONLON J.M.;
RL   FEBS LETT. 284:31-33(1991).
CC   -!- FUNCTION: MAY BE IMPORTANT IN REGULATION OF NEUROSECRETION.
CC   -!- SIMILARITY: MEMBER OF THE CHROMOGRANIN/SECRETOGRANIN PROTEIN
CC       FAMILY.
```

```
DR   PIR; S15867; S15867.
FT   NON_TER       1      1
FT   PEPTIDE       1     33       BRAIN PEPTIDE.
FT   NON_TER      33     33
SQ   SEQUENCE   33 AA;  3607 MW;  5190 CN;

Initial Score    =      4  Optimized Score  =      4  Significance =  3.28
Residue Identity =    40%  Matches          =      2  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

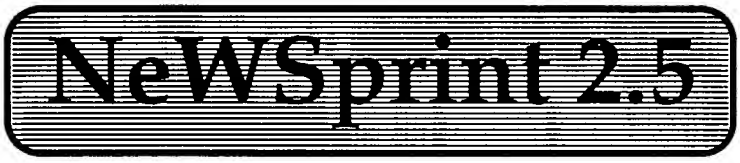
     X   X
    CXNXIX
      | |
     TNEIVEGQYTPQSLA
     X   X   10
```

maryh@stic **stdin**

NeWSprinter20

Fri May 19 10:55:23 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0



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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq3asq.res made by  on Fri 19 May 95 8:39:32-PDT.


Query sequence being compared:US-08-121-713B-3 (1-7)
Number of sequences searched:                53402
Number of scores above cutoff:                4001

     Results of the initial comparison of US-08-121-713B-3 (1-7) with:
   Data bank : A-GeneSeq 18, all entries

100000-
       -
N      -
U50000-
M      *
B      -
E      -
R      -
       -                                        *
O      -
F10000-
       -
S      -
E 5000-                  *
Q      -
U      -
E      -
N      -
C      -
E      -
S 1000-
       -
       -
   500-                                                    *
       -
       -
       -
       -
       -
       -
   100-
       -
       -
    50-
       -
       -
       -
       -
       -
       -
       -
    10-
       -
       -
```

SEQ 3

Salata 121713

```
     5-
      -
      -
      -
      -
      -
      -
      -
     0-------------------------------------------------------------------------
      |      |      |      | |      |      | |      |      |      |      |
SCORE 0      1      2      | 2      3      4 |      5      5      6      7
STDEV                      1                 2
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	1	2.26

Times:	CPU	Total Elapsed
	00:00:29.97	00:00:30.00

Number of residues:	6354270
Number of sequences searched:	53402
Number of scores above cutoff:	4001

Cut-off raised to 2.
Cut-off raised to 5.
Cut-off raised to 6.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

420 100% similar sequences to the query sequence were found:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1.	R47861	Alpha 2-Macroglobulin/LDL-rec	4544	7	7	2.65	0
2.	R43662	DEN1-S275/90 (ECACC V92042111	3396	7	7	2.65	0
3.	R26052	APC gene product in familial	2843	7	7	2.65	0
4.	P60053	Sequence of von Willebrand fa	2813	7	7	2.65	0
5.	P60462	Sequence of human von Willebr	2813	7	7	2.65	0
6.	R13887	Inositol-3-phosphate binding	2749	7	7	2.65	0
7.	R60021	Fibrinogen-alpha.	2446	7	7	2.65	0
8.	R28582	HCV amino acid sequence contg	2436	7	7	2.65	0
9.	R25135	HCV polypeptide 1.	2435	7	7	2.65	0
10.	R24306	Translation of ORF 2 contg. E	2408	7	7	2.65	0

11.	R29939	Deduced from Lelystad Agent g	2396	7	7	2.65	0
12.	P70373	Human fibronectin gene produc	2327	7	7	2.65	0
13.	R15468	Human fibronectin.	2327	7	7	2.65	0
14.	P81048	Sequence encoded by Rhinoviru	2150	7	7	2.65	0
15.	R05127	Complete human rhinovirus 2.	2150	7	7	2.65	0
16.	P60045	Sequence of viral proteins VP	2150	7	7	2.65	0
17.	P95645	Rabbit seletal muscle alpha-1	1873	7	7	2.65	0
18.	P91672	Primary amino acid sequence o	1764	7	7	2.65	0
19.	R22461	Masking protein high polymer	1712	7	7	2.65	0
20.	P81184	Sequence encoded by the 2nd r	1594	7	7	2.65	0
21.	R27640	Human calcium channel 27980/2	1493	7	7	2.65	0
22.	R11749	Human alpha-2 macroglobulin b	1484	7	7	2.65	0
23.	R11334	Recombinant human alpha-2 mac	1474	7	7	2.65	0
24.	R37508	Human DNA polymerase alpha ca	1462	7	7	2.65	0
25.	R24033	Soluble mannose receptor pept	1456	7	7	2.65	0
26.	R38304	Sequence of a serrate protein	1404	7	7	2.65	0
27.	R11061	Bovine Coronavirus E2 protein	1363	7	7	2.65	0
28.	R14584	TGF beta 1 binding protein en	1355	7	7	2.65	0
29.	R14481	LktA:lacZ fusion product.	1334	7	7	2.65	0
30.	R50290	lktA::lacZ fusion protein fro	1334	7	7	2.65	0
31.	R53787	Deep Vent DNA polymerase.	1312	7	7	2.65	0
32.	R28337	SFV4 structural polyprotein.	1253	7	7	2.65	0
33.	R45945	Glutamic acid receptor.	1239	7	7	2.65	0
34.	R49832	Beat-galactosidase/hepatitis	1217	7	7	2.65	0
35.	R26188	HVTA antigen.	1199	7	7	2.65	0
36.	R32882	Cardiac adenylyl cyclase type	1184	7	7	2.65	0
37.	R36728	Ubiquitin fusion protein, Ub-	1121	7	7	2.65	0
38.	R38861	GC-C.	1075	7	7	2.65	0
39.	R38096	Pyrococcus sp DNA polymerase.	1019	7	7	2.65	0
40.	R29648	AmEPV Spheroidin protein G5R.	1003	7	7	2.65	0
41.	R55576	AmEPV spheroidin.	1003	7	7	2.65	0
42.	R30742	Human pemphigus vulgaris 130k	999	7	7	2.65	0
43.	P50231	Sequence encoded by partial s	993	7	7	2.65	0
44.	R25141	JAK2.	986	7	7	2.65	0
45.	R42995	Glycosyltransferase.	985	7	7	2.65	0

1. US-08-121-713B-3 (1-7)
R47861 Alpha 2-Macroglobulin/LDL-receptor related protein

```
ID   R47861 standard; protein; 4544 AA.
AC   R47861;
DT   20-JUL-1994  (first entry)
DE   Alpha 2-Macroglobulin/LDL-receptor related protein.
KW   alpha-2 macroglobulin; Low Density Lipoprotein; LDL; receptor family;
KW   LDL receptor related protein; LRP; small rhinovirus receptor; deriv;
KW   minor Rhinovirus; alpha2MR/LRP.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Misc_difference 211..260
FT   /note= "50 residues not shown in SEQ.ID.No.4"
FT   Misc_difference 1990
FT   /note= "Residue not shown in SEQ.ID.No.4"
FT   Misc_difference 3050
FT   /note= "Residue not shown in SEQ.ID.No.4"
PN   WO9401553-A.
PD   20-JAN-1994.
PF   05-JUL-1993; E01728.
PR   08-JUL-1992; DE-222385.
PR   22-AUG-1992; DE-227892.
```



```
PR   19-FEB-1993; DE-305063.
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PI   Blaas D,  Gruenberger M,  Hofer F,  Huettinger M,  Kerjaschki D;
PI   Kowalski H,  Kuechler E,  Machat H;
DR   WPI; 94-035060/04.
PT   New peptide derivs. of receptor for rhinovirus - of the small
PT   receptor gp., and derived DNA, transformed cells and antibodies,
PT   used e.g. to treat or prevent rhinovirus infection
PS   Claim 5; Fig 2; 76pp; German.
CC   Functional derivatives of members of the Minor Rhinovirus Receptor
CC   group are claimed. The alpha-2 Macroglobulin/LDL-receptor related
CC   protein of sequence R47861 (Herz et al. EMBO J. 7;4119-4127 (1988))
CC   is a preferred parent receptor. The derivs, which are preferably
CC   soluble, extracellular forms of the native receptors, are useful
CC   for treating and preventing viral (esp. rhinoviral) infections.
CC   N.B. the SEQ.ID. listing includes a sequence (no.4) which differs
CC   from the alpha2-MR/LRP sequence as indicated in the Features Table.
SQ   Sequence   4544 AA;
SQ   249A; 277R; 249N; 393D; 0  B; 331C; 164Q; 235E; 0  Z; 376G; 129H;
SQ   196I; 305L; 173K; 72 M; 133F; 231P; 308S; 259T; 88 W; 131Y; 245V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.65
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    DCMDGSDEEACGTGVRTCPLDEFQCNN
    3640      3650  X   3660
```

2. US-08-121-713B-3 (1-7)
R43662 DEN1-S275/90 (ECACC V92042111).

```
ID   R43662 standard; Protein; 3396 AA.
AC   R43662;
DT   16-MAY-1994  (first entry)
DE   DEN1-S275/90 (ECACC V92042111).
KW   Dengue haemorrhagic fever; DHF; dengue fever; DF; dengue shock syndrome;
KW   DSS; DEN1 polypeptides.
OS   Dengue Fever Virus Type 1 strain S275/90.
FH   Key             Location/Qualifiers
FT   Protein         1..114
FT   /label= C
FT   Protein         15..114
FT   /label= C'
FT   Protein         115..205
FT   /label= PreM
FT   Protein         206..280
FT   /label= M
FT   Protein         281..774
FT   /label= E
FT   Protein         775..1128
FT   /label= NS1
FT   Protein         1129..1344
FT   /label= NS2A
FT   Protein         1345..1474
FT   /label= NS2B
FT   Protein         1475..2093
```

```
FT   /label= NS3
FT   Protein         2094..2242
FT   /label= NS4A
FT   Protein         2243..2492
FT   /label= NS4B
FT   Protein         2493..3396
FT   /label= NS5
PN   WO9322440-A.
PD   11-NOV-1993.
PF   28-APR-1993; CA0182.
PR   29-APR-1992; GB-009243.
PA   (UYSI-) UNIV SINGAPORE NAT.
PI   Chan Y,  Fu J,  Tan B,  Yap E,  Tan Y;
DR   WPI; 93-368799/46.
DR   N-PSDB; Q51476.
PT   New Dengue virus type 1 strain - used to obtain prods. for
PT   detection, diagnosis, vaccines and treatment involving virus
PS   Claim 9; Page 20-34; 55pp; English.
CC   DEN1 virus, strain S275/90 was isolated from the serum of a dengue
CC   haemorrhagic fever (DHF) patient.  RNA was isolated from the virus
CC   and used to prepare cDNA encoding DEN1 polypeptides.  Dengue Virus
CC   Type 1 prods. can be used for detection, diagnosis, vaccines
CC   (inactivated form) or treatment of DEN1 infections.  The sequences
CC   given in Q51477-86 are oligonucleotides used to prepare cDNA
CC   fragments corresp. to Dengue virus proteins, by PCR.
SQ   Sequence   3396 AA;
SQ   236A; 194R; 124N; 148D; 0  B; 60 C; 109Q; 220E; 0  Z; 279G; 74 H;
SQ   193I; 317L; 206K; 129M; 106F; 139P; 203S; 257T; 95 W; 74 Y; 233V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.65
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
   NSTHEMYWVSCGTGNIVSAVNMTSRML
      2710   X  2720      2730
```

3. US-08-121-713B-3 (1-7)
   R26052 APC gene product in familial adenomatous polyposis

```
ID   R26052 standard; Protein; 2843 AA.
AC   R26052;
DT   28-JAN-1993  (first entry)
DE   APC gene product in familial adenomatous polyposis.
KW   neoplasm; cancer; oncogene; tumour; growth; detection; diagnosis;
KW   prognosis; treatment; sporadic colorectal carcinomas; ss.
OS   Homo sapiens
PN   WO9213103-A.
PD   06-AUG-1992.
PF   16-JAN-1992; U00376.
PR   16-JAN-1991; GB-000963.
PR   08-AUG-1991; US-741940.
PA   (CANC-) CANCER INST.
PA   (ICIL ) IMPERIAL CHEM IND PLC.
PA   (UYJO ) UNIV.
PA   JOHNS HOPKINS.
PA   (UTAH ) UNIV UTAH.
```



```
PI   Albertsen H, Anand R, Carlson ML, Groden JL, Hedge PJ;
PI   Joslyng, Kinzler KW, Markham A, Nakamura Y, Thliveris A;
PI   Vogelstein B, Whiterl, Markham AF;
DR   WPI; 92-284685/34.
DR   N-PSDB; Q27234.
PT   Detection of somatic and germ-line alterations of human APC gene
PT   - used to diagnose, treat and study familial adenomatosus
PT   polyposis and sporadic colorectal cancer
PS   Disclosure; Page 47; 132pp; English.
CC   This sequence is encoded by the APC (Adenomatous Polyposis Coli)
CC   gene associated with tumorigenesis, found on chromosome 5q.
CC   The sequence may be mutated by deletions insertions, inversions, or
CC   point mutations of the gene. The APC gene is expressed in most normal
CC   tissues as well suggesting that APC is a tumour suppressor.
SQ   Sequence   2843 AA;
SQ   176A; 163R; 158N; 149D; 0  B; 38 C; 154Q; 208E; 0  Z; 149G; 67 H;
SQ   115I; 206L; 199K; 56 M; 47 F; 181P; 433S; 168T; 14 W; 50 Y; 112V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.65
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
   SHSLTIVSNACGTLWNLSARNPKDQEA
         680       690
```

4. US-08-121-713B-3 (1-7)
   P60053 Sequence of von Willebrand factor (vWF).

```
ID   P60053 standard; Protein; 2813 AA.
AC   P60053;
DT   22-JUL-1991  (first entry)
DE   Sequence of von Willebrand factor (vWF).
KW   Vascular injury; platelet plug formation.
OS   Homo sapiens.
PN   EP-197592-A.
PD   15-OCT-1986.
PF   26-MAR-1986; 200518.
PR   01-APR-1985; NL-000961.
PA   (VRIE-) STICHT VRIEND LANDS.
PA   (FRIN-) STICHT FRINDER RANT.
PI   Pannekoek H, Verwey CL, Diergaarde PJ, Hart MHL;
DR   WPI; 86-273504/42.
DR   N-PSDB; N60061.
PT   Recombinant cDNA plasmid or phage - contg. C-DNA fragment which
PT   codes for biological activity of human von Willebrand factor
PS   Disclosure; Fig 3; 37pp; English.
CC   vWF (glyco) protein having the AA sequence corresponding to the
CC   nucleotide sequence of 2518-8667 or 295-2517 of N60061 is claimed.
CC   Also claimed are new microorganisms, animal cell or human cell contg.
CC   the recombinant cDNA plasmid or phage; e.g. strain E.coli DH1 contg.
CC   the recombinant cDNA plasmid pSP8800vWF is deposited as C.B.S. No
CC   163.86.
SQ   Sequence   2813 AA;
SQ   160A; 137R; 101N; 160D; 0  B; 217C; 142Q; 181E; 0  Z; 207G; 77 H;
SQ   97 I; 233L; 104K; 55 M; 93 F; 173P; 201S; 146T; 27 W; 81 Y; 221V;
```

```
Initial Score    =      7  Optimized Score  =      7  Significance =  2.65
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    NCPKGQVYLQCGTPCNLTCRSLSYPDE
           660       670
```

5. US-08-121-713B-3 (1-7)
P60462 Sequence of human von Willebrand Factor (VWF) prec

```
 ID   P60462 standard; Protein; 2813 AA.
 AC   P60462;
 DT   25-JUN-1991  (first entry)
 DE   Sequence of human von Willebrand Factor (VWF) precursor.
 KW   Chronic renal failure; therapy; factor VIII C.
 OS   Homo sapiens.
 PN   WO8606096-A.
 PD   23-OCT-1986.
 PF   10-APR-1986; U00760.
 PR   11-APR-1985; US-722108.
 PA   (CHIL-) CHILDRENS MED CENT.
 PA   (GINS/) GINSBURG D.
 PI   Ginsburg D, Orkin SH, Kaufman RJ;
 DR   WPI; 86-291663/44.
 DR   N-PSDB; N60404.
 PT   Pure Von Willebrand Factor - produced using an expression vector
 PT   including a DNA sequence encoding functional VWF protein
 PS   Disclosure; Table 2, Pages 18-36A; 54pp; English.
 CC   cDNA clones pVWH33, pVWH5 and PVWE6 which span 9 kb pairs of DNA and
 CC   encompass the entire protein coding region of VWF, were selected to
 CC   construct full length cDNA (N60404). The pure VWF produced is useful
 CC   in the treatment of von Willebrand's disease (VWD) and the patients
 CC   with chronic renal failure whose abnormal bleeding times are
 CC   corrected by crude cryoprecipitate. Pure VWF can also be used to
 CC   carry, stabilise and improve the therapeutic efficacy of factor
 CC   VIII:C.
 SQ   Sequence   2813 AA;
 SQ   154A; 143R; 98 N; 155D; 0  B; 234C; 133Q; 181E; 0  Z; 205G; 70 H;
 SQ   95 I; 227L; 108K; 56 M; 89 F; 176P; 207S; 151T; 26 W; 79 Y; 226V;
```

```
Initial Score    =      7  Optimized Score  =      7  Significance =  2.65
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    NCPKGQVYLQCGTPCNLTCRSLSYPDE
           660       670
```

6. US-08-121-713B-3 (1-7)
R13887 Inositol-3-phosphate binding peptide.

```
 ID   R13887 standard; Protein; 2749 AA.
 AC   R13887;
```



```
 DT   27-NOV-1991  (first entry)
 DE   Inositol-3-phosphate binding peptide.
 KW   I-3-P; transformation; inositol.
 PN   J03183482-A.
 PD   09-AUG-1991.
 PF   14-DEC-1989; 324256.
 PR   14-DEC-1989; JP-324256.
 PA   (KYOW ) KYOWA HAKKO KOGYO KK.
 DR   WPI; 91-277584/38.
 DR   N-PSDB; Q13593.
 PT   New polypeptide having binding affinity to inositol-3-phosphate -
 PT   prepd. by culturing cell contg. recombinant plasmid comprising
 PT   DNA and vector DNA
 PS   Disclosure; Fig 2(1-3); 11pp; Japanese.
 CC   The sequence encoding this peptide may be included in a
 CC   plasmid/vector for transformation of a host cell and mass-prodn.
 CC   of the peptide.
 SQ   Sequence   2749 AA;
 SQ   146A; 155R; 144N; 154D; 0  B; 60 C; 128Q; 229E; 0  Z; 142G; 71 H;
 SQ   155I; 314L; 167K; 69 M; 123F; 99 P; 180S; 136T; 21 W; 71 Y; 185V;
```

```
Initial Score    =      7  Optimized Score  =      7  Significance =  2.65
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    IIFLMSFVGNCGTFTRGYRAMVLDVEF
      2370    X 2380      2390
```

7. US-08-121-713B-3 (1-7)
R60021 Fibrinogen-alpha.

```
 ID   R60021 standard; Protein; 2446 AA.
 AC   R60021;
 DT   23-FEB-1995  (first entry)
 DE   Fibrinogen-alpha.
 KW   Tissue binding; tissue sealing; wound healing; vulnerary;
 KW   tissue-binding domain; TBD; crosslinking domain; fibronectin;
 KW   fibrinogen-alpha; heparin-binding domain; collagen-binding domain;
 KW   cell-binding domain; hybrid protein.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   Domain          282..608
 FT   /label= collagen-binding_domain
 FT   /note= "acts as tissue-binding domain of hybrid
 FT   protein"
 FT   Domain          1812..2171
 FT   /label= heparin-binding_domain
 FT   /note= "acts as tissue-binding domain of hybrid
 FT   protein"
 PN   WO9416085-A.
 PD   21-JUL-1994.
 PF   30-DEC-1993; U12687.
 PR   30-DEC-1992; US-998271.
 PA   (ZYMO ) ZYMOGENETICS INC.
 PI   Irani MH;
 DR   WPI; 94-249231/30.
```

DR N-PSDB; Q70009.
PT New hybrid proteins for use in tissue sealing and wound healing -
PT comprising a tissue-binding domain from a protein covalently
PT linked to a crosslinking domain of another protein
PS Disclosure; Page 37-48; 87pp; English.
CC Hybrid proteins have a tissue-binding domain (TBD) from 1 protein
CC linked to a crosslinking domain from another protein. The TBD
CC comprises: aa 2-926, 928-1338 and especially 2-1336 of the sequence
CC given in R60019; the heparin-binding domain (aa 1812-2171 of R60021)
CC of fibronectin; the collagen-binding domain (aa 282-608 of R60021)
CC of fibronectin; or the cell-binding domain (aa 1357-1903 or 1532-
CC 1631 of R60020) of fibronectin. DNA encoding a fibronectin-
CC fibrinogen hybrid is given in Q70007, and sequences for fibronectin
CC and fibrinogen-alpha in Q70008 and Q70009, respectively.
SQ Sequence 2446 AA;
SQ 99 A; 125R; 99 N; 123D; 0 B; 63 C; 131Q; 142E; 0 Z; 204G; 48 H;
SQ 119I; 136L; 78 K; 27 M; 54 F; 191P; 198S; 267T; 40 W; 103Y; 199V;

Initial Score = 7 Optimized Score = 7 Significance = 2.65
Residue Identity = 42% Matches = 3 Mismatches = 4
Gaps = 0 Conservative Substitutions = 0

```
            X     X
            CGTXXXX
            |||
    SEGRRDNMKWCGTTQNYDADQKFGFCP
      440     X 450 X     460
```

8. US-08-121-713B-3 (1-7)
R28582 HCV amino acid sequence contg. antibody reactive p

ID R28582 standard; protein; 2436 AA.
AC R28582;
DT 22-MAR-1993 (first entry)
DE HCV amino acid sequence contg. antibody reactive peptides.
KW Hepatitis C virus; detection; peptides.
OS Hepatitis C virus.
FH Key Location/Qualifiers
FT Peptide 828..838
FT /note= "claimed peptide reactive to HCV antibody"
FT Peptide 1236..1261
FT /note= "claimed peptide reactive to HCV antibody"
FT Peptide 1254..1275
FT /note= "claimed peptide reactive to HCV antibody"
FT Peptide 1270..1295
FT /note= "claimed peptide reactive to HCV antibody"
FT Peptide 1288..1312
FT /note= "claimed peptide reactive to HCV antibody"
FT Peptide 1305..1325
FT /note= "claimed peptide reactive to HCV antibody"
FT Peptide 1318..1340
FT /note= "claimed peptide reactive to HCV antibody"
FT Peptide 1236..1275
FT /note= "claimed peptide reactive to HCV antibody"
PN J04288097-A.
PD 13-OCT-1992.
PF 07-NOV-1991; 301705.
PR 07-NOV-1991; JP-301705.
PA (OLYU) OLYMPUS OPTICAL CO LTD.

DR WPI; 92-387721/47.
PT New peptide(s) - are reactive to an antibody against type C
PT hepatitis virus, used to detect virus in patients
PS Disclosure; Fig 1; 11pp; Japanese.
CC The peptides (claimed) can be used to detect heptitis C virus (HCV)
CC antibody positive patients, post-transfusion hepatitis can be prevented
CC by screening a sample from a HCV antibody-positive patient with the
CC peptide.
SQ Sequence 2436 AA;
SQ 223A; 126R; 62 N; 105D; 0 B; 88 C; 75 Q; 105E; 0 Z; 189G; 52 H;
SQ 112I; 242L; 79 K; 45 M; 70 F; 174P; 168S; 185T; 53 W; 81 Y; 202V;

Initial Score = 7 Optimized Score = 7 Significance = 2.65
Residue Identity = 42% Matches = 3 Mismatches = 4
Gaps = 0 Conservative Substitutions = 0

```
            X     X
            CGTXXXX
            |||
    GPLTNSRGENCGTRRCRASGVLTTSCG
      2240    X  2250      2260
```

9. US-08-121-713B-3 (1-7)
R25135 HCV polypeptide 1.

ID R25135 standard; Protein; 2435 AA.
AC R25135;
DT 23-DEC-1992 (first entry)
DE HCV polypeptide 1.
KW Hepatitis C virus; blood transfusion.
OS Synthetic.
PN J04159298-A.
PD 02-JUN-1992.
PF 19-OCT-1990; 282431.
PR 19-OCT-1990; JP-282431.
PA (OLYU) OLYMPUS OPTICAL CO LTD.
DR WPI; 92-231947/28.
PT New peptides acting as antigenic analogues of human hepatitis C
PT virus - useful for detecting HCV antibody positive patients
PS Claim 1; Page 1; 14pp; Japanese.
CC The sequences given in R25135-36 are peptides from the hepatitis C
CC virus (HCV) which are recognised by the peptide sequences given in
CC R25130-24. These antigenic peptides can be used on their own or as
CC a mixture two different peptides. Using these peptides, HCV antibody
CC positive patients can be detected and hepatitis caused by blood
CC transfusion can be prevented.
SQ Sequence 2435 AA;
SQ 223A; 126R; 62 N; 105D; 0 B; 88 C; 76 Q; 106E; 0 Z; 188G; 52 H;
SQ 112I; 239L; 80 K; 45 M; 70 F; 174P; 168S; 185T; 53 W; 81 Y; 202V;

Initial Score = 7 Optimized Score = 7 Significance = 2.65
Residue Identity = 42% Matches = 3 Mismatches = 4
Gaps = 0 Conservative Substitutions = 0

```
            X     X
            CGTXXXX
            |||
    GPLTNSRGENCGTRRCRASGVLTTSCG
      2240    X  2250      2260
```

10. US-08-121-713B-3 (1-7)
R24306 Translation of ORF 2 contg. E.faecium protein VanS

ID R24306 standard; Protein; 2408 AA.
AC R24306;
DT 20-NOV-1992 (first entry)
DE Translation of ORF 2 contg. E.faecium protein VanS.
KW Glycopeptide antibiotic; vancomycin; teicoplanin; resistant;
KW D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;
KW inverted repeats; vanR; vanS; vanH; vanA; vanX;
KW open reading frame.
OS Enterococcus faecium BM4147.
FH Key Location/Qualifiers
FT Protein 727..1115
FT /label= VanS
FT /note= "see R24296"
PN WO9207942-A.
PD 14-MAY-1992.
PF 29-OCT-1991; F00855.
PR 31-OCT-1990; FR-013579.
PA (INSP) INST PASTEUR.
PI Arthur M, Courvalin P, Dutka-malen S, Molinas C;
DR WPI; 92-183677/22.
DR N-PSDB; Q25183.
PT Polypeptides involved in expression of glycopeptide antibiotic
PT resistance - useful in diagnosing presence of Gram-positive
PT enterococcal strains e.g. Enterococcus faecium and E gallinarum
PS Disclosure; Fig 5; 163pp; French.
CC A 7.3kb fragment of E.faecium DNA containing the five genes vanH,
CC vanA, vanX, vanR and vanS involved in antibiotic resistance was
CC translated in each of the three possible open reading frames.
CC Within ORF 2 there is the vanS gene. The "X"s in the sequence
CC indicate the position of nonsense codons.
CC See also Q25178-Q25182.
SQ Sequence 2408 AA;
SQ 120A; 200R; 100N; 70 D; 0 B; 78 C; 82 Q; 66 E; 0 Z; 118G; 52 H;
SQ 182I; 212L; 171K; 50 M; 97 F; 82 P; 198S; 120T; 28 W; 115Y; 110V;
SQ 157 Others;

Initial Score	=	7	Optimized Score	=	7	Significance =	2.65
Residue Identity	=	57%	Matches	=	4	Mismatches =	3
Gaps	=	0	Conservative Substitutions			=	0

```
            X     X
            CGTXXXX
            ||||
   QIRAFQSMYQCGTXIRDFRLYSSCAEE
1230      1240      1250
```

11. US-08-121-713B-3 (1-7)
R29939 Deduced from Lelystad Agent genome ORF 1A.

ID R29939 standard; Protein; 2396 AA.
AC R29939;
DT 28-APR-1993 (first entry)
DE Deduced from Lelystad Agent genome ORF 1A.
KW Mystery Swine Disease; MSD; Arteriviridae; coronavirus; RNA genome;

KW swine infertility and respiratory syndrome; CDI-NL-2.91;
KW Abortus Blauw; viral replicase; polymerase; open reading frame.
OS Lelystad Agent.
FH Key Location/Qualifiers
FT Modified site 257..259
FT /label= N-glycosylation_site
FT /note= "putative"
FT Modified site 842..844
FT /label= N-glycosylation_site
FT /note= "putative"
FT Modified site 2081..2083
FT /label= N-glycosylation_site
FT /note= "putative"
PN WO9221375-A.
PD 10-DEC-1992.
PF 05-JUN-1992; NL0096.
PR 06-JUN-1991; EP-201398.
PR 18-MAR-1992; EP-200781.
PA (DIER-) STICHTING CENT DIERGENEESKUNDIG INST.
PI Meulenberg JJM, Moormann RJM, Pol JMA, Terpstra C;
PI Wensvoort G;
DR WPI; 92-433379/52.
DR N-PSDB; Q32002.
PT Compsn. contg. source agent of unknown Swine disease - in live,
PT attenuated, dead or recombinant form, vaccine compsns. and
PT diagnostic kits, also causing agent specific nucleotide sequence
PS Claim 11; Fig 1; 77pp; English.
CC The genome of the Lelystad Agent consists of a genomic RNA molecule
CC (14.5 to 15.5kb) which replicates via a 3' nested set of subgenomic
CC RNAs. The nucleotide sequence was determined from overlapping cDNA
CC clones. The complete nucleotide sequence and the proteins deduced
CC from the 8 open reading frames (see R29939-R29946) are suitable for
CC vaccine development. Diagnosis of MSD will also be possible. ORF 1A
CC and ORF 1B are predicted to encode the viral replicase or polymerase,
CC ORFs 2-6 are predicted to encode structural viral membrane (envelope)
CC associated proteins and ORF 7 is predicted to encode the structural
CC viral nucleocapsid protein. The products deduced from ORFs 6 and 7
CC show significant similarity with VpX and Vp1, respectively, of Lactate
CC Dehydrogenase-Elevating Virus (LDV). The Lelystad Agent and LDV have
CC been classified with Equine Arteritis Virus in the new virus family,
CC the Arteriviridae which is part of the superfamily of coronaviruses.
SQ Sequence 2396 AA;
SQ 209A; 128R; 66 N; 115D; 0 B; 72 C; 85 Q; 105E; 0 Z; 183G; 54 H;
SQ 82 I; 256L; 89 K; 41 M; 102F; 173P; 199S; 139T; 46 W; 46 Y; 206V;

Initial Score	=	7	Optimized Score	=	7	Significance =	2.65
Residue Identity	=	42%	Matches	=	3	Mismatches =	4
Gaps	=	0	Conservative Substitutions			=	0

```
            X     X
            CGTXXXX
            |||
   TGPILCHVEHCGTESGDSSSPLDLSDA
   810      820   X   830
```

12. US-08-121-713B-3 (1-7)
P70373 Human fibronectin gene product.

ID P70373 standard; protein; 2327 AA.

```
AC   P70373;
DT   11-MAR-1991  (first entry)
DE   Human fibronectin gene product.
KW   FN; collagen; fibrin; heparin.
OS   Homo sapiens.
PN   EP-207751-A.
PD   07-JAN-1987.
PF   27-JUN-1986; 304998.
PR   28-JUN-1985; GB-016421.
PA   (DELT-) DELTA BIOTECHN.
PI   Baralle FE;
DR   WPI; 87-001441/01.
DR   N-PSDB; N70596.
PT   New fibronectin polypeptide sequence with affinity for collagen
PT   etc. - useful for targetting therapeutic substances on natural
PT   fibrin, for use in affinity purificn. of polypeptide(s) etc.
PS   Claim 11; Fig 3A; 32pp; English.
CC   The product may be expressed from a transformed micro-organism,
CC   esp. E.coli.
CC   FN binds to fibrin, heparin and Staphylococcus aureus, and may be
CC   used to target a therapuetic agent onto natural fibrin eg. a blood
CC   clot. It may also be used in affinity purification of a polypeptide,
CC   conjugated to the collagen binding site of FN and immobilised on a
CC   collagen surface.
SQ   Sequence   2327 AA;
SQ   93 A; 122R; 97 N; 117D; 0  B; 62 C; 128Q; 137E; 0  Z; 190G; 48 H;
SQ   108I; 122L; 77 K; 26 M; 52 F; 184P; 185S; 253T; 39 W; 98 Y; 189V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.65
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    SEGRRDNMKWCGTTQNYDADQKFGFCP
    410       420   X   430
```

13. US-08-121-713B-3 (1-7)
    R15468 Human fibronectin.

```
ID   R15468 standard; Protein; 2327 AA.
AC   R15468;
DT   12-MAR-1992  (first entry)
DE   Human fibronectin.
KW   Fibrin-imaging; atherosclerosis; thrombus inhibitor.
OS   Homo sapiens.
PN   WO9117765-A.
PD   28-NOV-1991.
PF   21-MAY-1991; U03584.
PR   21-MAY-1990; US-526397.
PA   (BIOT-) BIO-TECHN GEN CORP.
PI   Vogel T, Levanon A, Werber M, Guy R, Panet A, Hartman J;
PI   Shaked H.
DR   WPI; 91-369004/50.
DR   N-PSDB; Q15214.
PT   New fibrin binding domain polypeptide(s) - useful in imaging
PT   fibrin-contg. substances, to inhibit thrombus formation and treat
PT   wounds
```



```
PS   Disclosure; Fig 2; 191pp; English.
CC   The amino acid sequence is that of human fibronectin, this can be used
CC   to derive polypeptides which are identical to part of the fibrin-
CC   binding domain (FBD) of fibronectin. These polypeptides can be used
CC   to inhibit thrombus formation; or (coupled to a thrombolytic agent)
CC   to induce thrombolysis, or to treat wounds, e.g. in skin, eyes or
CC   tendons (in conjunction with a polypeptide which includes a part of
CC   the cell-binding domain (CBD) of fibronectin). These polypeptides are
CC   easier to prepare than the full 31kD polypeptide. It can also be
CC   used to image fibrin-contg. materials, esp. a thrombus or athero-
CC   sclerotic plaque, pref. using a gamma counter.
SQ   Sequence   2327 AA;
SQ   93 A; 122R; 97 N; 117D; 0  B; 62 C; 127Q; 137E; 0  Z; 190G; 49 H;
SQ   108I; 122L; 77 K; 26 M; 52 F; 184P; 186S; 252T; 39 W; 98 Y; 189V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.65
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    SEGRRDNMKWCGTTQNYDADQKFGFCP
    410       420   X   430
```

14. US-08-121-713B-3 (1-7)
    P81048 Sequence encoded by Rhinovirus 2 (HRV2) genome cDN

```
ID   P81048 standard; protein; 2150 AA.
AC   P81048;
DT   22-MAR-1991  (first entry)
DE   Sequence encoded by Rhinovirus 2 (HRV2) genome cDNA
KW   Passive immunity; diagnosis; therapy; ss.
OS   Rhinovirus.
FH   Key             Location/Qualifiers
FT   Protein         1..69
FT   /label=VP4
FT   Protein         70..330
FT   /label=VP2
FT   Protein         331..567
FT   /label=VP3
FT   Protein         568..856
FT   /label=VP1
FT   Protein         857..882
FT   /label=?
FT   /note="protein named '?'"
FT   Protein         883..992
FT   /label=P2-A
FT   Protein         993..1087
FT   /label=P2-B
FT   Protein         1088..1409
FT   /label=P2-C
FT   Protein         1410..1486
FT   /label=P3-A
FT   Protein         1487..1507
FT   /label=VPg
FT   Protein         1508..1690
FT   /label=PROTEASE
FT   Protein         1691..2150
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FT   /label=POLYMERASE
PN   EP-261403-A.
PD   30-MAR-1988.
PF   20-AUG-1987; 112104.
PR   17-JAN-1987; DE-701301.
PA   (BOEH) Boehringer Ingelheim.
PI   Duechler M, Skern T, Sommergruber W, Neubauer C, Grundler P, Blaas
PI   D, Kuchler E, Frasei L, Zorn M.
DR   WPI; 88-085735/13.
DR   N-PSDB; N81393.
PT   New DNA corresponding to viral RNA of rhino-virus HRV89 - useful for
PT   prodn. of polypeptide(s) for stimulating immune system against HRV
PT   89.
PS   Example; Fig 14; 66pp; German..
CC   DNA molecules corresponding to all or part of the RNA of rhinovirus
CC   strain HRV89 (Fig 4, N81390) is claimed, esp. the portion encoding
CC   the viral proteins VP1-VP4, P2A-P2C, P3A-P3C. Also claimed are the
CC   polypeptides encoded by any of these DNA molecules. The polypeptides
CC   are used for stimulating a protective immune response and for
CC   blocking cellular receptors. Ab are useful  for assay and for
CC   purificn. of the corresp. antigen, and can also be used for the
CC   therapeutic and diagnostic applications.
SQ   Sequence   2150 AA;
SQ   119A; 86 R; 120N; 124D; 0  B; 48 C; 71 Q; 102E; 0  Z; 124G; 60 H;
SQ   181I; 163L; 133K; 49 M; 89 F; 120P; 162S; 146T; 29 W; 93 Y; 131V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.65
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    TGSLRFSFMFCGTANTTVKLLLAYTPP
  440       450     X 460


15. US-08-121-713B-3 (1-7)
    R05127       Complete human rhinovirus 2.

ID   R05127 standard; protein; 2150 AA.
AC   R05127;
DT   17-JUL-1990  (first entry)
DE   Complete human rhinovirus 2.
KW   Human rhinovirus 2.
FH   Key             Location/Qualifiers
FT   Peptide         1..69
FT   /label=VP4
FT   Peptide         70..330
FT   /label=VP2
FT   Peptide         331..567
FT   /label=VP3
FT   Peptide         568..852
FT   /label=VP1
FT   Peptide         853..967
FT   /label=P2-A
FT   Peptide         993..1087
FT   /label=P2-B
FT   Peptide         1088..1486
FT   /label=P2-C
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FT   Peptide         1487..1507
FT   /label=VPg
FT   Protein         1508..1690
FT   /label=Protease
FT   Protein         1691..2150
FT   /label=Polymerase
PN   WO9001061-A.
PD   08-FEB-1990.
PF   22-JUL-1989; 0000861.
PR   24-JUN-1989; DE-920753.
PR   24-JUN-1989; DE-825189.
PA   (BOEH) Boehringer Ingelheim.
PI   Duelcher M, Skern T, Blaas D, Berger B, Sommergruber W, Keuchler E.
DR   WPI; 90-067175/09.
DR   N-PSDB; Q03418.
PT   New plasmid containing complete cDNA of human rhinovirus 2 under control
PT   of RNA polymerase promoter, transcribable in vitro to infectious RNA.
PS   Disclosure; Fig 3A-3E; 33pp; German.
CC   The HRV2 cDNA transcribed to infectious RNA allows study of
CC   viral behaviour. Effects of deletions, insertions or exchanges of amino
CC   acids can be examined directly and quantitatively. Viral polypeptides
CC   expressed by these plasmids can be used therapeutically, eg. to stimulate
CC   the immune system.
SQ   Sequence   2150 AA;
SQ   119 A;  86 R; 120 N; 124 D;  0 B;  48 C;  71 Q; 102 E;  0 Z; 124 G; 60 H;
SQ   181 I; 163 L; 133 K;  49 M; 89 F; 120 P; 162 S; 146 T; 29 W;  93 Y;131 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.65
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    TGSLRFSFMFCGTANTTVKLLLAYTPP
  440       450     X 460
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq3pir.res made by  on Fri 19 May 95 8:52:13-PDT.


Query sequence being compared:US-08-121-713B-3 (1-7)
Number of sequences searched:                75511
Number of scores above cutoff:                4999

      Results of the initial comparison of US-08-121-713B-3 (1-7) with:
   Data bank : PIR 43, all entries

100000-
      -
N     -
U50000-                                              *
M     -
B     -
E     -
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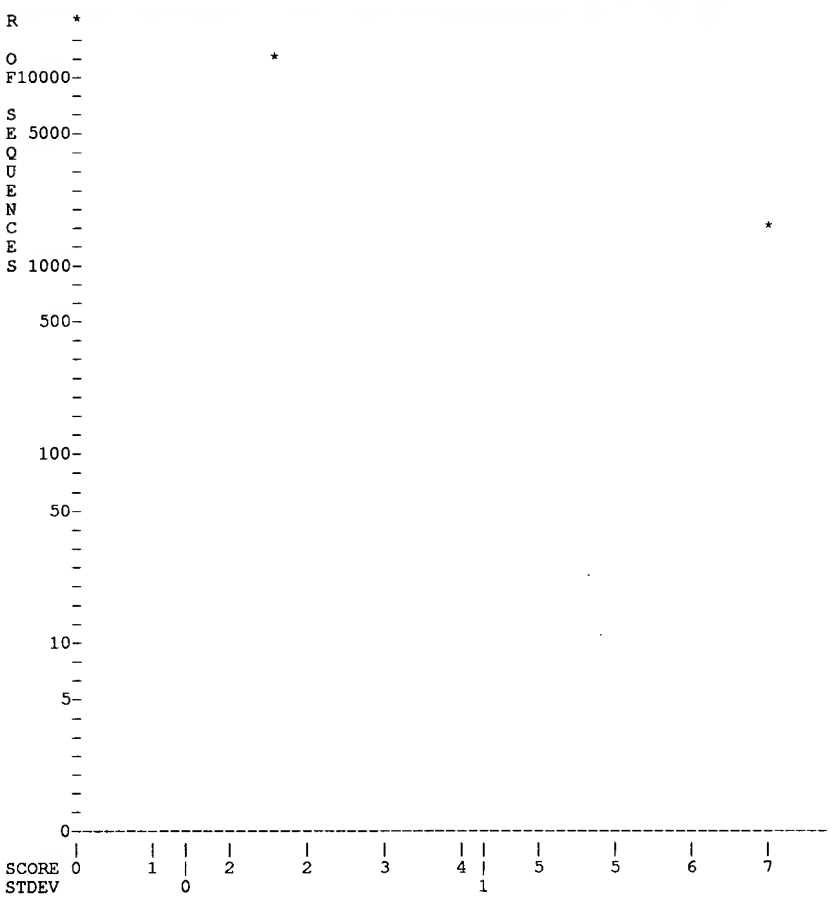

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

	Mean	Median	Standard Deviation
Scores:	3	6	2.18

	CPU	Total Elapsed
Times:	00:01:08.06	00:01:09.00

Number of residues: 22468834
Number of sequences searched: 75511
Number of scores above cutoff: 4999

Cut-off raised to 5.
Cut-off raised to 6.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

1473 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. IJFFTM	cadherin-related tumor suppre	5147	7	7	1.84	0
2. S02392	LDL receptor-related protein	4544	7	7	1.84	0
3. S25021	probable polyketide synthase	4427	7	7	1.84	0
4. S28600	hypothetical protein a - huma	4085	7	7	1.84	0
5. A40701	tenascin-X precursor - human	3566	7	7	1.84	0
6. A46112	genome polyprotein - rice tun	3473	7	7	1.84	0
7. S27927	polyprotein - rice tungro bac	3473	7	7	1.84	0
8. A42551	genome polyprotein - dengue v	3396	7	7	1.84	0
9. GNWVD3	genome polyprotein - dengue v	3390	7	7	1.84	0
10. S37536	macrogolgin - human	3259	7	7	1.84	0
11. S27852	hypothetical protein DGF-1 -	3229	7	7	1.84	0
12. A48450	putative cell-surface protein	3229	7	7	1.84	0
13. A44062	genome polyprotein - pepper m	3068	7	7	1.84	0
14. JQ1917	polyprotein - parsnip yellow	3027	7	7	1.84	0
15. B39658	polyposis coli protein DP2.5	2844	7	7	1.84	0
16. RBHUAP	adenomatous polyposis coli pr	2843	7	7	1.84	0
17. VWHU	von Willebrand factor precurs	2813	7	7	1.84	0
18. ACMSIT	inositol-trisphosphate recept	2749	7	7	1.84	0
19. A36579	inositol 1,4,5-triphosphate r	2749	7	7	1.84	0
20. B36579	inositol 1,4,5-triphosphate r	2734	7	7	1.84	0
21. A23475	G surface protein - Parameciu	2718	7	7	1.84	0
22. A34203	DNA-binding protein PRDII-BF1	2717	7	7	1.84	0
23. S28261	kinesin-related protein CENP-	2663	7	7	1.84	0
24. VFIHB2	RNA-directed RNA polymerase (	2652	7	7	1.84	0
25. A30788	mannose 6-phosphate receptor	2499	7	7	1.84	0
26. A28372	mannose 6-phosphate receptor	2491	7	7	1.84	0
27. A43908	fibronectin - African clawed	2481	7	7	1.84	0
28. S14428	fibronectin precursor - rat	2477	7	7	1.84	0
29. RNZQ2L	DNA-directed RNA polymerase (	2452	7	7	1.84	0
30. B36861	RNA-directed RNA polymerase (	2396	7	7	1.84	0
31. FNHU	fibronectin precursor - human	2386	7	7	1.84	0
32. S48405	hypothetical protein - yeast	2376	7	7	1.84	0
33. B47447	Ca2+ channel alpha 1 subunit	2326	7	7	1.84	0
34. FNBO	fibronectin - bovine	2265	7	7	1.84	0
35. S29236	calcium channel protein BII-1	2259	7	7	1.84	0

36. S06188	genome polyprotein 1 - grapev	2252	7	7	1.84	0
37. A47447	Ca2+ channel alpha 1 subunit	2223	7	7	1.84	0
38. A37490	calcium channel alpha 1 subun	2222	7	7	1.84	0
39. A41098	calcium channel protein alpha	2212	7	7	1.84	0
40. JQ1977	glutamate synthase (NADH) (EC	2194	7	7	1.84	0
41. S29237	calcium channel protein BII-2	2178	7	7	1.84	0
42. GNNY1B	genome polyprotein - human rh	2157	7	7	1.84	0
43. GNNYH2	genome polyprotein - human rh	2150	7	7	1.84	0
44. A35672	crumbs protein - fruit fly (D	2139	7	7	1.84	0
45. AGCH	agrin precursor - chicken	1955	7	7	1.84	0

1. US-08-121-713B-3 (1-7)
   IJFFTM cadherin-related tumor suppressor precursor - frui

```
ENTRY            IJFFTM     #type complete
TITLE            cadherin-related tumor suppressor precursor - fruit fly
                   (Drosophila melanogaster)
ORGANISM         #formal_name Drosophila melanogaster
DATE             30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                   08-Dec-1994
ACCESSIONS       A41087; B41087
REFERENCE        A41087
   #authors      Mahoney, P.A.; Weber, U.; Onofrechuk, P.; Biessmann, H.;
                   Bryant, P.J.; Goodman, C.S.
   #journal      Cell (1991) 67:853-868
   #title        The fat tumor suppressor gene in Drosophila encodes a novel
                   member of the cadherin gene superfamily.
   #cross-references MUID:92069752
   #accession    A41087
      ##molecule_type mRNA
      ##residues      143-485;1279-5147 ##label MAH
      ##cross-references GB:M80537
   #accession    B41087
      ##molecule_type DNA
      ##residues      1-142;487-1278 ##label MA2
      ##cross-references GB:M80537
      ##note          1229-Gly and 1233-Ser were also found
GENETICS
   #gene         fat
CLASSIFICATION   #superfamily cadherin-related tumor suppressor; cadherin
                   repeat homology; EGF homology
KEYWORDS         calcium binding; cell adhesion; duplication; transmembrane
                   protein

FEATURE
   1-35              #domain signal sequence #status predicted #label SIG\
   36-5147           #product cadherin-related tumor suppressor #status
                       predicted #label MAT\
   36-4583           #domain extracellular #label EXT\
   51-156            #domain cadherin repeat homology #label CR1\
   157-270           #domain cadherin repeat homology #label CR2\
   271-382           #domain cadherin repeat homology #label CR3\
   387-494           #domain cadherin repeat homology #label CR4\
   495-599           #domain cadherin repeat homology #label CR5\
   600-708           #domain cadherin repeat homology #label CR6\
   718-822           #domain cadherin repeat homology #label CR7\
   832-942           #domain cadherin repeat homology #label CR8\
   946-1049          #domain cadherin repeat homology #label CR9\
   1050-1153         #domain cadherin repeat homology #label C10\
   1154-1278         #domain cadherin repeat homology #label C11\
```



```
   1279-1384         #domain cadherin repeat homology #label C12\
   1385-1489         #domain cadherin repeat homology #label C13\
   1490-1601         #domain cadherin repeat homology #label C14\
   1605-1713         #domain cadherin repeat homology #label C15\
   1715-1823         #domain cadherin repeat homology #label C16\
   1824-1922         #domain cadherin repeat homology #label C17\
   1923-2027         #domain cadherin repeat homology #label C18\
   2028-2167         #domain cadherin repeat homology #label C19\
   2168-2278         #domain cadherin repeat homology #label C20\
   2279-2384         #domain cadherin repeat homology #label C99\
   2387-2491         #domain cadherin repeat homology #label C21\
   2492-2596         #domain cadherin repeat homology #label C22\
   2597-2703         #domain cadherin repeat homology #label C23\
   2705-2810         #domain cadherin repeat homology #label C24\
   2811-2913         #domain cadherin repeat homology #label C25\
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   3335-3439         #domain cadherin repeat homology #label C30\
   3440-3545         #domain cadherin repeat homology #label C31\
   3546-3651         #domain cadherin repeat homology #label C32\
   3652-3757         #domain cadherin repeat homology #label C33\
   3954-4010         #domain EGF homology #label EG1\
   4017-4048         #domain EGF homology #label EG2\
   4056-4089         #domain EGF homology #label EG3\
   4096-4127         #domain EGF homology #label EG4\
   4584-4609         #domain transmembrane #label TMM\
   4610-5147         #domain intracellular #label INT
SUMMARY          #length 5147  #molecular-weight 564895  #checksum 6994
SEQUENCE

Initial Score     =      7  Optimized Score  =      7  Significance =  1.84
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps              =      0  Conservative Substitutions             =     0

             X     X
             CGTXXXX
             |||
    SYTLNITASDCGTPSLSTTVLYNVLVV
       1460   X  1470      1480
```

2. US-08-121-713B-3 (1-7)
   S02392 LDL receptor-related protein precursor - human

```
ENTRY            S02392     #type complete
TITLE            LDL receptor-related protein precursor - human
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
                   28-Oct-1994
ACCESSIONS       S02392; S30027; S12538
REFERENCE        S02392
   #authors      Herz, J.; Hamann, U.; Rogne, S.; Myklebost, O.; Gausepohl,
                   H.; Stanley, K.K.
   #journal      EMBO J. (1988) 7:4119-4127
   #title        Surface location and high affinity for calcium of a 500-kd
                   liver membrane protein closely related to the LDL-receptor
                   suggest a physiological role as lipoprotein receptor.
   #cross-references MUID:89210795
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```
    #accession    S02392
       ##molecule_type mRNA
       ##residues      1-4544 ##label HER
       ##cross-references EMBL:X13916
       ##note         the nucleotide sequence is not given in this paper
REFERENCE        S30027
   #authors      Kristensen, T.
   #submission   submitted to the EMBL Data Library, October 1990
   #accession    S30027
      ##molecule_type mRNA
      ##residues      3275-3864 ##label KRI
      ##cross-references EMBL:X55077
REFERENCE        S12538
   #authors      Herz, J.; Kowal, R.C.; Goldstein, J.L.; Brown, M.S.
   #journal      EMBO J. (1990) 9:1769-1776
   #title        Proteolytic processing of the 600 kd low density lipoprotein
                  receptor-related protein (LRP) occurs in a trans-Golgi
                  compartment.
   #cross-references MUID:90269210
   #contents     annotation; site of proteolytic cleavage
CLASSIFICATION   #superfamily LDL receptor ligand-binding repeat homology; LDL
                  receptor/EGF precursor homology; LDL receptor
                  YWTD-containing repeat homology
KEYWORDS         calcium binding; glycoprotein; heterodimer; transmembrane
                  protein
FEATURE
   1-19              #domain signal sequence #status predicted #label SIG\
   20-3943           #product LDL receptor-related protein 515K chain #status
                       predicted #label 515K\
   27-64             #domain LDL receptor ligand-binding repeat homology
                       #label LDL1\
   72-108            #domain LDL receptor ligand-binding repeat homology
                       #label LDL2\
   292-334           #domain LDL receptor YWTD-containing repeat homology
                       #label YW1\
   335-378           #domain LDL receptor YWTD-containing repeat homology
                       #label YW2\
   379-420           #domain LDL receptor YWTD-containing repeat homology
                       #label YW3\
   571-613           #domain LDL receptor YWTD-containing repeat homology
                       #label YW4\
   614-659           #domain LDL receptor YWTD-containing repeat homology
                       #label YW5\
   660-710           #domain LDL receptor YWTD-containing repeat homology
                       #label YW6\
   711-752           #domain LDL receptor YWTD-containing repeat homology
                       #label YW7\
   753-799           #domain LDL receptor YWTD-containing repeat homology
                       #label YW8\
   854-890           #domain LDL receptor ligand-binding repeat homology
                       #label LDL3\
   895-931           #domain LDL receptor ligand-binding repeat homology
                       #label LDL4\
   936-971           #domain LDL receptor ligand-binding repeat homology
                       #label LDL5\
   976-1011          #domain LDL receptor ligand-binding repeat homology
                       #label LDL6\
   1015-1051         #domain LDL receptor ligand-binding repeat homology
                       #label LDL7\
   1062-1097         #domain LDL receptor ligand-binding repeat homology
```



```
                       #label LDL8\
   1104-1140         #domain LDL receptor ligand-binding repeat homology
                       #label LDL9\
   1145-1182         #domain LDL receptor ligand-binding repeat homology
                       #label LDLA\
   1309-1355         #domain LDL receptor YWTD-containing repeat homology
                       #label YW9\
   1356-1398         #domain LDL receptor YWTD-containing repeat homology
                       #label YWA\
   1399-1445         #domain LDL receptor YWTD-containing repeat homology
                       #label YWB\
   1446-1488         #domain LDL receptor YWTD-containing repeat homology
                       #label YWC\
   1489-1531         #domain LDL receptor YWTD-containing repeat homology
                       #label YWD\
   1582-1626         #domain LDL receptor YWTD-containing repeat homology
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   1627-1669         #domain LDL receptor YWTD-containing repeat homology
                       #label YWF\
   1670-1713         #domain LDL receptor YWTD-containing repeat homology
                       #label YWG\
   1714-1753         #domain LDL receptor YWTD-containing repeat homology
                       #label YWH\
   1754-1794         #domain LDL receptor YWTD-containing repeat homology
                       #label YWJ\
   1797-1846         #domain LDL receptor YWTD-containing repeat homology
                       #label YWK\
   1934-1976         #domain LDL receptor YWTD-containing repeat homology
                       #label YWL\
   1977-2019         #domain LDL receptor YWTD-containing repeat homology
                       #label YWM\
   2020-2063         #domain LDL receptor YWTD-containing repeat homology
                       #label YWN\
   2064-2105         #domain LDL receptor YWTD-containing repeat homology
                       #label YWO\
   2106-2151         #domain LDL receptor YWTD-containing repeat homology
                       #label YWP\
   2199-2252         #domain LDL receptor YWTD-containing repeat homology
                       #label YWQ\
   2253-2294         #domain LDL receptor YWTD-containing repeat homology
                       #label YWR\
   2344-2388         #domain LDL receptor YWTD-containing repeat homology
                       #label YWS\
   2389-2429         #domain LDL receptor YWTD-containing repeat homology
                       #label YWT\
   2430-2473         #domain LDL receptor YWTD-containing repeat homology
                       #label YWU\
   2524-2561         #domain LDL receptor ligand-binding repeat homology
                       #label LDLB\
   2566-2600         #domain LDL receptor ligand-binding repeat homology
                       #label LDLC\
   2605-2639         #domain LDL receptor ligand-binding repeat homology
                       #label LDLD\
   2644-2688         #domain LDL receptor ligand-binding repeat homology
                       #label LDLE\
   2696-2730         #domain LDL receptor ligand-binding repeat homology
                       #label LDLF\
   2734-2769         #domain LDL receptor ligand-binding repeat homology
                       #label LDLG\
   2774-2812         #domain LDL receptor ligand-binding repeat homology
```

```
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    2818-2853     #domain LDL receptor ligand-binding repeat homology
                  #label LDLI\
    2858-2897     #domain LDL receptor ligand-binding repeat homology
                  #label LDLJ\
    2904-2939     #domain LDL receptor ligand-binding repeat homology
                  #label LDLK\
    3069-3113     #domain LDL receptor YWTD-containing repeat homology
                  #label YWV\
    3114-3156     #domain LDL receptor YWTD-containing repeat homology
                  #label YWW\
    3157-3200     #domain LDL receptor YWTD-containing repeat homology
                  #label YWX\
    3201-3241     #domain LDL receptor YWTD-containing repeat homology
                  #label YWY\
    3242-3283     #domain LDL receptor YWTD-containing repeat homology
                  #label YWZ\
    3334-3369     #domain LDL receptor ligand-binding repeat homology
                  #label LDLL\
    3374-3408     #domain LDL receptor ligand-binding repeat homology
                  #label LDLM\
    3413-3448     #domain LDL receptor ligand-binding repeat homology
                  #label LDLN\
    3453-3489     #domain LDL receptor ligand-binding repeat homology
                  #label LDLO\
    3494-3531     #domain LDL receptor ligand-binding repeat homology
                  #label LDLP\
    3536-3570     #domain LDL receptor ligand-binding repeat homology
                  #label LDLQ\
    3575-3609     #domain LDL receptor ligand-binding repeat homology
                  #label LDLR\
    3613-3647     #domain LDL receptor ligand-binding repeat homology
                  #label LDLS\
    3654-3690     #domain LDL receptor ligand-binding repeat homology
                  #label LDLT\
    3695-3731     #domain LDL receptor ligand-binding repeat homology
                  #label LDLU\
    3741-3776     #domain LDL receptor ligand-binding repeat homology
                  #label LDLV\
    3912-3969     #domain LDL receptor YWTD-containing repeat homology
                  #label YWZU\
    3944-4544     #product LDL receptor-related protein 85K chain #status
                    predicted #label 85K\
    3944-4420     #domain extracellular #status predicted #label EXT\
    3970-4012     #domain LDL receptor YWTD-containing repeat homology
                  #label YWZX\
    4013-4056     #domain LDL receptor YWTD-containing repeat homology
                  #label YWZY\
    4057-4100     #domain LDL receptor YWTD-containing repeat homology
                  #label YWZZ\
    4421-4444     #domain transmembrane #status predicted #label TMM\
    4445-4544     #domain intracellular #status predicted #label INT\
    166,2998      #modified_site erythro-beta-hydroxyasparagine (Asn)
                    #status predicted\
    2958          #modified_site erythro-beta-hydroxyaspartic acid (Asp)
                    #status predicted\
    4075,4125,4278 #binding_site carbohydrate (Asn) (covalent) #status
                    predicted
SUMMARY          #length 4544  #molecular-weight 504571  #checksum 662
SEQUENCE
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Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    DCMDGSDEEACGTGVRTCPLDEFQCNN
    3640      3650  X   3660


3. US-08-121-713B-3 (1-7)
   S25021       probable polyketide synthase - Bacillus subtilis

 ENTRY            S25021     #type complete
 TITLE            probable polyketide synthase - Bacillus subtilis
 ORGANISM         #formal_name Bacillus subtilis
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S25021
 REFERENCE        S25021
    #authors      Scotti, C.; Piatti, M.; Cuzzoni, A.; Tognoni, A.; Grandi, G.;
                    Galizzi, A.; Albertini, A.M.
    #submission   submitted to the EMBL Data Library, July 1992
    #description  A Bacillus subtilis large ORF coding for a polypeptide highly
                    similar to polyketide synthases.
    #accession    S25021
       ##status       preliminary
       ##residues     1-4427 ##label SCO
       ##cross-references EMBL:Z14098
 SUMMARY          #length 4427  #molecular-weight 493405  #checksum 2187
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    HVAGAIDLIGCGTSHEHSMGWINWLQK
      3440    X 3450      3460


4. US-08-121-713B-3 (1-7)
   S28600       hypothetical protein a - human coronavirus

 ENTRY            S28600     #type complete
 TITLE            hypothetical protein a - human coronavirus
 ORGANISM         #formal_name human coronavirus
 DATE             25-Feb-1994; #sequence_revision 25-Feb-1994; #text_change
                    25-Feb-1994
 ACCESSIONS       S28600
 REFERENCE        S28600
    #authors      Herold, J.; Raabe, T.; Schelle-Prinz, B.; Siddell, S.G.
    #submission   submitted to the EMBL Data Library, December 1992
    #accession    S28600
       ##status       preliminary
       ##residues     1-4085 ##label HER
```

```
        ##cross-references EMBL:X69721
 SUMMARY          #length 4085  #molecular-weight 454209  #checksum 8951
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    NDGRVANGYVCGTGLWNLVFNILSMFS
    2720      2730  X   2740
```

5. US-08-121-713B-3 (1-7)
   A40701 tenascin-X precursor - human

```
 ENTRY            A40701     #type complete
 TITLE            tenascin-X precursor - human
 ORGANISM         #formal_name Homo sapiens #common_name man
 DATE             03-May-1994 #sequence_revision 03-May-1994 #text_change
                    02-Aug-1994
 ACCESSIONS       A40701; A33725
 REFERENCE        A40701
    #authors      Bristow, J.; Tee, M.K.; Gitelman, S.E.; Mellon, S.H.; Miller,
                    W.L.
    #journal      J. Cell Biol. (1993) 122:265-278
    #title        Tenascin-X: a novel extracellular matrix protein encoded by
                    the human XB gene overlapping P450c21B.
    #accession    A40701
       ##status        preliminary
       ##molecule_type DNA
       ##residues      1-3566 ##label BRI
       ##cross-references EMBL:X71937
 REFERENCE        A33725
    #authors      Morel, Y.; Bristow, J.; Gitelman, S.E.; Miller, W.L.
    #journal      Proc. Natl. Acad. Sci. U.S.A. (1989) 86:6582-6586
    #title        Transcript encoded on the opposite strand of the human
                    steroid 21-hydroxylase/complement component C4 gene locus.
    #cross-references MUID:89367293
    #accession    A33725
       ##molecule_type mRNA
       ##residues      2748-3199,'V',3201-3298,'E',3299-3314,'G',3316-3566
                        ##label MOR
       ##cross-references GB:M25813
 GENETICS
    #gene         XB
 KEYWORDS         extracellular matrix; glycoprotein; heptad repeat
 SUMMARY          #length 3566  #molecular-weight 385618  #checksum 7433
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    MCWPGYTGRDCGTRACPGDCRGRGRCV
```



```
          490 X     500
```

6. US-08-121-713B-3 (1-7)
   A46112 genome polyprotein - rice tungro spherical virus (

```
 ENTRY            A46112     #type complete
 TITLE            genome polyprotein - rice tungro spherical virus (strain Los
                    Banos)
 ORGANISM         #formal_name rice tungro spherical virus
 DATE             17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
                    10-Mar-1994
 ACCESSIONS       A46112
 REFERENCE        A46112
    #authors      Shen, P.; Kaniewska, M.; Smith, C.; Beachy, R.N.
    #journal      Virology (1993) 193:621-630
    #title        Nucleotide sequence and genomic organization of rice tungro
                    spherical virus.
    #accession    A46112
       ##molecule_type genomic RNA
       ##residues      1-3473 ##label SHE
       ##cross-references GB:S57835
 CLASSIFICATION   #superfamily rice tungro spherical virus genome polyprotein
 KEYWORDS         polyprotein
 SUMMARY          #length 3473  #molecular-weight 390260  #checksum 8842
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    VFRTFGVLRLCGTYVCMPAHYLDEITS
          2670      2680
```

7. US-08-121-713B-3 (1-7)
   S27927 polyprotein - rice tungro bacilliform virus

```
 ENTRY            S27927     #type complete
 TITLE            polyprotein - rice tungro bacilliform virus
 ORGANISM         #formal_name rice tungro bacilliform virus, RTBV
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S27927
 REFERENCE        S27927
    #authors      Shen, P.; Kaniewska, M.; Smith, C.; Beachy, R.N.
    #submission   submitted to the EMBL Data Library, June 1992
    #accession    S27927
       ##status        preliminary
       ##residues      1-3473 ##label SHE
       ##cross-references EMBL:M95497
 SUMMARY          #length 3473  #molecular-weight 390260  #checksum 8842
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0
```

```
            X     X
            CGTXXXX
            |||
   VFRTFGVLRLCGTYVCMPAHYLDEITS
         2670      2680
```

8. US-08-121-713B-3 (1-7)
   A42551 genome polyprotein - dengue virus type 1 (strain S

```
ENTRY            A42551     #type complete
TITLE            genome polyprotein - dengue virus type 1 (strain Singapore
                   S275/90)
CONTAINS         capsid protein; envelope protein; membrane protein;
                   nonstructural protein NS1; nonstructural protein NS2a;
                   nonstructural protein NS2b; nonstructural protein NS3;
                   nonstructural protein NS4a; nonstructural protein NS4b;
                   nonstructural protein NS5
ORGANISM         #formal_name dengue virus type 1
DATE             30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                   09-Sep-1994
ACCESSIONS       A42551
REFERENCE        A42551
   #authors      Fu, J.; Tan, B.H.; Yap, E.H.; Chan, Y.C.; Tan, Y.H.
   #journal      Virology (1992) 188:953-958
   #title        Full-length cDNA sequence of dengue type 1 virus (Singapore
                   strain S275/90).
   #accession    A42551
      ##molecule_type genomic RNA
      ##residues      1-3396 ##label FUJ
      ##cross-references GB:M87512
CLASSIFICATION   #superfamily yellow fever virus genome polyprotein
KEYWORDS         capsid protein; envelope protein; glycoprotein; nonstructural
                   protein; polyprotein; transmembrane protein

FEATURE
   1-114             #product capsid protein #status predicted #label CAP\
   115-281           #product membrane protein precursor #status predicted
                       #label MEP\
   115-204           #domain signal sequence #status predicted #label SIG\
   205-281           #product membrane protein #status predicted #label MEM\
   267-279           #domain transmembrane #status predicted #label TM1\
   282-774           #product envelope protein #status predicted #label ENV\
   753-769           #domain transmembrane #status predicted #label TM2\
   775-1127          #product nonstructural protein NS1 #status predicted
                       #label NS1\
   1128-1344         #product nonstructural protein NS2a #status predicted
                       #label N2A\
   1345-1474         #product nonstructural protein NS2b #status predicted
                       #label N2B\
   1475-2093         #product nonstructural protein NS3 #status predicted
                       #label NS3\
   2094-2243         #product nonstructural protein NS4a #status predicted
                       #label N4A\
   2244-2492         #product nonstructural protein NS4b #status predicted
                       #label N4B\
   2493-3396         #product nonstructural protein NS5 #status predicted
                       #label NS5\
   183,347,433       #binding_site carbohydrate (Asn) (covalent) #status
                       predicted
```



```
SUMMARY          #length 3396  #molecular-weight 379561  #checksum 3242
SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            CGTXXXX
            |||
   NSTHEMYWVSCGTGNIVSAVNMTSRML
      2710   X  2720      2730
```

9. US-08-121-713B-3 (1-7)
   GNWVD3 genome polyprotein - dengue virus type 3

```
ENTRY            GNWVD3     #type complete
TITLE            genome polyprotein - dengue virus type 3
CONTAINS         capsid protein; envelope protein; membrane protein;
                   nonstructural protein NS1; nonstructural protein NS2a;
                   nonstructural protein NS2b; nonstructural protein NS3;
                   nonstructural protein NS4a; nonstructural protein NS4b;
                   nonstructural protein NS5
ORGANISM         #formal_name dengue virus type 3
DATE             30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                   09-Sep-1994
ACCESSIONS       A34774
REFERENCE        A34774
   #authors      Osatomi, K.; Sumiyoshi, H.
   #journal      Virology (1990) 176:643-647
   #title        Complete nucleotide sequence of dengue type 3 virus genome
                   RNA.
   #cross-references MUID:90266483
   #accession    A34774
      ##molecule_type genomic RNA
      ##residues      1-3390 ##label OSA
CLASSIFICATION   #superfamily yellow fever virus genome polyprotein
KEYWORDS         capsid protein; envelope protein; glycoprotein; nonstructural
                   protein; polyprotein; transmembrane protein

FEATURE
   1-114             #product capsid protein #status predicted #label CAP\
   46-67             #domain transmembrane #status predicted #label TM1\
   115-280           #product membrane protein precursor #status predicted
                       #label MEP\
   115-205           #domain signal sequence #status predicted #label SIG\
   206-280           #product membrane protein #status predicted #label MEM\
   266-280           #domain transmembrane #status predicted #label TM3\
   281-773           #product envelope protein #status predicted #label ENV\
   724-746           #domain transmembrane #status predicted #label TM4\
   753-771           #domain transmembrane #status predicted #label TM5\
   774-1184          #product nonstructural protein NS1 #status predicted
                       #label NS1\
   1156-1175         #domain transmembrane #status predicted #label TM6\
   1185-1343         #product nonstructural protein NS2a #status predicted
                       #label N2A\
   1344-1473         #product nonstructural protein NS2b #status predicted
                       #label N2B\
   1474-2092         #product nonstructural protein NS3 #status predicted
                       #label NS3\
```

```
     2093-2378          #product nonstructural protein NS4a #status predicted
                          #label N4A\
     2379-2490          #product nonstructural protein NS4b #status predicted
                          #label N4B\
     2491-3390          #product nonstructural protein NS5 #status predicted
                          #label NS5\
     183,347,433,750,
     903,980,1132,1188,
     1661,2300,2304,
     2386,2456,2702,
     2712               #binding_site carbohydrate (Asn) (covalent) #status
                          predicted
  SUMMARY          #length 3390  #molecular-weight 378061  #checksum 1535
  SEQUENCE

 Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
 Residue Identity =    42%  Matches          =      3  Mismatches   =     4
 Gaps             =      0  Conservative Substitutions               =     0

              X     X
              CGTXXXX
              |||
     EGTTVVISENCGTRGPSLRTTTVSGKL
        1060    X  1070      1080


10. US-08-121-713B-3 (1-7)
     S37536       macrogolgin - human

  ENTRY            S37536     #type complete
  TITLE            macrogolgin - human
  ORGANISM         #formal_name Homo sapiens #common_name man
  DATE             09-Dec-1993; #sequence_revision 09-Dec-1993; #text_change
                     09-Dec-1993
  ACCESSIONS       S37536
  REFERENCE        S37536
     #authors      Seelig, H.P.; Schranz, P.; Schroeter, H.; Wiemann, C.;
                     Griffiths, G.; Renz, M.
     #submission   submitted to the EMBL Data Library, September 1993
     #accession    S37536
        ##status        preliminary
        ##residues      1-3259 ##label SEE
        ##cross-references EMBL:X75304
  SUMMARY          #length 3259  #molecular-weight 376075  #checksum 4495
  SEQUENCE

 Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
 Residue Identity =    42%  Matches          =      3  Mismatches   =     4
 Gaps             =      0  Conservative Substitutions               =     0

              X     X
              CGTXXXX
              |||
     DSSRTPIIGSCGTQEQALLIDLTSNSC
     3190      3200  X   3210


11. US-08-121-713B-3 (1-7)
     S27852       hypothetical protein DGF-1 - Trypanosoma cruzi
```



```
  ENTRY            S27852     #type complete
  TITLE            hypothetical protein DGF-1 - Trypanosoma cruzi
  ORGANISM         #formal_name Trypanosoma cruzi
  DATE             17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
                     30-Sep-1993
  ACCESSIONS       S27852
  REFERENCE        S27852
     #authors      Wincker, P.; Murta-Dovales, A.C.; Goldenberg, S.
     #submission   submitted to the EMBL Data Library, April 1992
     #description  Nucleotide sequence of a representative member of a
                     Trypanosoma cruzi dispersed gene family.
     #accession    S27852
        ##molecule_type DNA
        ##residues      1-3229 ##label WIN
        ##cross-references EMBL:M90534
  SUMMARY          #length 3229  #molecular-weight 334929  #checksum 5768
  SEQUENCE

 Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
 Residue Identity =    42%  Matches          =      3  Mismatches   =     4
 Gaps             =      0  Conservative Substitutions               =     0

              X     X
              CGTXXXX
              |||
     LFPGDVVVFSCGTCNDDAACYMPGTEL
           1020      1030


12. US-08-121-713B-3 (1-7)
     A48450       putative cell-surface protein (cysteine-rich repea

  ENTRY            A48450     #type complete
  TITLE            putative cell-surface protein (cysteine-rich repeat motif) -
                     Trypanosoma cruzi
  ORGANISM         #formal_name Trypanosoma cruzi
  DATE             01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
                     18-Nov-1994
  ACCESSIONS       A48450
  REFERENCE        A48450
     #authors      Wincker, P.; Murto-Dovales, A.C.; Goldenberg, S.
     #journal      Mol. Biochem. Parasitol. (1992) 55:217-220
     #title        Nucleotide sequence of a representative member of a
                     Trypanosoma cruzi dispersed gene family.
     #cross-references MUID:93063053
     #accession    A48450
        ##status        preliminary
        ##molecule_type DNA
        ##residues      1-3229 ##label WIN
        ##cross-references NCBIP:118407
        ##note          sequence extracted from NCBI backbone
        ##note          sequence not compared to nucleotide translation
  SUMMARY          #length 3229  #molecular-weight 334929  #checksum 5768
  SEQUENCE

 Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
 Residue Identity =    42%  Matches          =      3  Mismatches   =     4
 Gaps             =      0  Conservative Substitutions               =     0

             X     X
```

```
              CGTXXXX
              |||
    LFPGDVVVFSCGTCNDDAACYMPGTEL
          1020      1030
```

13. US-08-121-713B-3 (1-7)
    A44062 genome polyprotein - pepper mottle virus (strain C

```
 ENTRY            A44062     #type complete
 TITLE            genome polyprotein - pepper mottle virus (strain California)
 CONTAINS         29K protein; 34K protein; coat protein; cylindrical inclusion
                    protein; helper component protein; nuclear inclusion
                    protein a; nuclear inclusion protein b
 ORGANISM         #formal_name pepper mottle virus
 DATE             31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                    31-Dec-1993
 ACCESSIONS       A44062
 REFERENCE        A44062
    #authors      Vance, V.B.; Moore, D.; Turpen, T.H.; Bracker, A.; Hollowell,
                    V.C.
    #journal      Virology (1992) 191:19-30
    #title        The complete nucleotide sequence of pepper mottle virus
                    genomic RNA: comparison of the encoded polyprotein with
                    those of other sequenced potyviruses.
    #accession    A44062
       ##molecule_type genomic RNA
       ##residues      1-3068 ##label VAN
       ##cross-references GB:M96425
 CLASSIFICATION   #superfamily tobacco etch virus genome polyprotein
 KEYWORDS         coat protein; cylindrical inclusion protein; inclusion
                    protein; nucleus; polyprotein
 FEATURE
    1-287             #product 34K protein #status predicted #label KPT\
    288-743           #product helper component protein #status predicted
                        #label HCP\
    744-1156          #product 29K protein #status predicted #label KPR\
    1157-1790         #product cylindrical inclusion protein #status predicted
                        #label CIP\
    1791-2276         #product nuclear inclusion protein a #status predicted
                        #label NIA\
    2277-2799         #product nuclear inclusion protein b #status predicted
                        #label NIB\
    2800-3068         #product coat protein #status predicted #label CPT
 SUMMARY          #length 3068  #molecular-weight 348653  #checksum 2964
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions              =     0

            X     X
            CGTXXXX
            |||
    YFADADEEFECGTYEVRHQSSSRSDTL
    2780      2790  X   2800
```

14. US-08-121-713B-3 (1-7)
    JQ1917 polyprotein - parsnip yellow fleck virus


```
 ENTRY            JQ1917     #type complete
 TITLE            polyprotein - parsnip yellow fleck virus
 ORGANISM         #formal_name parsnip yellow fleck virus, PYFV
 DATE             31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                    31-Dec-1993
 ACCESSIONS       JQ1917
 REFERENCE        JQ1917
    #authors      Turnbull-Ross, A.D.; Reavy, B.; Mayo, M.A.; Murant, A.F.
    #journal      J. Gen. Virol. (1992) 73:3203-3211
    #title        The nucleotide sequence of parsnip yellow fleck virus: a
                    plant picorna-like virus.
    #contents     Strain P-121
    #accession    JQ1917
       ##molecule_type mRNA
       ##residues      1-3027 ##label TUR
 KEYWORDS         polyprotein
 SUMMARY          #length 3027  #molecular-weight 336244  #checksum 9823
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.84
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions              =     0

            X     X
            CGTXXXX
            |||
    YIFSTTNVPGCGTKHGLADPGAFMRRR
        1570 X    1580
```

15. US-08-121-713B-3 (1-7)
    B39658 polyposis coli protein DP2.5 - human

```
 ENTRY            B39658     #type complete
 TITLE            polyposis coli protein DP2.5 - human
 ORGANISM         #formal_name Homo sapiens #common_name man
 DATE             21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change
                    30-Sep-1993
 ACCESSIONS       B39658
 REFERENCE        A39658
    #authors      Joslyn, G.; Carlson, M.; Thliveris, A.; Albertsen, H.;
                    Gelbert, L.; Samowitz, W.; Groden, J.; Stevens, J.; Spirio,
                    L.; Robertson, M.; Sargeant, L.; Krapcho, K.; Wolff, E.;
                    Burt, R.; Hughes, J.P.; Warrington, J.; McPherson, J.;
                    Wasmuth, J.; Le Paslier, D.; Abderrahim, H.; Cohen, D.;
                    Leppert, M.; White, R.
    #journal      Cell (1991) 66:601-613
    #title        Identification of deletion mutations and three new genes at
                    the familial polyposis locus.
    #cross-references MUID:91330307
    #accession    B39658
       ##status       preliminary
       ##molecule_type DNA
       ##residues      1-2844 ##label JOS
       ##cross-references GB:M73548
 CLASSIFICATION   #superfamily adenomatous polyposis coli protein
 SUMMARY          #length 2844  #molecular-weight 311654  #checksum 7518
 SEQUENCE
```

```
Initial Score     =      7  Optimized Score  =      7  Significance =  1.84
Residue Identity  =    42%  Matches          =      3  Mismatches   =     4
Gaps              =      0  Conservative Substitutions               =     0

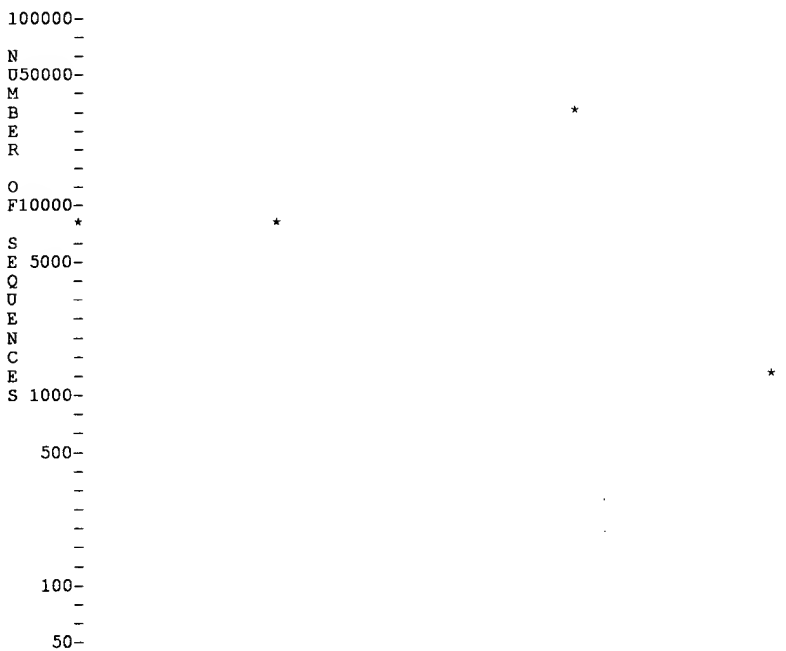
             X     X
             CGTXXXX
             |||
    SHSLTIVSNACGTLWNLSARNPKDQEA
          680       690
> O <
O| |O  IntelliGenetics
> O <

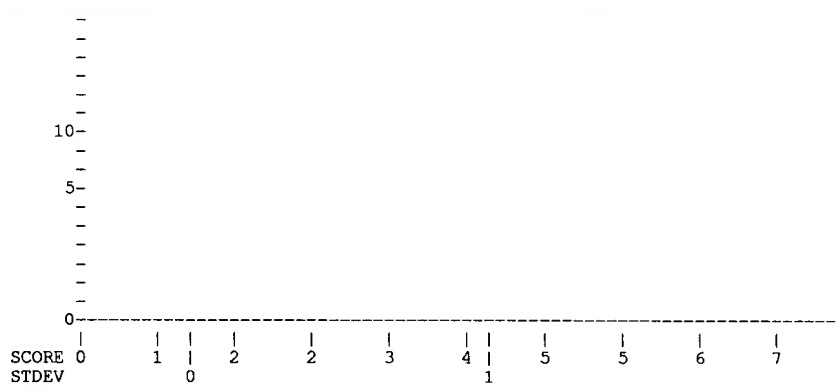
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq3spt.res made by  on Fri 19 May 95 8:54:49-PDT.


Query sequence being compared:US-08-121-713B-3 (1-7)
Number of sequences searched:                43470
Number of scores above cutoff:                4588

      Results of the initial comparison of US-08-121-713B-3 (1-7) with:
   Data bank : Swiss-Prot 31, all entries
```





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	3	6	2.02

Times:	CPU	Total Elapsed
	00:00:44.00	00:00:46.00

```
Number of residues:              15335248
Number of sequences searched:       43470
Number of scores above cutoff:       4588

Cut-off raised to 5.
Cut-off raised to 6.

The scores below are sorted by initial score.
Significance is calculated based on initial score.


1019 100% similar sequences to the query sequence were found:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. FAT_DROME	CADHERIN-RELATED TUMOR SUPPRE	5147	7	7	1.98	0
2. PKSI_BACSU	PUTATIVE POLYKETIDE SYNTHASE	4427	7	7	1.98	0

3.	RRPA_CVH22	RNA-DIRECTED RNA POLYMERASE (	4085	7	7	1.98	0
4.	RPOA_LELV	RNA-DIRECTED RNA POLYMERASE (	3859	7	7	1.98	0
5.	POLG_DEN1S	GENOME POLYPROTEIN (CONTAINS:	3396	7	7	1.98	0
6.	POLG_DEN3	GENOME POLYPROTEIN (CONTAINS:	3390	7	7	1.98	0
7.	POLG_PEMVC	GENOME POLYPROTEIN (CONTAINS:	3068	7	7	1.98	0
8.	POLG_PYFV1	GENOME POLYPROTEIN (CONTAINS:	3027	7	7	1.98	0
9.	APC_HUMAN	ADENOMATOUS POLYPOSIS COLI PR	2843	7	7	1.98	0
10.	VWF_HUMAN	VON WILLEBRAND FACTOR PRECURS	2813	7	7	1.98	0
11.	IP3R_MOUSE	INOSITOL 1,4,5-TRISPHOSPHATE-	2749	7	7	1.98	0
12.	IP3R_RAT	INOSITOL 1,4,5-TRISPHOSPHATE-	2749	7	7	1.98	0
13.	ZEP1_HUMAN	ZINC FINGER PROTEIN 40 (HUMAN	2717	7	7	1.98	0
14.	G156_PARPR	156G SURFACE PROTEIN PRECURSO	2715	7	7	1.98	0
15.	CENE_HUMAN	CENTROMERIC PROTEIN E (CENP-E	2663	7	7	1.98	0
16.	RRPB_IBVB	RNA-DIRECTED RNA POLYMERASE (	2652	7	7	1.98	0
17.	MPRI_BOVIN	CATION-INDEPENDENT MANNOSE-6-	2499	7	7	1.98	0
18.	MPRI_HUMAN	CATION-INDEPENDENT MANNOSE-6-	2491	7	7	1.98	0
19.	FINC_RAT	FIBRONECTIN PRECURSOR (FN).	2477	7	7	1.98	0
20.	RPB1_PLAFD	DNA-DIRECTED RNA POLYMERASE I	2452	7	7	1.98	0
21.	CCB2_RABIT	BRAIN CALCIUM CHANNEL BI-2 PR	2424	7	7	1.98	0
22.	FINC_HUMAN	FIBRONECTIN PRECURSOR.	2386	7	7	1.98	0
23.	YIM9_YEAST	HYPOTHETICAL 269.9 KD PROTEIN	2376	7	7	1.98	0
24.	FAB1_YEAST	FAB1 PROTEIN.	2278	7	7	1.98	0
25.	MUC2_HUMAN	MUCIN 2 (INTESTINAL MUCIN 2)	2274	7	7	1.98	0
26.	CCB1_RABIT	BRAIN CALCIUM CHANNEL BI-1 PR	2273	7	7	1.98	0
27.	FINC_BOVIN	FIBRONECTIN (FN).	2265	7	7	1.98	0
28.	CCB3_RABIT	BRAIN CALCIUM CHANNEL BII-1 P	2259	7	7	1.98	0
29.	POL1_GCMV	RNA1 POLYPROTEIN (250 KD PROT	2252	7	7	1.98	0
30.	GLSN_MEDSA	GLUTAMATE SYNTHASE (NADH) PRE	2194	7	7	1.98	0
31.	CCB4_RABIT	BRAIN CALCIUM CHANNEL BII-2 P	2178	7	7	1.98	0
32.	POLG_HRV1B	GENOME POLYPROTEIN (COAT PROT	2157	7	7	1.98	0
33.	POLG_HRV2	GENOME POLYPROTEIN (COAT PROT	2150	7	7	1.98	0
34.	CRB_DROME	CRUMBS PROTEIN PRECURSOR (95F	2139	7	7	1.98	0
35.	AGRI_CHICK	AGRIN PRECURSOR.	1955	7	7	1.98	0
36.	RRPO_ACLSV	RNA-DIRECTED RNA POLYMERASE (	1884	7	7	1.98	0
37.	CIC1_RABIT	DIHYDROPRYRIDINE-SENSITIVE L-	1873	7	7	1.98	0
38.	BRC1_HUMAN	BREAST CANCER TYPE 1 SUSCEPTI	1863	7	7	1.98	0
39.	RPB1_CAEEL	DNA-DIRECTED RNA POLYMERASE I	1859	7	7	1.98	0
40.	POLR_EPMV	RNA REPLICASE POLYPROTEIN (EC	1839	7	7	1.98	0
41.	LMB1_HUMAN	LAMININ BETA-1 CHAIN PRECURSO	1786	7	7	1.98	0
42.	LMB1_MOUSE	LAMININ BETA-1 CHAIN PRECURSO	1786	7	7	1.98	0
43.	RRPO_SHVX	RNA REPLICATION PROTEIN (CONT	1718	7	7	1.98	0
44.	TGFB_RAT	TRANSFORMING GROWTH FACTOR BE	1712	7	7	1.98	0
45.	RPOC_THEMA	DNA-DIRECTED RNA POLYMERASE B	1690	7	7	1.98	0

1. US-08-121-713B-3 (1-7)
FAT_DROME CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT P

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ID   FAT_DROME      STANDARD;      PRT;  5147 AA.
AC   P33450;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE   CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).
GN   FT.
OS   DROSOPHILA MELANOGASTER (FRUIT FLY).
OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92069752
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RA   MAHONEY P.A., WEBER U., ONOFRECHUK P., BIESSMANN H., BRYANT P.J.,
RA   GOODMAN C.S.;
RL   CELL 67:853-868(1991).
CC   -!- FUNCTION: COULD FUNCTION AS A CELL-ADHESION PROTEIN.
CC   -!- DISEASE: RECESSIVE LETAL MUTATIONS IN FAT CAUSE HYPERPLASTIC,
CC       TUMOR-LIKE OVERGROWTH OF LARVAL IMAGINAL DISCS, DEFECTS IN
CC       DIFFERENTIATION AND MORPHOGENESIS, AND DEAT DURING THE PUPAL
CC       STAGE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY OF CELL ADHESION
CC       MOLECULES. CONTAINS 37 CADHERINS-TYPE REPEATS.
CC   -!- SIMILARITY: THE PROTEIN INCLUDES 4 EGF-LIKE REPEATS.
DR   EMBL; M80537; DMFAT.
DR   PIR; A41087; IJFFTM.
DR   FLYBASE; FBGN0001075; FT.
DR   PROSITE; PS00022; EGF.
DR   PROSITE; PS00232; CADHERIN.
KW   CELL ADHESION; SIGNAL; TRANSMEMBRANE; CYTOSKELETON; GLYCOPROTEIN;
KW   CALCIUM-BINDING; REPEAT; EGF-LIKE DOMAIN;
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36   5147       CADHERIN-RELATED TUMOR SUPPRESSOR.
FT   DOMAIN       36   4583       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   4584   4609       POTENTIAL.
FT   DOMAIN     4610   5147       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       36    156       CADHERIN 1.
FT   REPEAT      157    270       CADHERIN 2.
FT   REPEAT      271    382       CADHERIN 3.
FT   REPEAT      383    494       CADHERIN 4.
FT   REPEAT      495    599       CADHERIN 5.
FT   REPEAT      600    708       CADHERIN 6.
FT   REPEAT      709    820       CADHERIN 7.
FT   REPEAT      821    942       CADHERIN 8.
FT   REPEAT      943   1049       CADHERIN 9.
FT   REPEAT     1050   1153       CADHERIN 10.
FT   REPEAT     1154   1278       CADHERIN 11.
FT   REPEAT     1279   1384       CADHERIN 12.
FT   REPEAT     1385   1489       CADHERIN 13.
FT   REPEAT     1490   1601       CADHERIN 14.
FT   REPEAT     1602   1713       CADHERIN 15.
FT   REPEAT     1714   1823       CADHERIN 16.
FT   REPEAT     1824   1922       CADHERIN 17.
FT   REPEAT     1923   2027       CADHERIN 18.
FT   REPEAT     2028   2167       CADHERIN 19.
FT   REPEAT     2168   2278       CADHERIN 20.
FT   REPEAT     2279   2385       CADHERIN 21.
FT   REPEAT     2386   2491       CADHERIN 22.
FT   REPEAT     2492   2596       CADHERIN 23.
FT   REPEAT     2597   2703       CADHERIN 24.
FT   REPEAT     2704   2810       CADHERIN 25.
FT   REPEAT     2811   2913       CADHERIN 26.
FT   REPEAT     2914   3013       CADHERIN 27.
FT   REPEAT     3014   3124       CADHERIN 28.
FT   REPEAT     3125   3229       CADHERIN 29.
FT   REPEAT     3230   3334       CADHERIN 30.
FT   REPEAT     3335   3439       CADHERIN 31.
FT   REPEAT     3440   3545       CADHERIN 32.
FT   REPEAT     3546   3651       CADHERIN 33.
FT   REPEAT     3652   3756       CADHERIN 34.
FT   REPEAT     3954   4016       EGF-LIKE 1.
FT   REPEAT     4017   4055       EGF-LIKE 2.
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FT   REPEAT     4056   4095       EGF-LIKE 3.
FT   REPEAT     4096   4134       EGF-LIKE 4.
FT   CARBOHYD    239    239       POTENTIAL.
FT   CARBOHYD    257    257       POTENTIAL.
FT   CARBOHYD    276    276       POTENTIAL.
FT   CARBOHYD    280    280       POTENTIAL.
FT   CARBOHYD    402    402       POTENTIAL.
FT   CARBOHYD    461    461       POTENTIAL.
FT   CARBOHYD    605    605       POTENTIAL.
FT   CARBOHYD    631    631       POTENTIAL.
FT   CARBOHYD   1155   1155       POTENTIAL.
FT   CARBOHYD   1367   1367       POTENTIAL.
FT   CARBOHYD   1458   1458       POTENTIAL.
FT   CARBOHYD   1751   1751       POTENTIAL.
FT   CARBOHYD   1831   1831       POTENTIAL.
FT   CARBOHYD   1880   1880       POTENTIAL.
FT   CARBOHYD   2080   2080       POTENTIAL.
FT   CARBOHYD   2171   2171       POTENTIAL.
FT   CARBOHYD   2247   2247       POTENTIAL.
FT   CARBOHYD   2290   2290       POTENTIAL.
FT   CARBOHYD   2437   2437       POTENTIAL.
FT   CARBOHYD   2581   2581       POTENTIAL.
FT   CARBOHYD   2799   2799       POTENTIAL.
FT   CARBOHYD   2920   2920       POTENTIAL.
FT   CARBOHYD   2946   2946       POTENTIAL.
FT   CARBOHYD   2967   2967       POTENTIAL.
FT   CARBOHYD   3167   3167       POTENTIAL.
FT   CARBOHYD   3303   3303       POTENTIAL.
FT   CARBOHYD   3386   3386       POTENTIAL.
FT   CARBOHYD   3389   3389       POTENTIAL.
FT   CARBOHYD   3525   3525       POTENTIAL.
FT   CARBOHYD   3852   3852       POTENTIAL.
FT   CARBOHYD   3865   3865       POTENTIAL.
FT   CARBOHYD   3905   3905       POTENTIAL.
FT   CARBOHYD   4306   4306       POTENTIAL.
FT   CARBOHYD   4414   4414       POTENTIAL.
FT   CARBOHYD   4471   4471       POTENTIAL.
FT   CARBOHYD   4487   4487       POTENTIAL.
FT   CARBOHYD   4539   4539       POTENTIAL.
FT   CARBOHYD   4550   4550       POTENTIAL.
FT   VARIANT    1229   1229       S -> G.
FT   VARIANT    1233   1233       G -> S.
SQ   SEQUENCE   5147 AA;  564885 MW;  23531637 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    SYTLNITASDCGTPSLSTTVLYNVLVV
       1460   X  1470      1480
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2. US-08-121-713B-3 (1-7)
   PKSL_BACSU   PUTATIVE POLYKETIDE SYNTHASE PKSL (PKS).

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ID   PKSL_BACSU     STANDARD;      PRT;  4427 AA.
AC   Q05470;
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DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   PUTATIVE POLYKETIDE SYNTHASE PKSL (PKS).
GN   PKSL OR PKSX OR PKSA OR OUTG.
OS   BACILLUS SUBTILIS.
OC   PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168 / PB1424;
RM   93345824
RA   SCOTTI C., PIATTI M., CUZZONI A., PERANI P., TOGNONI A., GRANDI G.,
RA   GALIZZI A., ALBERTINI A.M.;
RL   GENE 130:65-71(1993).
CC   -!- FUNCTION: POTENTIALLY INVOLVED IN SOME INTERMEDIATE STEPS FOR
CC       THE SYNTHESIS OF A POLYKETIDE MOLECULE WHICH MAY BE INVOLVED IN
CC       SECONDARY METABOLISM.
CC   -!- SIMILARITY: TO FATTY ACID SYNTHASE (FAS).
DR   EMBL; M97902; BSPKSX.
DR   EMBL; U11039; BS11039.
DR   PIR; S25021; S25021.
DR   SUBTILIST; BG10698; PKSL.
KW   TRANSFERASE; ACYLTRANSFERASE; ANTIBIOTIC BIOSYNTHESIS; NADP;
KW   PHOSPHOPANTETHEINE; MULTIFUNCTIONAL ENZYME; REPEAT.
FT   DOMAIN      184    282       ACYL CARRIER (ACP).
FT   DOMAIN      382    759       BETA-KETOACYL SYNTHASE (KS).
FT   DOMAIN      937   1115       DEHYDRATASE.
FT   DOMAIN     1409   1602       BETA-KETOACYL REDUCTASE (KR).
FT   DOMAIN     1665   1761       ACYL CARRIER (ACP).
FT   DOMAIN     1876   2253       BETA-KETOACYL SYNTHASE (KS).
FT   DOMAIN     2469   2560       ACYL CARRIER (ACP).
FT   DOMAIN     2609   2702       ACYL CARRIER (ACP).
FT   DOMAIN     2823   3182       BETA-KETOACYL SYNTHASE (KS).
FT   DOMAIN     3575   3776       BETA-KETOACYL REDUCTASE (KR).
FT   DOMAIN     3834   3925       ACYL CARRIER (ACP).
FT   DOMAIN     4019   4373       BETA-KETOACYL SYNTHASE (KS).
FT   BINDING    2523   2523       PHOSPHOPANTETHEINE (POTENTIAL).
FT   BINDING    2664   2664       PHOSPHOPANTETHEINE (POTENTIAL).
SQ   SEQUENCE   4427 AA;  493398 MW;  21754976 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    HVAGAIDLIGCGTSHEHSMGWINWLQK
      3440   X 3450      3460
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3. US-08-121-713B-3 (1-7)
   RRPA_CVH22   RNA-DIRECTED RNA POLYMERASE (ORF1A) (EC 2.7.7.48).

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ID   RRPA_CVH22     STANDARD;      PRT;  4085 AA.
AC   Q05002;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE   RNA-DIRECTED RNA POLYMERASE (ORF1A) (EC 2.7.7.48).
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OS   HUMAN CORONAVIRUS (STRAIN 229E).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; CORONAVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   93331726
RA   HEROLD J., RAABE T., SCHELLE-PRINZ B., SIDDELL S.G.;
RL   VIROLOGY 195:680-691(1993).
CC   -!- FUNCTION: THE RNA DEPENDENT RNA POLYMERASE OF CORONAVIRUSES IS
CC       A MULTIFUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECESSARY
CC       FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA, LEADER RNA,
CC       SUBGENOMIC MRNAS AND PROGENY VIRION RNA.
CC   -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
CC       + RNA(N).
DR   EMBL; X69721; HCVORF1AB.
DR   PIR; S28600; S28600.
KW   RNA-DIRECTED RNA POLYMERASE.
SQ   SEQUENCE   4085 AA;  454206 MW;  19863052 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    NDGRVANGYVCGTGLWNLVFNILSMFS
    2720      2730  X   2740
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4. US-08-121-713B-3 (1-7)
   RPOA_LELV RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (ORF1A/1

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ID   RPOA_LELV      STANDARD;      PRT;  3859 AA.
AC   Q04561;
DT   01-OCT-1993 (REL. 27, CREATED)
DT   01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (ORF1A/1B).
GN   POL.
OS   LELYSTAD VIRUS (LV) (PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME
OS   VIRUS).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; TOGAVIRIDAE;
OC   ARTERIVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   93297139
RA   MEULENBERG J.J.M., HULST M.M., DE MEIJER E.J., MOONEN P.L.J.M.,
RA   DEN BESTEN A., DE KLUYVER E.P., WENSVOORT G., MOORMANN R.J.M.;
RL   VIROLOGY 192:62-72(1993).
RN   [2]
RP   SEQUENCE OF 3328-3859 FROM N.A.
RC   STRAIN=BOXMEER 10;
RM   93174942
RA   CONZELMANN K.K., VISSER N., VAN WOENSEL P., THIEL H.J.;
RL   VIROLOGY 193:329-339(1993).
CC   -!- FUNCTION: RNA-DIRECTED RNA POLYMERASE & POSSIBLE HELICASE. A
CC       ROLE FOR NTP-BINDING PROTEINS IN RNA DUPLEX UNWINDING HAS BEEN
CC       SUGGESTED. POSSIBLE CONTAINS A PROTEASE DOMAIN (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE =
CC       N PYROPHOSPHATE + RNA(N).
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CC   -!- SIMILARITY: WITH THE POLYMERASE PROTEIN OF OTHER CORONAVIRUSES AND
CC       OF TOROVIRUSES.
DR   EMBL; M96262; LEYPOLYEN.
DR   EMBL; L04493; PRWPOLGLY.
DR   PIR; A36861; A36861.
DR   PIR; A45392; A45392.
KW   RNA-DIRECTED RNA POLYMERASE; HELICASE; ATP-BINDING; HYDROLASE;
KW   SERINE PROTEASE.
FT   CHAIN         1   2396       ORF1A.
FT   CHAIN      2397   3859       ORF1B.
FT   DOMAIN      262    290       CYS-RICH.
FT   DOMAIN      472    525       CYS-RICH.
FT   DOMAIN      792   1506       HELICASE.
FT   DOMAIN     1203   1284       CYS-RICH.
FT   DOMAIN     1724   1830       TRYPSIN-LIKE SERINE PROTEASE.
FT   DOMAIN     2010   2108       CYS-RICH.
FT   DOMAIN     2768   2972       POLYMERASE.
FT   ACT_SITE   1732   1732       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   1757   1757       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   1810   1810       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   NP_BIND    2587   2595       ATP (BY SIMILARITY).
FT   ZN_FING    3042   3094       BY SIMILARITY.
FT   CONFLICT   3506   3506       T -> V (IN REF. 2).
FT   CONFLICT   3744   3744       V -> I (IN REF. 2).
SQ   SEQUENCE   3859 AA;  421843 MW;  21900374 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    TGPILCHVEHCGTESGDSSSPLDLSDA
    810       820   X   830
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5. US-08-121-713B-3 (1-7)
   POLG_DEN1S GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CO

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ID   POLG_DEN1S     STANDARD;      PRT;  3396 AA.
AC   P33478;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE   GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
DE   PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
DE   PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
DE   RNA POLYMERASE (EC 2.7.7.48) (NS5)).
OS   DENGUE VIRUS TYPE 1 (STRAIN SINGAPORE S275/90).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
OC   FLAVIVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92263809
RA   FU J., TAN B.H., YAP E.H., CHAN Y.C., TAN Y.H.;
RL   VIROLOGY 188:953-958(1992).
CC   -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC       LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF THREE PROTEINS:
CC       PROTEIN PRM, PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A
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CC       COMPLEX OF PROTEIN C AND MRNA.
DR   EMBL; M87512; DENT1SEQ.
DR   PIR; A42551; A42551.
KW   POLYPROTEIN; GLYCOPROTEIN; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN;
KW   COAT PROTEIN; ENVELOPE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE;
KW   NONSTRUCTURAL PROTEIN.
FT   CHAIN         1    114       CAPSID PROTEIN C (POTENTIAL).
FT   PROPEP      115    205
FT   CHAIN       206    280       ENVELOPE GLYCOPROTEIN M (POTENTIAL).
FT   CHAIN       281    774       MAJOR ENVELOPE PROTEIN E (POTENTIAL).
FT   CHAIN       775   1127       NONSTRUCTURAL PROTEIN NS1 (POTENTIAL).
FT   CHAIN      1128   1344       NONSTRUCTURAL PROTEIN NS2A (POTENTIAL).
FT   CHAIN      1345   1474       NONSTRUCTURAL PROTEIN NS2B (POTENTIAL).
FT   CHAIN      1475   2093       HELICASE (NS3) (POTENTIAL).
FT   CHAIN      2094   2243       NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).
FT   CHAIN      2244   2492       NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).
FT   CHAIN      2493   3396       RNA-DIRECTED RNA POLYMERASE (NS5)
FT                                (POTENTIAL).
FT   NP_BIND    1668   1675       ATP (POTENTIAL).
FT   SITE       1759   1762       DEAH BOX.
FT   TRANSMEM    267    279       POTENTIAL.
FT   TRANSMEM    753    769       POTENTIAL.
FT   CARBOHYD    183    183       POTENTIAL.
FT   CARBOHYD    347    347       POTENTIAL.
FT   CARBOHYD    433    433       POTENTIAL.
SQ   SEQUENCE   3396 AA;  379558 MW;  22686711 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =      4
Gaps             =      0  Conservative Substitutions               =      0

            X     X
            CGTXXXX
            |||
   NSTHEMYWVSCGTGNIVSAVNMTSRML
      2710   X  2720      2730


6. US-08-121-713B-3 (1-7)
   POLG_DEN3    GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CO

ID   POLG_DEN3      STANDARD;      PRT;  3390 AA.
AC   P27915;
DT   01-AUG-1992 (REL. 23, CREATED)
DT   01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT   01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE   GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
DE   PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E;
DE   NONSTRUCTURAL PROTEINS NS1, NS2, NS4A AND NS4B; HELICASE (NS3);
DE   RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (NS5)).
OS   DENGUE VIRUS TYPE 3.
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
OC   FLAVIVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   90266483
RA   OSATOMI K., SUMIYOSHI H.;
RL   VIROLOGY 176:643-647(1990).
CC   -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC       LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
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CC       PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC       PROTEIN C AND MRNA.
DR   EMBL; M93130; DENCME.
DR   PIR; A34774; GNWVD3.
KW   POLYPROTEIN; GLYCOPROTEIN; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN;
KW   COAT PROTEIN; ENVELOPE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE;
KW   NONSTRUCTURAL PROTEIN.
FT   CHAIN         1    114       CAPSID PROTEIN C.
FT   PROPEP      115    205
FT   CHAIN       206    280       ENVELOPE GLYCOPROTEIN M.
FT   CHAIN       281    773       MAJOR ENVELOPE PROTEIN E.
FT   CHAIN       774   1184       NONSTRUCTURAL PROTEIN NS1.
FT   CHAIN      1185   1343       NONSTRUCTURAL PROTEIN NS2A.
FT   CHAIN      1344   1473       NONSTRUCTURAL PROTEIN NS2B.
FT   CHAIN      1474   2092       HELICASE (NS3).
FT   CHAIN      2093   2378       NONSTRUCTURAL PROTEIN NS4A.
FT   CHAIN      2379   2490       NONSTRUCTURAL PROTEIN NS4B.
FT   CHAIN      2491   3390       RNA-DIRECTED RNA POLYMERASE (NS5).
FT   NP_BIND    1667   1674       ATP (POTENTIAL).
FT   SITE       1758   1761       DEAH BOX.
FT   TRANSMEM     46     67       POTENTIAL.
FT   TRANSMEM    266    280       POTENTIAL.
FT   TRANSMEM    724    746       POTENTIAL.
FT   TRANSMEM    753    771       POTENTIAL.
FT   TRANSMEM   1156   1175       5 (POTENTIAL).
FT   CARBOHYD    183    183       POTENTIAL.
FT   CARBOHYD    347    347       POTENTIAL.
FT   CARBOHYD    433    433       POTENTIAL.
FT   CARBOHYD    750    750       POTENTIAL.
FT   CARBOHYD    903    903       POTENTIAL.
FT   CARBOHYD    980    980       POTENTIAL.
FT   CARBOHYD   1132   1132       POTENTIAL.
FT   CARBOHYD   1188   1188       POTENTIAL.
FT   CARBOHYD   1661   1661       POTENTIAL.
FT   CARBOHYD   2300   2300       POTENTIAL.
FT   CARBOHYD   2304   2304       POTENTIAL.
FT   CARBOHYD   2456   2456       POTENTIAL.
FT   CARBOHYD   2702   2702       POTENTIAL.
FT   CARBOHYD   2712   2712       POTENTIAL.
SQ   SEQUENCE   3390 AA;  378057 MW;  22373526 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =      4
Gaps             =      0  Conservative Substitutions               =      0

            X     X
            CGTXXXX
            |||
   EGTTVVISENCGTRGPSLRTTTVSGKL
     1060   X  1070      1080


7. US-08-121-713B-3 (1-7)
   POLG_PEMVC   GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN;

ID   POLG_PEMVC     STANDARD;      PRT;  3068 AA.
AC   Q01500;
DT   01-OCT-1993 (REL. 27, CREATED)
DT   01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
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DE   GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN; HELPER COMPONENT-
DE   PROTEINASE (HC-PRO); 42-50 KD PROTEIN; CYTOPLASMIC INCLUSION PROTEIN
DE   (CI); 6 KD PROTEIN; NUCLEAR INCLUSION PROTEIN A (NI-A) (EC 3.4.-.-)
DE   (49K PROTEINASE) (49 KD-PRO); NUCLEAR INCLUSION PROTEIN B (NI-B)
DE   (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN).
OS   PEPPER MOTTLE VIRUS (CALIFORNIA ISOLATE) (PEMV).
OC   VIRIDAE; SS-RNA NONENVELOPED VIRUSES; POTYVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   93033110
RA   VANCE V.B., MOORE D., TURPEN T.H., BRACKER A., HOLLOWELL V.C.;
RL   VIROLOGY 191:19-30(1992).
CC   -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC       TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC   -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC       MAY BE INVOLVED IN REPLICATION.
CC   -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A, OR THE N-TERMINAL PART OF
CC       IT, VPG, IS COVALENTLY LINKED TO THE GENOMIC RNA. NI-A ALSO HAS
CC       PROTEOLYTIC ACTIVITY.
CC   -!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC       POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC       PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC       INDIVIDUAL PROTEINS.
CC   -!- SIMILARITY: TO OTHER POTYVIRUSES POLYPROTEINS.
DR   EMBL; M96425; PMVCG.
DR   PIR; A44062; A44062.
KW   HYDROLASE; PROTEASE; RNA-DIRECTED RNA POLYMERASE; COAT PROTEIN;
KW   POLYPROTEIN; COVALENT PROTEIN-RNA LINKAGE.
FT   CHAIN         1    287       N-TERMINAL PROTEIN.
FT   CHAIN       288    743       HELPER COMPONENT-PROTEINASE.
FT   CHAIN       744   1156       29 KD PROTEIN.
FT   CHAIN      1157   1790       CYTOPLASMIC INCLUSION PROTEIN.
FT   CHAIN      1791   1842       6 KD PROTEIN.
FT   CHAIN      1843   2276       NUCLEAR INCLUSION PROTEIN A.
FT   CHAIN      2277   2795       NUCLEAR INCLUSION PROTEIN B.
FT   CHAIN      2796   3068       COAT PROTEIN.
FT   BINDING    1906   1906       COVALENT LINKAGE OF VIRAL RNA
FT                                (BY SIMILARITY).
SQ   SEQUENCE   3068 AA;  348651 MW;  22258851 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    YFADADEEFECGTYEVRHQSSSRSDTL
    2780      2790  X   2800


8. US-08-121-713B-3 (1-7)
   POLG_PYFV1   GENOME POLYPROTEIN (CONTAINS: 22.5 KD PROTEIN; 26

 ID   POLG_PYFV1     STANDARD;      PRT;  3027 AA.
 AC   Q05057;
 DT   01-FEB-1994 (REL. 28, CREATED)
 DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT   01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
 DE   GENOME POLYPROTEIN (CONTAINS: 22.5 KD PROTEIN; 26 KD PROTEIN; 31 KD
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 DE   PROTEIN; PROBABLE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48)).
 OS   PARSNIP YELLOW FLECK VIRUS (ISOLATE P-121) (PYFV).
 OC   VIRIDAE; SS-RNA NONENVELOPED VIRUSES; SEQUIVIRIDAE.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RM   93107855
 RA   TURNBULL-ROSS A.D., REAVY B., MAYO M.A., MURANT A.F.;
 RL   J. GEN. VIROL. 73:3203-3211(1992).
 CC   -!- SIMILARITY: SOME, TO THE CMPV AND TBRV POLYPROTEINS.
 DR   EMBL; D14066; PYFPOLYP.
 DR   PIR; JQ1917; JQ1917.
 KW   POLYPROTEIN; ATP-BINDING; COAT PROTEIN; RNA-DIRECTED RNA POLYMERASE.
 FT   NP_BIND    1467   1474       ATP (POTENTIAL).
 FT   VARIANT     962    962       T -> I.
 FT   VARIANT    1373   1373       L -> F.
 SQ   SEQUENCE   3027 AA;  336242 MW;  22418420 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    YIFSTTNVPGCGTKHGLADPGAFMRRR
        1570 X    1580


9. US-08-121-713B-3 (1-7)
   APC_HUMAN    ADENOMATOUS POLYPOSIS COLI PROTEIN (APC PROTEIN).

 ID   APC_HUMAN      STANDARD;      PRT;  2843 AA.
 AC   P25054;
 DT   01-MAY-1992 (REL. 22, CREATED)
 DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
 DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE   ADENOMATOUS POLYPOSIS COLI PROTEIN (APC PROTEIN).
 GN   APC OR DP2.5.
 OS   HOMO SAPIENS (HUMAN).
 OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC   EUTHERIA; PRIMATES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RM   91335210
 RA   KINZLER K.W., NILBERT M.C., SU L.-K., VOGELSTEIN B., BRYAN T.M.,
 RA   LEVY D.B., SMITH K.J., PREISINGER A.C., HEDGE P., MCKECHNIE D.,
 RA   FINNIEAR R., MARKHAM A., GROFFEN J., BOGUSKI M.S., ALTSCHUL S.F.,
 RA   HORII A., ANDO H., MIYOSHI Y., MIKI Y., NISHISHO I., NAKAMURA Y.;
 RL   SCIENCE 253:661-665(1991).
 RN   [2]
 RP   VARIANTS FAP.
 RM   91335211
 RA   NISHISHO I., NAKAMURA Y., MIYOSHI Y., MIKI Y., ANDO H., HORII A.,
 RA   KOYAMA K., UTSUNOMIYA J., BABA S., HEDGE P., MARKHAM A., KRUSH A.J.,
 RA   PETERSEN G., HAMILTON S.R., NILBERT M.C., LEVY D.B., BRYAN T.M.,
 RA   PREISINGER A.C., SMITH K.J., SU L.-K., KINZLER K.W., VOGELSTEIN B.;
 RL   SCIENCE 253:665-669(1991).
 RN   [3]
 RP   VARIANTS FAP.
 RM   93265030
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RA   MIYOSHI Y., NAGASE H., ANDO H., ICHII S., NAKATSURU S., AOKI T.,
RA   MIKI Y., MORI T., NAKAMURA Y.;
RL   HUM. MOL. GENET. 1:229-233(1992).
RN   [4]
RP   VARIANTS FAP.
RM   93244793
RA   NAKATSURU S., YANAGISAWA A., ICHII S., TAHARA E., KATO Y.,
RA   NAKAMURA Y., HORII A.;
RL   HUM. MOL. GENET. 1:559-563(1992).
CC   -!- DISEASE: MUTATIONS OF THE GENE FOR THIS PROTEIN WERE FOUND IN
CC       PATIENTS WITH FAMILIAL ADENOMATOUS POLYPOSIS (FAP) AND GARDNERS
CC       SYNDROME (GS), THAT CONTRIBUTE TO TUMOR DEVELOPMENT IN PATIENTS
CC       WITH NONINHERITED FORMS OF COLORECTAL CANCER.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES TYPES.
DR   EMBL; M74088; HSFAPAPC.
DR   PIR; A37261; RBHUAP.
DR   MIM; 175100; 11TH EDITION.
KW   ANTI-ONCOGENE; DISEASE MUTATION.
FT   DOMAIN        1    730       LEUCINE-RICH.
FT   DOMAIN        7     72       COIL (POTENTIAL).
FT   DOMAIN      185    227       COIL (POTENTIAL).
FT   DOMAIN      731   2832       SER-RICH.
FT   DOMAIN     1131   1156       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN     1558   1577       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN     1866   1893       HIGHLY CHARGED.
FT   VARIANT     414    414       R -> C (IN A FAP).
FT   VARIANT     817    817       G -> C (IN A GASTRIC CANCER).
FT   VARIANT     880    880       I -> T (IN A GASTRIC CANCER).
FT   VARIANT     911    911       E -> G (IN A FAP).
FT   VARIANT     942    942       N -> D (IN A GASTRIC CANCER).
FT   VARIANT    1120   1120       G -> E (IN A GASTRIC CANCER).
FT   VARIANT    1171   1171       R -> H (IN A GASTRIC CANCER).
FT   VARIANT    1197   1197       F -> S (IN A GASTRIC CANCER).
FT   VARIANT    1259   1259       I -> T (IN A GASTRIC CANCER).
FT   VARIANT    1312   1312       G -> E (IN A GASTRIC CANCER).
FT   VARIANT    1313   1313       T -> A (IN A FAP).
FT   VARIANT    1326   1326       V -> A (IN A GASTRIC CANCER).
SQ   SEQUENCE   2843 AA;  311658 MW;  18964414 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    SHSLTIVSNACGTLWNLSARNPKDQEA
          680       690


10. US-08-121-713B-3 (1-7)
    VWF_HUMAN    VON WILLEBRAND FACTOR PRECURSOR.

ID   VWF_HUMAN      STANDARD;      PRT;  2813 AA.
AC   P04275;
DT   20-MAR-1987 (REL. 04, CREATED)
DT   01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   VON WILLEBRAND FACTOR PRECURSOR.
GN   F8VWF OR VWF.
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OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   90062044
RA   MANCUSO D.J., TULEY E.A., WESTFIELD L.A., WORRALL N.K.,
RA   SHELTON-INLOES B.B., SORACE J.M., ALEVY Y.G., SADLER J.E.;
RL   J. BIOL. CHEM. 264:19514-19527(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RM   87016349
RA   BONTHRON D., ORR E.C., MITSOCK L.M., MITSOCK L.M., GINSBURG D.,
RA   HANDIN R.I., ORKIN S.H.;
RL   NUCLEIC ACIDS RES. 14:7125-7128(1986).
RN   [3]
RP   SEQUENCE OF 1-1400 FROM N.A.
RM   87004550
RA   VERWEIJ C.L., DIERGAARDE P.J., HART M., PANNEKOEK H.;
RL   EMBO J. 5:1839-1847(1986).
RN   [4]
RP   ERRATUM.
RA   VERWEIJ C.L., DIERGAARDE P.J., HART M., PANNEKOEK H.;
RL   EMBO J. 5:3074-3074(1986).
RN   [5]
RP   SEQUENCE OF 764-2813.
RM   86269895
RA   TITANI K., KUMAR S., TAKIO K., ERICSSON L.H., WADE R.D., ASHIDA K.,
RA   WALSH K.A., CHOPEK M.W., SADLER J.E., FUJIKAWA K.;
RL   BIOCHEMISTRY 25:3171-3184(1986).
RN   [6]
RP   SEQUENCE OF 781-1424 FROM N.A.
RM   86269894
RA   SHELTON-INLOES B.B., TITANI K., SADLER J.E.;
RL   BIOCHEMISTRY 25:3164-3171(1986).
RN   [7]
RP   SEQUENCE OF 764-873 AND 1289-2813 FROM N.A.
RM   86016708
RA   SADLER J.E., SHELTON-INLOES B.B., SORACE J.M., HARLAN J.M.,
RA   TITANI K., DAVIE E.W.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 82:6394-6398(1985).
RN   [8]
RP   SEQUENCE OF 2731-2813 FROM N.A.
RM   85269603
RA   VERWEIJ C.L., DE VRIES C.J.M., DISTEL B., VAN ZONNEVELD A.-J.,
RA   VAN KESSEL A.G., VAN MOURIK J.A., PANNEKOEK H.;
RL   NUCLEIC ACIDS RES. 13:4699-4717(1985).
RN   [9]
RP   SEQUENCE OF 1-177 FROM N.A.
RM   88111704
RA   BONTHRON D., ORKIN S.H.;
RL   EUR. J. BIOCHEM. 171:51-57(1988).
RN   [10]
RP   STRUCTURE OF CARBOHYDRATES.
RM   86274702
RA   SAMOR B., MICHALSKI J.C., DEBRAY H., MAZURIER C., GOUDEMAND M.,
RA   VAN HALBEEK H., VLIEGENTHART J.F.G., MONTREUIL J.;
RL   EUR. J. BIOCHEM. 158:295-298(1986).
RN   [11]
RP   VARIANT NORMANDY-1.
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RM 91296824
RA TULEY E.A., GAUCHER C., JORIEUX S., WORRALL N.K., SADLER J.E.,
RA MAZURIER C.;
RL PROC. NATL. ACAD. SCI. U.S.A. 88:6377-6381(1991).
RN [12]
RP VARIANTS NORMANDY-2 AND NORMANDY-3.
RM 92001464
RA GAUCHER C., MERCIER B., JORIEUX S., OUFKIR D., MAZURIER C.;
RL BR. J. HAEMATOL. 78:506-514(1991).
RN [13]
RP VARIANT LEU-1266.
RM 93253064
RA HOLMBERG L., DENT J.A., SCHNEPPENHEIM R., BUDDE U., WARE J.,
RA RUGGERI Z.M.;
RL J. CLIN. INVEST. 91:2169-2177(1993).
RN [14]
RP VARIANT ASP-1268.
RM 93388627
RA RABINOWITZ I., RANDI A.M., SHINDLER K.S., TULEY E.A., RUSTAGI P.K.,
RA SADLER J.E.;
RL J. BIOL. CHEM. 268:20497-20501(1993).
RN [15]
RP VARIANT ARG-1272.
RM 93041232
RA LAVERGNE J.-M., DE PAILLETTE L., BAHNAK B.R., RIBBA A.-S.,
RA FRESSINAUD E., MEYER D., PIETU G.;
RL BR. J. HAEMATOL. 82:66-72(1992).
RN [16]
RP VARIANTS TRP-1306; CYS-1308 AND PRO-1613.
RM 91185601
RA RANDI A.M., RABINOWITZ I., MANCUSO D.J., MANNUCCI P.M., SADLER J.E.,
RL J. CLIN. INVEST. 87:1220-1226(1991).
RN [17]
RP VARIANTS TRP-1306; CYS-1308; LEU-1314 AND LEU-1318.
RM 93041230
RA DONNER M., KRISTOFFERSSON A.C., LENK H., SCHEIBEL E., DAHLBACK B.,
RA NILSSON I.M., HOLMBERG L.;
RL BR. J. HAEMATOL. 82:58-65(1992).
RN [18]
RP VARIANTS TRP-1306; MET-1316; THR-1628 AND SER-1648.
RM 93042596
RA PIETU G., RIBBA A.S., DE PAILLETTE L., CHEREL G., LAVERGNE J.M.,
RA BAHNAK B.R., MEYER D.;
RL BLOOD COAGUL. FIBRINOLYSIS 3:415-421(1992).
RN [19]
RP VARIANT CYS-1308.
RM 92104315
RA DONNER M., ANDERSSON A.-M., KRISTOFFERSSON A.-C., NILSSON I.M.,
RA DAHLBACK B., HOLMBERG L.;
RL EUR. J. HAEMATOL. 47:342-345(1991).
RN [20]
RP VARIANT CYS-1313.
RM 91187908
RA WARE J., DENT J.A., AZUMA H., SUGIMOTO M., KYRLE P.A., YOSHIOKA A.,
RA RUGGERI Z.M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 88:2946-2950(1991).
RN [21]
RP VARIANT LEU-1314.
RM 93041230
RA DONNER M., KRISTOFFERSSON A.C., LENK H., SCHEIBEL E., DAHLBACK B.,

RA NILSSON I.M., HOLMBERG L.;
RL BR. J. HAEMATOL. 82:58-65(1992).
RN [22]
RP VARIANT MET-1316.
RM 92109240
RA MURRAY E.W., GILES A.R., LILLICRAP D.;
RL AM. J. HUM. GENET. 50:199-207(1992).
RN [23]
RP VARIANT SER-1324.
RM 93028560
RA RABINOWITZ I., TULEY E.A., MANCUSO D.J., RANDI A.M., FIRKIN B.G.,
RA HOWARD M.A., SADLER J.E.;
RL PROC. NATL. ACAD. SCI. U.S.A. 89:9846-9849(1992).
RN [24]
RP VARIANTS TRP-1306; CYS-1308; MET-1316; GLN-1341 AND HIS-1399.
RM 91185602
RA COONEY K.A., NICHOLS W.C., BRUCK M.E., BAHOU W.F., SHAPIRO A.D.,
RA BOWIE E.J.W., GRALNICK H.R., GINSBURG D.;
RL J. CLIN. INVEST. 87:1227-1233(1991).
RN [25]
RP VARIANT CYS-1514.
RM 93168632
RA GAUCHER C., HANSS M., DECHAVANNE M., MAZURIER C.;
RL BR. J. HAEMATOL. 83:94-99(1993).
RN [26]
RP VARIANTS TRP-1597 AND ASP-1607.
RM 89264495
RA GINSBURG D., KONKLE B.A., GILL J.C., MONTGOMERY R.R.,
RA BOCKENSTEDT P.L., JOHNSON T.A., YANG A.Y.;
RL PROC. NATL. ACAD. SCI. U.S.A. 86:3723-3727(1989).
RN [27]
RP VARIANTS GLN-1597; ARG-1609 AND GLU-1665.
RM 93333089
RA INBAL A., ENGLENDER T., KORNBROT N., RANDI A.M., CASTAMAN G.,
RA MANNUCCI P.M., SADLER J.E.;
RL BLOOD 82:830-836(1993).
RN [28]
RP VARIANT THR-1628.
RM 91196734
RA IANNUZZI M.C., HIDAKA N., BOEHNKE M., BRUCK M.E., HANNA W.T.,
RA COLLINS F.S., GINSBURG D.;
RL AM. J. HUM. GENET. 48:757-763(1991).
RN [29]
RP VARIANT LYS-1638.
RM 93054652
RA RIBBA A.S., VOORBERG J., MEYER D., PANNEKOEK H., PIETU G.;
RL J. BIOL. CHEM. 267:23209-23215(1992).
RN [30]
RP VARIANT TYR-2739.
RM 94375013
RA ZHANG Z.P., BLOMBAECK M., EGBERG N., FALK G., ANVRET M.;
RL GENOMICS 21:188-193(1994).
CC -!- FUNCTION: VWF HAS AN IMPORTANT FUNCTION IN THE MAINTENANCE OF
CC HOMEOSTASIS, IT PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS
CC BY FORMING A NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT
CC THE SITE OF VASCULAR INJURY.
CC -!- SUBUNIT: MULTIMERIC.
CC -!- TISSUE SPECIFICITY: BLOOD.
CC -!- PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
CC INTERCHAIN DISULFIDE BONDS.

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CC   -!- THE A DOMAINS APPEAR TO BE RELATED TO 225 RESIDUES OF COMPLEMENT
CC       FACTOR B (THE LAST 5 RESIDUES OF BA AND THE AMINO-TERMINAL 220
CC       RESIDUES OF BB).
CC   -!- DISEASE: DEFICIENCIES IN VWF ARE ASSOCIATED WITH VARIOUS FORMS
CC       OF VON WILLEBRAND DISEASE (VWD) CHARACTERIZED BY FREQUENT BLEEDING
CC       (GINGIVAL, MINOR SKIN LACERATIONS, MENORRHAGIA, ETC.). TYPE I VWD
CC       IS ASSOCIATED WITH A QUANTATIVE DEFICIENCY OF VWF; TYPE II BY
CC       NORMAL TO DECREASED PLASMA LEVEL OF VWF; TYPE III BY A VIRTUAL
CC       ABSENCE OF VWF. THERE ARE SUBTYPES (A TO H) OF TYPE II VWD; FOR
CC       EXAMPLE: TYPE IIA IS CHARACTERIZED BY THE ABSENCE OF VWF HIGH
CC       MOLECULAR WEIGHT MULTIMERS IN PLASMA.
DR   EMBL; M25828; HSVWFA01.
DR   EMBL; M25829; HSVWFA02.
DR   EMBL; M25830; HSVWFA03.
DR   EMBL; M25831; HSVWFA04.
DR   EMBL; M25832; HSVWFA05.
DR   EMBL; M25833; HSVWFA06.
DR   EMBL; M25834; HSVWFA07.
DR   EMBL; M25835; HSVWFA08.
DR   EMBL; M25836; HSVWFA09.
DR   EMBL; M25837; HSVWFA10.
DR   EMBL; M25838; HSVWFA11.
DR   EMBL; M25839; HSVWFA12.
DR   EMBL; M25840; HSVWFA13.
DR   EMBL; M25841; HSVWFA14.
DR   EMBL; M25842; HSVWFA15.
DR   EMBL; M25843; HSVWFA16.
DR   EMBL; M25844; HSVWFA17.
DR   EMBL; M25845; HSVWFA18.
DR   EMBL; M25846; HSVWFA19.
DR   EMBL; M25847; HSVWFA20.
DR   EMBL; M25848; HSVWFA21.
DR   EMBL; M25849; HSVWFA22.
DR   EMBL; M25850; HSVWFA23.
DR   EMBL; M25851; HSVWFA24.
DR   EMBL; M25852; HSVWFA25.
DR   EMBL; M25853; HSVWFA26.
DR   EMBL; M25854; HSVWFA27.
DR   EMBL; M25855; HSVWFA28.
DR   EMBL; M25856; HSVWFA29.
DR   EMBL; M25857; HSVWFA30.
DR   EMBL; M25858; HSVWFA31.
DR   EMBL; M25859; HSVWFA32.
DR   EMBL; M25860; HSVWFA33.
DR   EMBL; M25861; HSVWFA34.
DR   EMBL; M25862; HSVWFA35.
DR   EMBL; M25863; HSVWFA36.
DR   EMBL; M25864; HSVWFA37.
DR   EMBL; M25865; HSVWFA38.
DR   EMBL; M10321; HSVWF1.
DR   EMBL; M10320; HSVWF2.
DR   EMBL; X04146; HSVWFR.
DR   EMBL; X02672; HSVWFC.
DR   EMBL; X04385; HSVWFR1.
DR   EMBL; X06828; HSVWF123.
DR   EMBL; X06829; HSVWF45.
DR   PIR; A03212; VWHU.
DR   PIR; A34480; A34480.
DR   PIR; A25298; A25298.
DR   PIR; A25469; A25469.
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DR   PIR; S02377; S02377.
DR   PIR; S07363; S07363.
DR   MIM; 193400; 11TH EDITION.
DR   MIM; 277480; 11TH EDITION.
KW   BLOOD COAGULATION; PLATELET; GLYCOPROTEIN; EXTRACELLULAR MATRIX;
KW   PLASMA; ENDOTHELIAL CELL; REPEAT; CELL ADHESION; SIGNAL;
KW   DISEASE MUTATION; POLYMORPHISM; VON WILLEBRAND DISEASE.
FT   SIGNAL        1     22
FT   PROPEP       23    763       D1/D2.
FT   CHAIN       764   2813       VON-WILLEBRAND FACTOR.
FT   DOMAIN      764    787       AMINO-TERMINAL.
FT   DOMAIN      788    833       E1.
FT   DOMAIN      826    853       CX.
FT   DOMAIN      842   1130       D3.
FT   DOMAIN     1260   1479       A1.
FT   DOMAIN     1480   1672       A2.
FT   DOMAIN     1673   1874       A3.
FT   DOMAIN     1934   2203       D4.
FT   DOMAIN     2216   2261       E2.
FT   DOMAIN     2296   2330       B1.
FT   DOMAIN     2340   2365       B2.
FT   DOMAIN     2375   2399       B3.
FT   DOMAIN     2400   2515       C1.
FT   DOMAIN     2544   2662       C2.
FT   DOMAIN     2663   2813       CARBOXYL-TERMINAL.
FT   REPEAT      788    833       E DOMAIN.
FT   REPEAT     2216   2261       E DOMAIN.
FT   REPEAT      826    853       C DOMAIN.
FT   REPEAT     2400   2515       C DOMAIN.
FT   REPEAT     2544   2662       C DOMAIN.
FT   REPEAT      842   1130       D DOMAIN.
FT   REPEAT     1934   2203       D DOMAIN.
FT   REPEAT     1260   1479       A DOMAIN.
FT   REPEAT     1480   1672       A DOMAIN.
FT   REPEAT     1673   1874       A DOMAIN.
FT   REPEAT     2296   2330       B DOMAIN.
FT   REPEAT     2340   2365       B DOMAIN.
FT   REPEAT     2375   2399       B DOMAIN.
FT   SIMILAR    1260   1479       WITH COMPLEMENT FACTOR B.
FT   SIMILAR    1480   1672       WITH COMPLEMENT FACTOR B.
FT   SIMILAR    1673   1874       WITH COMPLEMENT FACTOR B.
FT   SITE       2507   2509       CELL ATTACHMENT SITE.
FT   DISULFID   1272   1458
FT   CARBOHYD    857    857
FT   CARBOHYD   1147   1147
FT   CARBOHYD   1231   1231
FT   CARBOHYD   1248   1248       PROBABLE.
FT   CARBOHYD   1255   1255       PROBABLE.
FT   CARBOHYD   1256   1256       PROBABLE.
FT   CARBOHYD   1263   1263       PROBABLE.
FT   CARBOHYD   1468   1468       PROBABLE.
FT   CARBOHYD   1477   1477       PROBABLE.
FT   CARBOHYD   1486   1486       PROBABLE.
FT   CARBOHYD   1487   1487       PROBABLE.
FT   CARBOHYD   1515   1515
FT   CARBOHYD   1574   1574
FT   CARBOHYD   1679   1679       PROBABLE.
FT   CARBOHYD   2223   2223
FT   CARBOHYD   2290   2290
FT   CARBOHYD   2298   2298       PROBABLE.
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FT   CARBOHYD   2357   2357
FT   CARBOHYD   2400   2400
FT   CARBOHYD   2546   2546
FT   CARBOHYD   2585   2585
FT   CARBOHYD   2790   2790
FT   VARIANT     789    789       T -> A.
FT   VARIANT     791    791       T -> M (IN NORMANDY-1).
FT   VARIANT     816    816       R -> W (IN NORMANDY-2).
FT   VARIANT     852    852       R -> Q.
FT   VARIANT     854    854       R -> Q (IN NORMANDY-3).
FT   VARIANT     857    857       N -> D.
FT   VARIANT    1266   1266       P -> L (IN VWD TYPE I).
FT   VARIANT    1268   1268       H -> D (IN VWD TYPE IIB).
FT   VARIANT    1272   1272       C -> R (IN VWD TYPE IIA).
FT   VARIANT    1306   1306       R -> W (IN VWD TYPE IIB).
FT   VARIANT    1308   1308       R -> C (IN VWD TYPE IIB).
FT   VARIANT    1313   1313       W -> C (IN VWD TYPE IIB).
FT   VARIANT    1314   1314       V -> L (IN VWD TYPE IIB).
FT   VARIANT    1316   1316       V -> M (IN VWD TYPE IIB).
FT   VARIANT    1318   1318       V -> L (IN VWD TYPE IIB).
FT   VARIANT    1324   1324       G -> S (IN VWD TYPE IIB).
FT   VARIANT    1341   1341       R -> Q (IN VWD TYPE IIB).
FT   VARIANT    1381   1381       A -> T.
FT   VARIANT    1399   1399       R -> H.
FT   VARIANT    1514   1514       F -> C (IN VWD TYPE IIA).
FT   VARIANT    1597   1597       R -> W (IN VWD TYPE IIA).
FT   VARIANT    1597   1597       R -> Q (IN VWD TYPE IIA).
FT   VARIANT    1607   1607       V -> D (IN VWD TYPE IIA).
FT   VARIANT    1609   1609       G -> R (IN VWD TYPE IIA).
FT   VARIANT    1613   1613       S -> P (IN VWD TYPE IIA).
FT   VARIANT    1628   1628       I -> T (IN VWD TYPE IIA).
FT   VARIANT    1638   1638       E -> K (IN VWD TYPE IIA).
FT   VARIANT    1648   1648       P -> S (IN VWD TYPE IIA).
FT   VARIANT    1665   1665       V -> E (IN VWD TYPE IIA).
FT   VARIANT    2739   2739       C -> Y (IN VWD TYPE III).
FT   CONFLICT    471    471       I -> V (IN REF. 2 AND 3).
FT   CONFLICT    484    484       H -> R (IN REF. 3).
FT   CONFLICT    770    770       P -> H (IN REF. 4 AND 7).
FT   CONFLICT    804    804       C -> S (IN REF. 4 TO 7).
FT   CONFLICT   1472   1472       H -> D (IN REF. 5).
FT   CONFLICT   1914   1914       S -> T (IN REF. 2).
FT   CONFLICT   2168   2168       C -> S (IN REF. 5).
SQ   SEQUENCE   2813 AA;  309296 MW;  19889791 CN;

Initial Score     =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity  =    42%  Matches          =      3  Mismatches   =      4
Gaps              =      0  Conservative Substitutions              =      0

             X     X
             CGTXXXX
             |||
    NCPKGQVYLQCGTPCNLTCRSLSYPDE
           660       670


11. US-08-121-713B-3 (1-7)
    IP3R_MOUSE   INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE

 ID   IP3R_MOUSE      STANDARD;      PRT;  2749 AA.
 AC   P11881;
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DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 1 RECEPTOR
DE   (INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN P(400)) (TYPE 1 INSP3
DE   RECEPTOR).
GN   INSP3R.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CERBELLA PURKINJE NEURONS;
RM   90044039
RA   FURUICHI T., YOSHIKAWA S., MIYAWAKI A., WADA K., MAEDA N.,
RA   MIKOSHIBA K.;
RL   NATURE 342:32-38(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR; TISSUE=CEREBELLUM;
RM   89345101
RA   FURUICHI T., YOSHIKAWA S., MIKOSHIBA K.;
RL   NUCLEIC ACIDS RES. 17:5385-5386(1989).
RN   [3]
RP   ALTERNATIVE SPLICING.
RM   91296797
RA   NAKAGAWA T., OKANO H., FURUICHI T., ARUGA J., MIKOSHIBA K.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 88:6244-6248(1991).
CC   -!- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND
CC       MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
CC       THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL
CC       EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-
CC       BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE
CC       PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- PTM: PHOSPHORYLATED BY CYCLIC-AMP KINASE. PHOSPHORYLATION PREVENTS
CC       THE LIGAND-INDUCED OPENING OF THE CALCIUM CHANNELS.
CC   -!- CALCIUM APPEARS TO INHIBIT LIGAND BINDING TO THE RECEPTOR, MOST
CC       PROBABLY BY INTERACTING WITH A DISTINCT CALCIUM-BINDING PROTEIN
CC       WHICH THEN INHIBITS THE RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
CC       RETICULUM.
CC   -!- ALTERNATIVE PRODUCTS: ADDITIONAL SUBTYPES OF INSP3R ARISE BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE.
CC   -!- SIMILARITY: TO RYANODINE RECEPTOR.
DR   EMBL; X15373; MMP400.
DR   PIR; S04844; ACMSIT.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION;
KW   ENDOPLASMIC RETICULUM; IONIC CHANNEL; ION TRANSPORT; CALCIUM CHANNEL;
KW   ALTERNATIVE SPLICING.
FT   DOMAIN        1   2273       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   2274   2294       M1 (POTENTIAL).
FT   TRANSMEM   2308   2326       M2 (POTENTIAL).
FT   TRANSMEM   2334   2356       M3 (POTENTIAL).
FT   TRANSMEM   2365   2387       M4 (POTENTIAL).
FT   TRANSMEM   2391   2407       M5 (POTENTIAL).
FT   TRANSMEM   2440   2462       M6 (POTENTIAL).
FT   TRANSMEM   2530   2549       M7 (POTENTIAL).
FT   TRANSMEM   2570   2589       M8 (POTENTIAL).
FT   DOMAIN     2590   2749       CYTOPLASMIC (POTENTIAL).
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FT   VARSPLIC    318    332       MISSING (IN INSP3R SI-).
FT   VARSPLIC   1692   1731       MISSING (IN INSP3R SIIABC-).
FT   VARSPLIC   1715   1715       MISSING (IN INSP3R SIIB-).
FT   VARSPLIC   1715   1731       MISSING (IN INSP3R SIIBC-).
FT   MOD_RES    1588   1588       PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   MOD_RES    1755   1755       PHOSPHORYLATION (BY CAPK) (POTENTIAL).
SQ   SEQUENCE   2749 AA;  313193 MW;  22837568 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            CGTXXXX
            |||
    IIFLMSFVGNCGTFTRGYRAMVLDVEF
      2370    X 2380      2390
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12. US-08-121-713B-3 (1-7)
    IP3R_RAT INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE

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ID   IP3R_RAT       STANDARD;      PRT;  2749 AA.
AC   P29994;
DT   01-APR-1993 (REL. 25, CREATED)
DT   01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 1 RECEPTOR
DE   (INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN P(400)) (TYPE 1 INSP3
DE   RECEPTOR).
GN   INSP3R.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   90324264
RA   MIGNERY G.A., NEWTON C.L., ARCHER B.T. III, SUEDHOF T.C.;
RL   J. BIOL. CHEM. 265:12679-12685(1990).
CC   -!- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND
CC       MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
CC       THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL
CC       EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-
CC       BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE
CC       PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- PTM: PHOSPHORYLATED BY CYCLIC-AMP KINASE. PHOSPHORYLATION PREVENTS
CC       THE LIGAND-INDUCED OPENING OF THE CALCIUM CHANNELS.
CC   -!- CALCIUM APPEARS TO INHIBIT LIGAND BINDING TO THE RECEPTOR, MOST
CC       PROBABLY BY INTERACTING WITH A DISTINCT CALCIUM-BINDING PROTEIN
CC       WHICH THEN INHIBITS THE RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
CC       RETICULUM.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED.
CC   -!- SIMILARITY: TO RYANODINE RECEPTOR.
DR   EMBL; J05510; RRI145TR.
DR   PIR; A36579; A36579.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION;
KW   ENDOPLASMIC RETICULUM; IONIC CHANNEL; ION TRANSPORT; CALCIUM CHANNEL;
KW   ALTERNATIVE SPLICING.
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FT   DOMAIN        1   2273       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   2274   2294       M1 (POTENTIAL).
FT   TRANSMEM   2308   2326       M2 (POTENTIAL).
FT   TRANSMEM   2334   2356       M3 (POTENTIAL).
FT   TRANSMEM   2365   2387       M4 (POTENTIAL).
FT   TRANSMEM   2391   2407       M5 (POTENTIAL).
FT   TRANSMEM   2440   2462       M6 (POTENTIAL).
FT   TRANSMEM   2530   2549       M7 (POTENTIAL).
FT   TRANSMEM   2570   2589       M8 (POTENTIAL).
FT   DOMAIN     2590   2749       CYTOPLASMIC (POTENTIAL).
FT   MOD_RES    1589   1589       PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   MOD_RES    1755   1755       PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   VARSPLIC    322    336       MISSING (IN VARIANT).
FT   VARIANT    1372   1372       MISSING (IN ALL, BUT P17 CLONES).
SQ   SEQUENCE   2749 AA;  313132 MW;  22831603 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            CGTXXXX
            |||
    IIFLMSFVGNCGTFTRGYRAMVLDVEF
      2370    X 2380      2390
```

13. US-08-121-713B-3 (1-7)
    ZEP1_HUMAN ZINC FINGER PROTEIN 40 (HUMAN IMMUNODEFICIENCY VIR

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ID   ZEP1_HUMAN     STANDARD;      PRT;  2717 AA.
AC   P15822;
DT   01-APR-1990 (REL. 14, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   ZINC FINGER PROTEIN 40 (HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-
DE   BINDING PROTEIN 1) (HIV-EP1) (MAJOR HISTOCOMPATIBILITY COMPLEX BINDING
DE   PROTEIN 1) (MBP-1) (POSITIVE REGULATORY DOMAIN II BINDING FACTOR 1)
DE   (PRDII-BF1).
GN   HIVEP1 OR ZNF40.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   90169514
RA   FAN C.M., MANIATIS T.;
RL   GENES DEV. 4:29-42(1990).
RN   [2]
RP   STRUCTURE BY NMR OF 2113-2142.
RM   91064333
RA   OMICHINSKI J.G., CLORE G.M., APPELLA E., SAKAGUCHI K.,
RA   GRONENBORN A.M.;
RL   BIOCHEMISTRY 29:9324-9334(1990).
RN   [3]
RP   STRUCTURE BY NMR OF 2087-2142.
RM   92232684
RA   OMICHINSKI J.G., CLORE G.M., ROBIEN M., SAKAGUCHI K., APPELLA E.,
RA   GRONENBORN A.M.;
RL   BIOCHEMISTRY 31:3907-3917(1992).
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CC   -!- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE
CC       5'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF
CC       NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1.
CC       IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS
CC       OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I
CC       MHC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT
CC       IN T-CELL ACTIVATION.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED
CC       AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH ZINC-FINGER
CC       IN-BETWEEN.
CC   -!- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
CC   -!- SIMILARITY: 70% BETWEEN THE TWO ZINC-FINGER DOMAINS.
CC   -!- SIMILARITY: STRONG, TO HIV-EP2.
DR   EMBL; X51435; HSZFPBF1.
DR   PIR; A34203; A34203.
DR   PDB; 3ZNF; 15-JAN-92.
DR   PDB; 4ZNF; 15-JAN-92.
DR   PDB; 1BBO; 31-OCT-93.
DR   TRANSFAC; T00497; -.
DR   MIM; 194540; 11TH EDITION.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2.
KW   TRANSCRIPTION REGULATION; ZINC-FINGER; METAL-BINDING; DNA-BINDING;
KW   NUCLEAR PROTEIN; 3D-STRUCTURE.
FT   DOMAIN      406    456       ZINC-FINGERS.
FT   ZN_FING     406    428       C2H2-TYPE.
FT   ZN_FING     434    456       C2H2-TYPE.
FT   ZN_FING     955    981       CC-X(13)-HC MOTIF (POTENTIAL).
FT   DOMAIN     2087   2139       ZINC-FINGERS.
FT   ZN_FING    2087   2109       C2H2-TYPE.
FT   ZN_FING    2115   2139       C2H2-TYPE.
FT   STRAND     2088   2088
FT   TURN       2090   2092
FT   STRAND     2095   2095
FT   HELIX      2099   2108
FT   TURN       2109   2109
FT   STRAND     2115   2116
FT   STRAND     2123   2124
FT   HELIX      2127   2135
SQ   SEQUENCE   2717 AA;  297217 MW;  19898490 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    TDNSECISSHCGTTSPSYTNTAFDVLL
        180   X   190       200
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14. US-08-121-713B-3 (1-7)
    G156_PARPR 156G SURFACE PROTEIN PRECURSOR.

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ID   G156_PARPR     STANDARD;      PRT;  2715 AA.
AC   P13837;
DT   01-JAN-1990 (REL. 13, CREATED)
DT   01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT   01-AUG-1990 (REL. 15, LAST ANNOTATION UPDATE)
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DE   156G SURFACE PROTEIN PRECURSOR.
GN   156G.
OS   PARAMECIUM PRIMAURELIA.
OC   EUKARYOTA; PROTOZOA; CILIOPHORA; CILIATA; HOLOTRICHA; HYMENOSTOMATIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=156;
RM   87060934
RA   PRAT A., KATINKA M., CARON F., MEYER E.;
RL   J. MOL. BIOL. 189:47-60(1986).
CC   -!- FUNCTION: THIS PROTEIN IS THE SURFACE ANTIGEN OR IMMOBILIZATION
CC       ANTIGEN OF PARAMECIUM PRIMAURELIA.
CC   -!- IT HAS INTERNAL HOMOLOGIES AND A HIGHLY PERIODIC STRUCTURE WITH
CC       37 PERIODS OF ABOUT 75 RESIDUES, EACH PERIOD CONTAINING 8
CC       CYSTEINES, EXCEPT FOR FOUR HALF PERIODS. A VARIABLE PART OF 475
CC       RESIDUES COMPRISES 4 ALMOST IDENTICAL PERIODS IN THE MIDDLE OF THE
CC       PROTEIN.
CC   -!- EXPRESSION OF G PROTEIN OCCURS AT LOW TEMPERATURES (14-32
CC       DEGREE CELSIUS).
CC   -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC   -!- SIMILARITY: 98% TO THE ALLELIC FORM 168G PROTEIN (P17053) IN
CC       PERIODIC STRUCTURE AND 80% IN VARIABLE DOMAIN IN THE MIDDLE OF
CC       THE PROTEIN.
DR   EMBL; X03882; PPSGP.
DR   PIR; A23475; A23475.
DR   HSSP; P06620; 1INA.
KW   SIGNAL; REPEAT; ANTIGEN; MEMBRANE; GPI-ANCHOR.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21   2715       156G SURFACE PROTEIN.
FT   DOMAIN      106   2560       37 X 75 AA APPROXIMATE REPEATS.
FT   SIMILAR       1    222       88% TO PARAMECIUM TETRAURELIA A
FT                                PROTEIN.
SQ   SEQUENCE   2715 AA;  279551 MW;  16284274 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             CGTXXXX
             |||
    ITGTGLTTAICGTYDAGCVANVNGTAC
 1070      1080    X 1090
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15. US-08-121-713B-3 (1-7)
    CENE_HUMAN CENTROMERIC PROTEIN E (CENP-E PROTEIN).

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ID   CENE_HUMAN     STANDARD;      PRT;  2663 AA.
AC   Q02224;
DT   01-JUL-1993 (REL. 26, CREATED)
DT   01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT   01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE   CENTROMERIC PROTEIN E (CENP-E PROTEIN).
GN   CENPE.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
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RM   93024922
RA   YEN T.J., LI G., SCHAAR B.T., SZILAK I., CLEVELAND D.W.;
RL   NATURE 359:536-539(1992).
CC   -!- FUNCTION: PROBABLE KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE
CC       MITOSIS AT THE G2 PHASE OF THE CELL CYCLE. PROBABLY IMPORTANT
CC       FOR CHROMOSOME MOVEMENT AND/OR SPINDLE ELONGATION.
CC   -!- SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CC       CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS
CC       QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
CC   -!- SIMILARITY: BELONGS TO A FAMILY OF KINESIN-LIKE PROTEINS
CC       CHARACTERIZED BY THE PRESENCE OF A MECHANOCHEMICAL DOMAIN TETHERED
CC       TO DIFFERENT PROTEIN BINDING DOMAINS.
DR   EMBL; Z15005; HSCENPE.
DR   PIR; S28261; S28261.
DR   MIM; 117143; 11TH EDITION.
DR   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN.
KW   MOTOR PROTEIN; CELL DIVISION; ATP-BINDING; COILED COIL; MITOSIS;
KW   CELL CYCLE; CENTROMERE.
FT   DOMAIN        1    335       MECHANOCHEMICAL (MOTOR).
FT   DOMAIN      336   2471       COILED COIL (POTENTIAL).
FT   DOMAIN     2472   2663       GLOBULAR (POTENTIAL).
FT   NP_BIND      86     93       ATP (BY SIMILARITY).
SQ   SEQUENCE   2663 AA;  312087 MW;  23820152 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.98
Residue Identity =    42%  Matches          =      3  Mismatches   =     4
Gaps             =      0  Conservative Substitutions              =     0

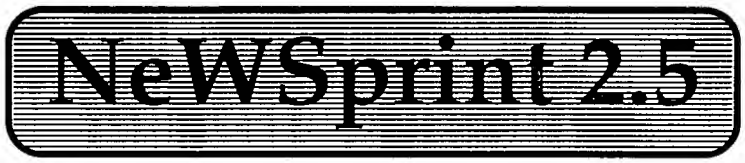
             X     X
             CGTXXXX
             |||
    IYNETITDLLCGTQKMKPLIIREDVNR
       140   X   150       160
```

maryh@stic **stdin**

NeWSprinter20

Fri May 19 10:59:04 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0



Salata 121713

SEQ 7

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O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq7asq.res made by  on Fri 19 May 95 8:39:35-PDT.


Query sequence being compared:US-08-121-713B-7 (1-7)
Number of sequences searched:                53402
Number of scores above cutoff:                4072

     Results of the initial comparison of US-08-121-713B-7 (1-7) with:
   Data bank : A-GeneSeq 18, all entries

100000-
      -
N     -
U50000*
M     -
B     -
E     -
R     -
      -
O     -
F10000-
      -                                                              *
S     -
E 5000-
Q     -
U     -
E     -
N     -
C     -
E     -
S 1000-
      -
      -
   500-
      -
      -
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      -
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      -
   100-
      -
      -
    50-
      -
      -
      -
      -
      -
      -
    10-
      -
      -
```



```
    5-
      -
      -
      -
      -
      -
      -
      -
    0-------------------------------------------------------------------------
      |       |  |   |       |       |       |       |  |  |       |       |
SCORE 0       1  |   2       2       3       4       5  |  5       6       7
STDEV            1                   2                  3
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PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	0	1	2.39

Times:	CPU	Total Elapsed
	00:00:32.00	00:00:32.00

Number of residues: 6354270
Number of sequences searched: 53402
Number of scores above cutoff: 4072

Cut-off raised to 1.
Cut-off raised to 2.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

4072 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. R54099	NANBHV E1/E2 protein.	3014	7	7	2.92	0
2. R53417	Blood transmiscible NANBHV pr	3010	7	7	2.92	0
3. R59921	RAS associated GAP NF201.	2485	7	7	2.92	0
4. R59922	RAS associated GAP NF204.	2485	7	7	2.92	0
5. R55694	Carbamoyl-phosphate-synthetas	2391	7	7	2.92	0
6. R52580	RPTP-beta amino acid sequence	2308	7	7	2.92	0
7. R67819	Acetyl CoA carboxylase.	2240	7	7	2.92	0
8. R53257	Human collagen (Type V).	1838	7	7	2.92	0

9.	R55273	Beta subunit of integrin cell	1822	7	7	2.92	0
10.	R59751	Type II collagen.	1418	7	7	2.92	0
11.	R60292	Varicella zoster virus IEP175	1310	7	7	2.92	0
12.	R54841	HER4.	1308	7	7	2.92	0
13.	R52701	Plasmid pASK60-Strep reading	1277	7	7	2.92	0
14.	R52702	Plasmid pASK60-Strep reading	1277	7	7	2.92	0
15.	R54074	CryET5.	1229	7	7	2.92	0
16.	R55764	Sequence encoded by the cDNA	1153	7	7	2.92	0
17.	R55272	Alpha subunit of integrin cel	1073	7	7	2.92	0
18.	R54843	HER4 with alternate 3'-end wi	1058	7	7	2.92	0
19.	R54066	Non-A, non-B hepatitis virus	1051	7	7	2.92	0
20.	R54067	Non-A, non-B hepatitis virus	1031	7	7	2.92	0
21.	R53921	HCV fusion protein corresp. t	980	7	7	2.92	0
22.	R52566	Phosphoenol pyruvate carboxyl	964	7	7	2.92	0
23.	R52567	Phosphoenol pyruvate carboxyl	964	7	7	2.92	0
24.	R56990	Bacillus deramificans pullula	957	7	7	2.92	0
25.	R56989	Bacillus deramificans mature	928	7	7	2.92	0
26.	R53963	VEF.	901	7	7	2.92	0
27.	R60252	NF-ATp.	890	7	7	2.92	0
28.	R59924	Human GAP protein.	870	7	7	2.92	0
29.	R53732	S. cerevisiae Plc1 protein.	869	7	7	2.92	0
30.	R53404	S-Locus receptor (serine/thre	858	7	7	2.92	0
31.	R53228	Rice starch branching enzyme.	820	7	7	2.92	0
32.	R55692	hnRNP U protein.	806	7	7	2.92	0
33.	R57283	Bovine enterokinase.	798	7	7	2.92	0
34.	R52690	HCV CKS-33-BCD antigen.	781	7	7	2.92	0
35.	R55708	Glycosyltransferase hybrid.	767	7	7	2.92	0
36.	R55709	Glycosyltransferase hybrid.	767	7	7	2.92	0
37.	R54611	Native CD26.	766	7	7	2.92	0
38.	R53778	Sequence of human amyloid pro	763	7	7	2.92	0
39.	R54612	Delta3-9 CD26.	759	7	7	2.92	0
40.	R59784	Human pro-hormone convertase	753	7	7	2.92	0
41.	R67764	Murine pro-hormone convertase	753	7	7	2.92	0
42.	R55097	Prostate-specific membrane an	750	7	7	2.92	0
43.	R55206	Human zona pellucida ZPA prot	745	7	7	2.92	0
44.	R54867	Hepatitis C Virus core protei	743	7	7	2.92	0
45.	R54613	Delta24-34 CD26.	739	7	7	2.92	0

1. US-08-121-713B-7 (1-7)
R54099 NANBHV E1/E2 protein.

```
ID   R54099 standard; Protein; 3014 AA.
AC   R54099;
DT   09-FEB-1995  (first entry)
DE   NANBHV E1/E2 protein.
KW   E1/E2 protein; non-A, non-B hepatitits virus; NANBHV; signal peptide;
KW   heterogenic; virus; transformation; insect cell; antigen; anti-NANBHV;
KW   antibody; hepatitis C virus; HCV; vaccine.
OS   Non-A, non-B hepatitis virus.
FH   Key             Location/Qualifiers
FT   Peptide         832..847
FT   /note= "Peptide fragment not given in the specification,
FT   but encoded by the given cDNA sequence"
FT   Peptide         1296..1311
FT   /note= "Peptide fragment not given in the specification,
FT   but encoded by the given cDNA sequence"
FT   Peptide         1760..1775
FT   /note= "Peptide fragment not given in the specification,
FT   but encoded by the given cDNA sequence"
```



```
FT   Peptide         2688..2703
FT   /note= "Peptide fragment not given in the specification,
FT   but encoded by the given cDNA sequence"
PN   J06141873-A.
PD   24-MAY-1994.
PF   13-MAR-1992; 089371.
PR   13-MAR-1992; JP-089371.
PA   (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
DR   WPI; 94-205030/25.
DR   N-PSDB; Q64175.
PT   Virus vector contg hepatitis C virus and signal sequence - useful
PT   in vaccines and in immunological detection
PS   Disclosure; Page 7-19; 23pp; Japanese.
CC   This sequence represents the E1/E2 protein from non-A, non-B hepatitits
CC   virus (NANBHV).  The cDNA encoding this sequence may be linked to a
CC   signal peptide (r54100) from a heterogenic virus so the the NANBHV
CC   protein may be expressed by a transformed insect cell.  This protein
CC   may be used as an antigen in the generation of anti-NANBHV antibodies.
CC   These antibodies may be used in a hepatitis C vaccine.
SQ   Sequence   3014 AA;
SQ   293A; 178R; 91 N; 127D; 0  B; 97 C; 88 Q; 112E; 0  Z; 252G; 68 H;
SQ   129I; 301L; 95 K; 61 M; 86 F; 205P; 216S; 216T; 65 W; 99 Y; 235V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                  |
    RVLEDGVNYATGNMPGCSFSIFLLALL
      160     X 170 X     180
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2. US-08-121-713B-7 (1-7)
R53417 Blood transmiscible NANBHV protein.

```
ID   R53417 standard; Protein; 3010 AA.
AC   R53417;
DT   17-JAN-1995  (first entry)
DE   Blood transmiscible NANBHV protein.
KW   Polymerase chain reaction; PCR; amplify; primer; non-A, non-B hepatitis;
KW   NANBH; virus; blood transmissible; detection; hepatitis virus; RT-PCR;
KW   C100 antibody; HCV RNA; NS5 region.
OS   Non-A, non-B hepatitis virus.
FH   Key             Location/Qualifiers
FT   Misc_difference 222
FT   /label= His, Arg
FT   Misc_difference 226
FT   /label= Cys, Arg
FT   Misc_difference 246
FT   /label= Leu, Phe
FT   Misc_difference 263
FT   /label= Asp, Asn
FT   Misc_difference 291
FT   /label= Phe, Ser
FT   Misc_difference 311
FT   /label= Gly, Asp
FT   Misc_difference 398
FT   /label= Ser, Arg, Gly
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FT   Misc_difference 400
FT   /label= Thr, Ala
FT   Misc_difference 405
FT   /label= Gln, Pro, Leu
FT   Misc_difference 410
FT   /label= Lys, Arg
FT   Misc_difference 418
FT   /label= Gly, Asp
FT   Misc_difference 430
FT   /label= Asn, Asp
FT   Misc_difference 438
FT   /label= Phe, Leu
FT   Misc_difference 478
FT   /label= Arg, Lys
FT   Misc_difference 759
FT   /label= Leu, Val
FT   Misc_difference 1017
FT   /label= Ser, Asn
FT   Misc_difference 1036
FT   /label= Thr, Ala
FT   Misc_difference 1056
FT   /label= Glu, Asp
FT   Misc_difference 1201
FT   /label= Met, Thr
FT   Misc_difference 1205
FT   /label= Met, Ile
FT   Misc_difference 1255
FT   /label= Asn, Tyr
FT   Misc_difference 1263
FT   /label= Gly, Asp
FT   Misc_difference 1455
FT   /label= Asn, Asp
FT   Misc_difference 1828
FT   /label= Ala, Thr
FT   Misc_difference 1895
FT   /label= Gly, Arg
FT   Misc_difference 1896
FT   /label= Gly, Ile
FT   Misc_difference 2143
FT   /label= Glu, Val
FT   Misc_difference 2144
FT   /label= Asp, Glu
FT   Misc_difference 2462
FT   /label= Cys, Arg
FT   Misc_difference 2486
FT   /label= Val, Met
FT   Misc_difference 2488
FT   /label= Lys, Gln
FT   Misc_difference 2844
FT   /label= Leu, Met
FT   Misc_difference 2862
FT   /label= Leu, Gln
FT   Misc_difference 2917
FT   /label= Arg, Leu
FT   Misc_difference 2968
FT   /label= Ser, Gly
FT   Misc_difference 2989
FT   /label= Cys, Arg
FT   Misc_difference 2990
FT   /label= Tyr, Cys
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PN   J06105690-A.
PD   19-APR-1994.
PF   10-MAR-1992; 051885.
PR   10-MAR-1992; JP-051885.
PA   (KAEN/) KAENNO K.
DR   WPI; 94-163130/20.
DR   N-PSDB; Q63499.
PT   Blood-transmissible non-A non-B hepatitis virus DNA - used for
PT   detection of hepatitis virus
PS   Claim 1; Page 8-20; 22pp; Japanese.
CC   This sequence is encoded by the genome of a blood transmissible non-A,
CC   non-B hepatitis (NANBH) virus. The cDNA sequence was isolated using the
CC   primers given in Q63500-35.  The amplified fragments are used in the
CC   detection of hepatitis virus.  The target DNA was isolated from serum
CC   of chronically infected NANBH patients who were C100 antibody-positive
CC   and HCV RNA (NS5 region) positive.  Reverse transcription-PCR and PCR
CC   were performed on cDNA and the total human NANBH DNA was constructed
CC   from 23 clones.
SQ   Sequence   3010 AA;
SQ   289A; 166R; 80 N; 124D; 0  B; 96 C; 94 Q; 113E; 0  Z; 241G; 63 H;
SQ   134I; 295L; 97 K; 57 M; 88 F; 204P; 216S; 225T; 64 W; 100Y; 227V;
SQ   37 Others;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                  |
    RKHPEATYTKCGSGPWLTPRCIVDYPY
     590       600  X    610
```

3. US-08-121-713B-7 (1-7)
   R59921 RAS associated GAP NF201.

```
ID   R59921 standard; protein; 2485 AA.
AC   R59921;
DT   22-FEB-1995  (first entry)
DE   RAS associated GAP NF201.
KW   Ras; GTPase activating protein; GAP; GAP related domain; GRD;
KW   pkT10; pkP11; Saccharomyces cerevisiae; RAS2; v-Ras; heat shock;
KW   neurofibromatosis type 1; NF1.
OS   Homo sapiens.
PN   WO9416069-A.
PD   21-JUL-1994.
PF   12-JAN-1994; U00198.
PR   15-JAN-1993; US-004824.
PA   (SCHE ) SCHERING CORP.
PI   Kaziro Y,  Nakafuku M;
DR   WPI; 94-249216/30.
PT   Blocking Ras-induced effects on a cell - by introducing a GTPase
PT   activating protein to the cell, used esp. in treatment of cancers
PS   Disclosure; Page 36-44; 87pp; English.
CC   Human neurofibromatosis type 1 (NF1)-GAP related domain (GRD) was
CC   cloned into the yeast expression vector pkT10 to obtain pkP11.  The
CC   pkP11 DNA was mutagenized by hydroxylamine in vitro and transformed
CC   into S. cerevisiae TK161-R2V-D, which carries an oncogenic-type
CC   RAS2Val19 mutation.  The heat shock sensitivity of the clones was
```

```
CC   checked.  Plasmid DNAs were recovered, re-transformed into TK161-
CC   R2V-D, and phenotypic reversion was examined.  2 Clones, NF201 and
CC   NF204 (given in R59922), which had strong suppression activity for
CC   RAS2Val19, were selected.  The mutant NF1-GRDs were also able to
CC   inhibit v-Ras-induced transformation in mammalian cells.
SQ   Sequence   2485 AA;
SQ   159A; 109R; 110N; 113D; 0  B; 51 C; 111Q; 146E; 0  Z; 110G; 80 H;
SQ   127I; 312L; 141K; 75 M; 104F; 112P; 221S; 156T; 28 W; 63 Y; 157V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                   |
   LITGLVQLVPQSHMPEIAQEAMEALLV
          200       210


4. US-08-121-713B-7 (1-7)
   R59922       RAS associated GAP NF204.

ID   R59922 standard; protein; 2485 AA.
AC   R59922;
DT   22-FEB-1995  (first entry)
DE   RAS associated GAP NF204.
KW   Ras; GTPase activating protein; GAP; GAP related domain; GRD;
KW   pkT10; pkP11; Saccharomyces cerevisiae; RAS2; v-Ras; heat shock;
KW   neurofibromatosis type 1; NF1.
OS   Homo sapiens.
PN   WO9416069-A.
PD   21-JUL-1994.
PF   12-JAN-1994; U00198.
PR   15-JAN-1993; US-004824.
PA   (SCHE ) SCHERING CORP.
PI   Kaziro Y,  Nakafuku M;
DR   WPI; 94-249216/30.
PT   Blocking Ras-induced effects on a cell - by introducing a GTPase
PT   activating protein to the cell, used esp. in treatment of cancers
PS   Disclosure; Page 44-52; 87pp; English.
CC   Human neurofibromatosis type 1 (NF1)-GAP related domain (GRD) was
CC   cloned into the yeast expression vector pkT10 to obtain pkP11.  The
CC   pkP11 DNA was mutagenized by hydroxylamine in vitro and transformed
CC   into S. cerevisiae TK161-R2V-D, which carries an oncogenic-type
CC   RAS2Val19 mutation.  The heat shock sensitivity of the clones was
CC   checked.  Plasmid DNAs were recovered, re-transformed into TK161-
CC   R2V-D, and phenotypic reversion was examined.  2 Clones, NF201
CC   (given in R59921) and NF204, which had strong suppression activity
CC   for RAS2Val19, were selected.  The mutant NF1-GRDs were also able
CC   to inhibit v-Ras-induced transformation in mammalian cells.
SQ   Sequence   2485 AA;
SQ   160A; 108R; 110N; 113D; 0  B; 52 C; 111Q; 146E; 0  Z; 109G; 81 H;
SQ   125I; 313L; 136K; 76 M; 106F; 114P; 221S; 156T; 28 W; 63 Y; 157V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
```



```
             XXXXPXX
                   |
   LITGLVQLVPQSHMPEIAQEAMEALLV
          200       210


5. US-08-121-713B-7 (1-7)
   R55694       Carbamoyl-phosphate-synthetase II.

ID   R55694 standard; Protein; 2391 AA.
AC   R55694;
DT   06-DEC-1994  (first entry)
DE   Carbamoyl-phosphate-synthetase II.
KW   Carbamoyl-phosphate-synthetase II; CPSII; psCPSII gene;
KW   malaria.
OS   Plasmodium falciparum.
FH   Key             Location/Qualifiers
FT   Domain          1..690
FT   /note= "glutamine-amidotransferase domain"
FT   Domain          1..270
FT   /note= "structural subdomain"
FT   Peptide         271..482
FT   /note= "insert sequence"
FT   Domain          483..690
FT   /note= "glutaminase subdomain"
FT   Domain          691..2391
FT   /note= "carbamoyl-phosphate-synthase domain"
FT   Domain          691..1254
FT   /note= "ATP binding subdomain CPSa"
FT   Peptide         1255..1857
FT   /note= "insert sequence"
FT   Domain          1858..2391
FT   /note= "ATP binding subdomain CPSb"
PN   WO9412643-A.
PD   09-JUN-1994.
PF   02-DEC-1993; AU0617.
PR   03-DEC-1992; AU-006206.
PR   16-DEC-1992; AU-006380.
PA   (UNIX ) UNISEARCH LTD.
PI   Flores MV,  Osullivan WJ,  Stewart TS;
DR   WPI; 94-200271/24.
DR   N-PSDB; Q62924.
PT   Nucleic acid encoding carbamoyl phosphate synthetase II -
PT   isolated from Plasmodium falciparum, used to develop prods. for
PT   the treatment of malaria.
PS   Disclosure; Page 6-16; 31pp; English.
CC   The cDNA sequence encoding the carbamoyl-phosphate-transferase II
CC   (CPSII) of Plasmodium falciparum was determined.  The cDNA encodes
CC   a protein that includes 2 insert sequences not found in other CPSII
CC   proteins.  The first separates the putative structural subdomain and
CC   the glutaminase subdomain of the glutamine-amidotransferase subunit
CC   of CPSII, while the second separates 2 ATP binding subdomains of the
CC   CPSII subunit, CPSa and CPSb.
SQ   Sequence   2391 AA;
SQ   68 A; 61 R; 328N; 150D; 0  B; 53 C; 48 Q; 164E; 0  Z; 110G; 53 H;
SQ   219I; 185L; 234K; 42 M; 100F; 45 P; 176S; 97 T; 7  W; 135Y; 116V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0
```

```
            X     X
            XXXXPXX
                 |
   KRIDAIHQAFHLNMPMDKIHELTHIDY
        1120 X    1130
```

6. US-08-121-713B-7 (1-7)
R52580 RPTP-beta amino acid sequence.

```
ID   R52580 standard; protein; 2308 AA.
AC   R52580;
DT   02-FEB-1995  (first entry)
DE   RPTP-beta amino acid sequence.
KW   Receptor protein tyrosine phosphatase; RPTP-beta; extracellular; CAM;
KW   carbonic anhydrase; structural domain; cytoplasmic; phosphatase domains;
KW   ligand; receptor-ligand complex; cell adhesion molecule; N-CAM; Ng-CAM;
KW   growth factor; extracellular matrix component; enzymatic activity;
KW   differentiation; metabolism; cell cycle control; neuronal function;
KW   contractility; contact inhibition; viral receptor interactions;
KW   inflammations; cellular transformation; cancer; type 2; NIDDM;
KW   non-insulin dependant diabetes melitus.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         1..21
FT   /note= "Signal peptide"
FT   Domain          33..301
FT   /note= "Carbonic anhydrase domain"
FT   Modified_site   108
FT   /note= "N-linked glycosylation site"
FT   Modified_site   134
FT   /note= "N-linked glycosylation site"
FT   Modified_site   223
FT   /note= "N-linked glycosylation site"
FT   Modified_site   232
FT   /note= "N-linked glycosylation site"
FT   Modified_site   325
FT   /note= "N-linked glycosylation site"
FT   Modified_site   381
FT   /note= "N-linked glycosylation site"
FT   Modified_site   480
FT   /note= "N-linked glycosylation site"
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FT   /note= "N-linked glycosylation site"
FT   Modified_site   1562
FT   /note= "N-linked glycosylation site"
FT   Modified_site   1618
FT   /note= "N-linked glycosylation site"
FT   Domain          1635..1662
FT   /note= "Transmembrane domain"
FT   Domain          1743..1984
FT   /note= "DI phosphatase domain"
FT   Domain          2041..2274
FT   /note= "DII phosphatase domain"
PN   WO9409037-A.
PD   28-APR-1994.
PF   14-OCT-1993; U09838.
PR   15-OCT-1992; US-961235.
PA   (UYNY-) UNIV NEW YORK MEDICAL CENT.
PI   Barnea G,  Grumet MH,  Margolis RU,  Schlessinger J;
DR   WPI; 94-151249/18.
PT   New class of receptor protein tyrosine phosphatase molecule -
PT   useful for identifying cpds which modulate the enzymatic activity
PT   of the receptors
PS   Claim 3; Fig 1; 66pp; English.
CC   This sequence represents the receptor protein tyrosine phosphatase,
CC   RPTP-beta.  This protein comprises an extracellular carbonic
CC   anhydrase structural domain and two cytoplasmic phosphatase domains.
CC   RPTP-beta non-covalently binds a ligand  to form a receptor-ligand
CC   complex.  The ligand is pref. a cell adhesion molecule (CAM), esp. N-
CC   CAM or Ng-CAM, or a growth factor or extracellular matrix component.
CC   The endogenous enzymatic activity of RPTP-beta may be increased or
CC   decreased.  This modulation regulates cellular functions comprising
CC   differentiation, metabolism, cell cycle control or neuronal function.
CC   The modulation pref. regulates cellular behaviour comprising
CC   contractility or contact inhibition.  It esp. regulates abnormal or
CC   deleterious processes comprising viral receptor interactions,
CC   inflammations, cellular transformation to a cancerous state, or
CC   development of type 2 NIDDM.
SQ   Sequence   2308 AA;
SQ   144A; 47 R; 86 N; 135D; 0  B; 32 C; 96 Q; 166E; 0  Z; 119G; 67 H;
SQ   123I; 186L; 109K; 58 M; 88 F; 122P; 286S; 179T; 20 W; 74 Y; 159V;
SQ   12 Others;
```

```
Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0
```

```
            X     X
            XXXXPXX
                 |
   PVMSQGPSVTDLEMPHYSTFAYFDTEV
    700        710  X    720
```

7. US-08-121-713B-7 (1-7)
R67819 Acetyl CoA carboxylase.

```
ID   R67819 standard; Protein; 2240 AA.
AC   R67819;
DT   01-MAR-1995  (first entry)
DE   Acetyl CoA carboxylase.
KW   Acetyl CoA; carboxylase; lipid; fatty acid; biosynthesis;
KW   metabolism; Brassica napus.
OS   Brassica napus.
PN   DE4317260-A.
PD   28-JUL-1994.
PF   24-MAY-1993; 317260.
PR   22-JAN-1993; DE-301694.
PR   24-MAY-1993; DE-317260.
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PI   Schell J,  Schulte W,  Toepfer R;
DR   WPI; 94-236136/29.
DR   N-PSDB; Q67676.
PT   Acetyl CoA-carboxylase from plants, e.g. brassica napus - is
PT   useful for modifying the oil and fatty acid prodn. in plants or
PT   for conferring resistance to certain herbicides
PS   Disclosure; Figure 7; 31pp; German.
CC   Acetyl CoA carboxylase (ACC) is an enzyme which appears to be part of
CC   the lipid storage system.  ACC is end product regulated and is also
CC   the limiting enzyme in de novo fatty acid biosynthesis.  A changed
CC   enzyme can interfere with both the lipid and fatty acid metabolism in
CC   plants.
SQ   Sequence   2240 AA;
SQ   177A; 134R; 81 N; 109D; 0  B; 34 C; 84 Q; 157E; 0  Z; 162G; 58 H;
SQ   121I; 220L; 114K; 62 M; 84 F; 108P; 162S; 98 T; 30 W; 65 Y; 180V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                  |
    DKIGSSLIAQAADVPTLPWSGSHVKIP
       260   X   270       280
```

8. US-08-121-713B-7 (1-7)
   R53257 Human collagen (Type V).

```
ID   R53257 standard; Protein; 1838 AA.
AC   R53257;
DT   12-JAN-1995  (first entry)
DE   Human collagen (Type V).
KW   Human collagen; alpha 1; V type collagen; placental mRNA.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         1..38
FT   /label= signal_peptide
FT   Region          444..538
FT   /note= "contains (Gly-X-Y) repeats"
FT   Binding_site    645..647
FT   /label= RGD
FT   /note= "cell adhesion motif"
FT   Binding_site    663..665
FT   /label= RGD
```



```
FT   /note= "cell adhesion motif"
FT   Domain          897..933
FT   /label= heparin_binding_domain
FT   Region          1573..1838
FT   /label= C-terminal_region
FT   /note= "contains 8 Cys residues"
PN   J06105687-A.
PD   19-APR-1994.
PF   27-DEC-1991; 358300.
PR   27-DEC-1991; JP-358300.
PA   (TAKI ) TAKARA SHUZO CO LTD.
DR   WPI; 94-163129/20.
DR   N-PSDB; Q64556.
PT   Human collagen V-type gene - is used for diagnosis of human
PT   collagen V-type related diseases
PS   Claim 1; Page 6-14; 19pp; Japanese.
CC   This amino acid sequence of type V collagen contains several distinct
CC   domains including a region comprising repeated (Gly-X-Y) motifs and a
CC   central domain containing two copies of the Arg-Gly-Asp cell adhesion
CC   motif. The cDNA sequence encoding type V collagen was isolated from a
CC   human placental library and will be useful for diagnosis of diseases
CC   related to type V collagen.
SQ   Sequence   1838 AA;
SQ   92 A; 72 R; 34 N; 105D; 0  B; 12 C; 74 Q; 118E; 0  Z; 428G; 17 H;
SQ   52 I; 97 L; 98 K; 23 M; 39 F; 334P; 72 S; 70 T; 7  W; 40 Y; 54 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                  |
    GRRGRAGSDGARGMPGQTGPKGDRGFD
     610       620  X    630
```

9. US-08-121-713B-7 (1-7)
   R55273 Beta subunit of integrin cell surface receptor.

```
ID   R55273 standard; Protein; 1822 AA.
AC   R55273;
DT   31-JAN-1995  (first entry)
DE   Beta subunit of integrin cell surface receptor.
KW   Integrin; alpha; beta; subunit; glycoprotein; heterodimer;
KW   transmembrane; extracellular matrix; cell signalling; cytoskeleton;
KW   behaviour; signal transduction; receptor.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         28..42
FT   /note= "N-terminal peptide."
FT   Modified_site   491
FT   /note= "Potential N-linked glycosylation site."
FT   Modified_site   617
FT   /note= "Potential N-linked glycosylation site."
FT   Modified_site   695
FT   /note= "Potential N-linked glycosylation site."
FT   Domain          711..733
FT   /note= "Putative transmembrane domain."
FT   Modified_site   980
```

```
FT   /note= "Potential N-linked glycosylation site."
FT   Modified site   1593
FT   /note= "Potential N-linked glycosylation site."
PN   US5320942-A.
PD   14-JUN-1994.
PF   19-FEB-1987; 016552.
PR   19-FEB-1987; US-016552.
PR   04-JAN-1989; US-293384.
PR   01-OCT-1990; US-591105.
PA   (KAJI/) KAJIJI S.
PA   (QUAR/) QUARANTA V.
PI   Kajiji S,  Quaranta V;
DR   WPI; 94-191533/23.
DR   N-PSDB; Q65674.
PT   Diagnosing presence of abnormal epithelial tissue in vitro -
PT   utilises monoclonal antibodies to alpha6 beta4 cell surface protein
PS   Example 5; Figure 9; 34pp; English.
CC   Integrins are heterodimers comrised of alpha and beta subunits, that
CC   are non-covalently associated transmembrane glycoproteins.  11 alpha
CC   chains and 6 beta chains have been recognised in man.  Each alpha
CC   subunit tends to associate with only one type of beta subunit but
CC   there are several exceptions.  Integrins mediate (in part) the
CC   interaction of cells with the extracellular matrix, forming a link
CC   between the extracellular matrix and the cytoskeleton.  They may
CC   transmit signals from the extracellular to the intracellular
CC   environment, affecting cell behaviour.  This sequence is the beta4
CC   subunit of an alpha6 beta4 integrin.
SQ   Sequence   1822 AA;
SQ   102A; 128R; 62 N; 102D; 0  B; 65 C; 88 Q; 123E; 0  Z; 135G; 46 H;
SQ   64 I; 175L; 63 K; 32 M; 58 F; 123P; 149S; 118T; 20 W; 50 Y; 119V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

     X     X
     XXXXPXX
       |
    MAGPRPSPWARLLLAALI
     X      10
```

10. US-08-121-713B-7 (1-7)
    R59751 Type II collagen.

```
ID   R59751 standard; protein; 1418 AA.
AC   R59751;
DT   14-FEB-1995  (first entry)
DE   Type II collagen.
KW   Collagen; triple helix; articular cartilage; collagenase;
KW   degradation; monoclonal antibody; epitope; matrix;
KW   metalloproteinase.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         1..24
FT   /label= Signal peptide.
PN   WO9414070-A.
PD   23-JUN-1994.
PF   06-DEC-1993; CA0522.
PR   04-DEC-1992; US-984123.
```



```
PA   (SHRI-) SHRINERS HOSPITALS FOR CRIPPLED CHILDREN.
PI   Hollander AP,  Poole AR;
DR   WPI; 94-234222/28.
PT   Determn. of cartilage degradation - using a monoclonal antibody
PT   to measure the amt. of unwound collagen or fragments in samples
PS   Disclosure; Figure 1; 119pp; English.
CC   Type II collagen constitutes the bulk of the fibrillar backbone of
CC   cartilage matrix.  It is composed of a tightly wound triple helix
CC   which can only be cleaved by the metalloproteinase collagenase to
CC   produce 3/4 and 1/4 length alpha chain fragments. The destruction of
CC   articular cartilage is due, in part, to the degradation of collagen.
CC   Incapable of maintaining its helical structure at  physiological
CC   temperatures, collagenase-cleaved collagens unwind and become
CC   susceptible to further degradation by other proteinases.  By
CC   producing monoclonal antibodies directed against epitopes which are
CC   only revealed when collagen is unwound, the antibodies provide a
CC   means of determining the degredation of cartilage in a biological
CC   sample.  The antibodies do not bind to native helical collagen.
CC   Epitopes used in the production of such antibodies are described in
CC   R59749, R59750 and R67742.
SQ   Sequence   1418 AA;
SQ   129A; 71 R; 30 N; 54 D; 0  B; 10 C; 58 Q; 74 E; 0  Z; 400G; 8  H;
SQ   30 I; 54 L; 64 K; 17 M; 23 F; 262P; 46 S; 40 T; 6  W; 9  Y; 33 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
               |
   GPPGAQGPPGLQGMPGERGAAGIAGPK
  670       680    X  690
```

11. US-08-121-713B-7 (1-7)
    R60292 Varicella zoster virus IEP175/IE62.

```
ID   R60292 standard; Protein; 1310 AA.
AC   R60292;
DT   21-FEB-1995  (first entry)
DE   Varicella zoster virus IEP175/IE62.
KW   VZV; immediate early protein; IEP175; IE62; phosphoprotein; human;
KW   T cells; vaccine; secretable; cytotoxic T lymphocyte; virions.
OS   Varicella-zoster virus.
PN   WO9414962-A.
PD   07-JUL-1994.
PF   17-DEC-1993; E03626.
PR   23-DEC-1992; GB-026768.
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PI   Bollen A,  Haumont M,  Jacobs P,  Massaer M;
DR   WPI; 94-234697/28.
DR   N-PSDB; Q70362.
PT   Pure varicella zoster virus immediate early protein 175 - and its
PT   fusion proteins, useful in vaccines, also related vectors
PS   Claim 2; Fig 1; 29pp; English.
CC   This sequence represents the Varicella-zoster virus (VZV) immediate
CC   early protein 175 (IEP175).  IEP175 is encoded by an open reading
CC   frame designated ORF62 and the protein itself is sometimes referred
CC   to as IE62.  The protein is a phosphoprotein with a relative
```

```
CC   molecular weight of 175 kD.  It is recognised by human T cells and
CC   is thought to be an important immune target.  This protein and
CC   derivatives of it may be used in vaccines to treat or prevent VZV
CC   diseases.  Preferred derivatives include a secretable derivative in
CC   which amino acids 226-257 and amino acids 648-733 have been deleted.
CC   IEP175 should induce cytotoxic T lymphocyte at an early stage,
CC   preventing assembly of new virions and spreading to new cells.
SQ   Sequence   1310 AA;
SQ   143A; 127R; 21 N; 87 D; 0  B; 12 C; 40 Q; 72 E; 0  Z; 120G; 25 H;
SQ   30 I; 97 L; 35 K; 14 M; 30 F; 148P; 120S; 61 T; 18 W; 20 Y; 90 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                   |
    TSGPVVDPPAVITMPLDGPAPNGGFRR
    730       740   X   750
```

12. US-08-121-713B-7 (1-7)
    R54841 HER4.

```
ID   R54841 standard; Protein; 1308 AA.
AC   R54841;
DT   11-JAN-1995  (first entry)
DE   HER4.
KW   Human epidermal growth factor receptor; HER; EGF; tyrosine kinase;
KW   cancer; neuronal tissue; muscle tissue; neoplasm;
KW   carcinoma; primer; probe; PCR.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Region          1..1308
FT   /note= "claim 12"
FT   Region          26..1308
FT   /note= "claim 12"
FT   Region          1..1045
FT   /note= "claim 12"
FT   Region          26..1045
FT   /note= "claim 12"
FT   Region          772..1308
FT   /note= "claim 12"
PN   EP-599274-A.
PD   01-JUN-1994.
PF   23-NOV-1993; 118837.
PR   24-NOV-1992; US-981165.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
PI   Culouscou J,  Plowman GD,  Shoyab M;
DR   WPI; 94-169599/21.
DR   N-PSDB; Q64896.
PT   New recombinant nucleic acid expressing HER4 - a new receptor
PT   tyrosine kinase expressed in some cancer cells, and related
PT   vectors, antibodies, ligands etc, for diagnosis and treatment of
PT   cancers
PS   Claim 12; Fig 1; 104pp; English.
CC   HER4 is the fourth member of the EGFR-family of tyrosine kinases and
CC   is expressed in some human cancers and in some tissues of neuronal
CC   or muscle origin.  HER4 polynucleotides, opt. labelled, are useful
```



```
CC   in assays (e.g. of HER4 mRNA to detect certain neoplasms, esp.
CC   breast carcinoma) and as primers in PCR or as probes.
SQ   Sequence   1308 AA;
SQ   69 A; 68 R; 76 N; 69 D; 0  B; 58 C; 47 Q; 84 E; 0  Z; 91 G; 32 H;
SQ   68 I; 110L; 66 K; 29 M; 48 F; 90 P; 80 S; 76 T; 16 W; 53 Y; 78 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                   |
    QGCNGPTSHDCIYYPWTGHSTLPQHAR
         630  X    640
```

13. US-08-121-713B-7 (1-7)
    R52701 Plasmid pASK60-Strep reading frame "b" translation

```
ID   R52701 standard; Protein; 1277 AA.
AC   R52701;
DT   11-JAN-1995  (first entry)
DE   Plasmid pASK60-Strep reading frame "b" translation.
KW   Streptavidin binding peptide; fusion protein; pASK60-Strep;
KW   affinity chromatography; purification; peptide tag; detection.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Region          1..1277
FT   /note= "translated from reading frame 'b' of
FT   pASK60-Strep; all X's correspond to nonsense
FT   codons"
FT   Peptide         443..463
FT   /label= OmpA_signal_peptide
PN   GB2272698-A.
PD   25-MAY-1994.
PF   01-NOV-1993; 022501.
PR   03-NOV-1992; DE-237113.
PA   (KUEH-) KUEHN KONSTRUKTION GMBH & CO KG KLAUS.
PA   (BIOA-) INST BIOANALYTIK GEMEINNUETZIGE GMBH.
PI   Schmidt T,  Skerra A;
DR   WPI; 94-153484/19.
DR   N-PSDB; Q62676.
PT   New fusion peptide(s) - have easily controlled binding properties
PT   and are capable of binding to streptavidin
PS   Example 5; Fig 8; 53pp; English.
CC   Plasmid pASK60-Strep was produced starting from pASK40
CC   (Biotechnology 9, 273-278, 1991) using site-directed mutagenesis
CC   and PCR. The plasmid contains an improved set of unique restriction
CC   sites, including two sites located directly at the 3' end of the
CC   region coding for the OmpA signal peptide. The polylinker is
CC   followed by a DNA sequence coding for a streptavidin binding
CC   peptide. The plasmid pASK60-Strep is useful for the expression of
CC   polypeptides fused to a streptavidin binding peptide. The
CC   production of such fusion proteins can be specifically detected
CC   using a streptavidin-alkaline phosphatase conjugate.
SQ   Sequence   1277 AA;
SQ   122A; 84 R; 40 N; 51 D; 0  B; 21 C; 56 Q; 54 E; 0  Z; 83 G; 26 H;
SQ   60 I; 144L; 49 K; 26 M; 55 F; 71 P; 100S; 79 T; 13 W; 28 Y; 82 V;
SQ   33 Others;
```

```
Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                 |
    LNEAIPNDERDTTMPVAMATTLRKLLT
        890   X   900        910
```

14. US-08-121-713B-7 (1-7)
    R52702 Plasmid pASK60-Strep reading frame "c" translation

```
 ID   R52702 standard; Protein; 1277 AA.
 AC   R52702;
 DT   11-JAN-1995  (first entry)
 DE   Plasmid pASK60-Strep reading frame "c" translation.
 KW   Streptavidin binding peptide; fusion protein; pASK60-Strep;
 KW   affinity chromatography; purification; peptide tag; detection.
 OS   Synthetic.
 FH   Key             Location/Qualifiers
 FT   Region          1..1277
 FT   /note= "translated from reading frame 'c' of
 FT   pASK60-Strep; all X's correspond to nonsense
 FT   codons"
 FT   Peptide         482..491
 FT   /label= streptavidin-binding peptide
 PN   GB2272698-A.
 PD   25-MAY-1994.
 PF   01-NOV-1993; 022501.
 PR   03-NOV-1992; DE-237113.
 PA   (KUEH-) KUEHN KONSTRUKTION GMBH & CO KG KLAUS.
 PA   (BIOA-) INST BIOANALYTIK GEMEINNUETZIGE GMBH.
 PI   Schmidt T,  Skerra A;
 DR   WPI; 94-153484/19.
 DR   N-PSDB; Q62676.
 PT   New fusion peptide(s) - have easily controlled binding properties
 PT   and are capable of binding to streptavidin
 PS   Example 5; Fig 8; 53pp; English.
 CC   Plasmid pASK60-Strep was produced starting from pASK40
 CC   (Biotechnology 9, 273-278, 1991) using site-directed mutagenesis
 CC   and PCR. The plasmid contains an improved set of unique restriction
 CC   sites, including two sites located directly at the 3' end of the
 CC   region coding for the OmpA signal peptide. The polylinker is
 CC   followed by a DNA sequence coding for a streptavidin binding
 CC   peptide. The plasmid pASK60-Strep is useful for the expression of
 CC   polypeptides fused to a streptavidin binding peptide. The
 CC   production of such fusion proteins can be specifically detected
 CC   using a streptavidin-alkaline phosphatase conjugate.
 SQ   Sequence   1277 AA;
 SQ   87 A; 137R; 44 N; 23 D; 0  B; 38 C; 37 Q; 25 E; 0  Z; 54 G; 33 H;
 SQ   60 I; 113L; 58 K; 22 M; 64 F; 95 P; 111S; 63 T; 51 W; 29 Y; 63 V;
 SQ   70 Others;
```

```
Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0
```



```
             X     X
             XXXXPXX
                 |
    XMXNQXRYTMSQSMPVSLIRPFPAWXT
       30     X  40 X      50
```

15. US-08-121-713B-7 (1-7)
    R54074 CryET5.

```
 ID   R54074 standard; Protein; 1229 AA.
 AC   R54074;
 DT   02-FEB-1995  (first entry)
 DE   CryET5.
 KW   cryET4; cryET5; Lepidoptera; lepidopteran insect; insecticidal;
 KW   toxin; insecticidal crystal protein; ICP.
 OS   Bacillus thuringiensis.
 PN   US5322687-A.
 PD   21-JUN-1994.
 PF   29-JUL-1993; 100709.
 PR   29-JUL-1993; US-100709.
 PA   (ECOG-) ECOGEN INC.
 PI   Donovan WP,  Gonzalez JM,  Jany CS,  Tan Y;
 DR   WPI; 94-199503/24.
 DR   N-PSDB; Q64112.
 PT   Isolated cryET4 gene and Bacillus thuringiensis cultures
 PT   transformed with this gene - used in compsns. against
 PT   lepidopteran insects.
 PS   Disclosure; Col 29-38; 51pp; English.
 CC   B. thuringiensis strain EG5847 exhibits insecticidal activity
 CC   against lepidopteran insects.  Two novel toxin genes from B.
 CC   thuringiensis EG5847 designated cryET4 and cryET5 produce
 CC   insecticidal proteins with activity against a broad spectrum of
 CC   lepidopteran insects.  The gene sequences are given in Q64111-12.
 SQ   Sequence   1229 AA;
 SQ   74 A; 81 R; 89 N; 62 D; 0  B; 18 C; 47 Q; 100E; 0  Z; 77 G; 28 H;
 SQ   70 I; 104L; 31 K; 9  M; 52 F; 55 P; 79 S; 97 T; 20 W; 59 Y; 77 V;
```

```
Initial Score    =      7  Optimized Score  =      7  Significance =  2.92
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                 |
    YSFLVGELWPSGRDPWEIFLEHVEQLI
          90 X     100
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq7pir.res made by  on Fri 19 May 95 8:52:16-PDT.


Query sequence being compared:US-08-121-713B-7 (1-7)
Number of sequences searched:                75511
Number of scores above cutoff:                4262
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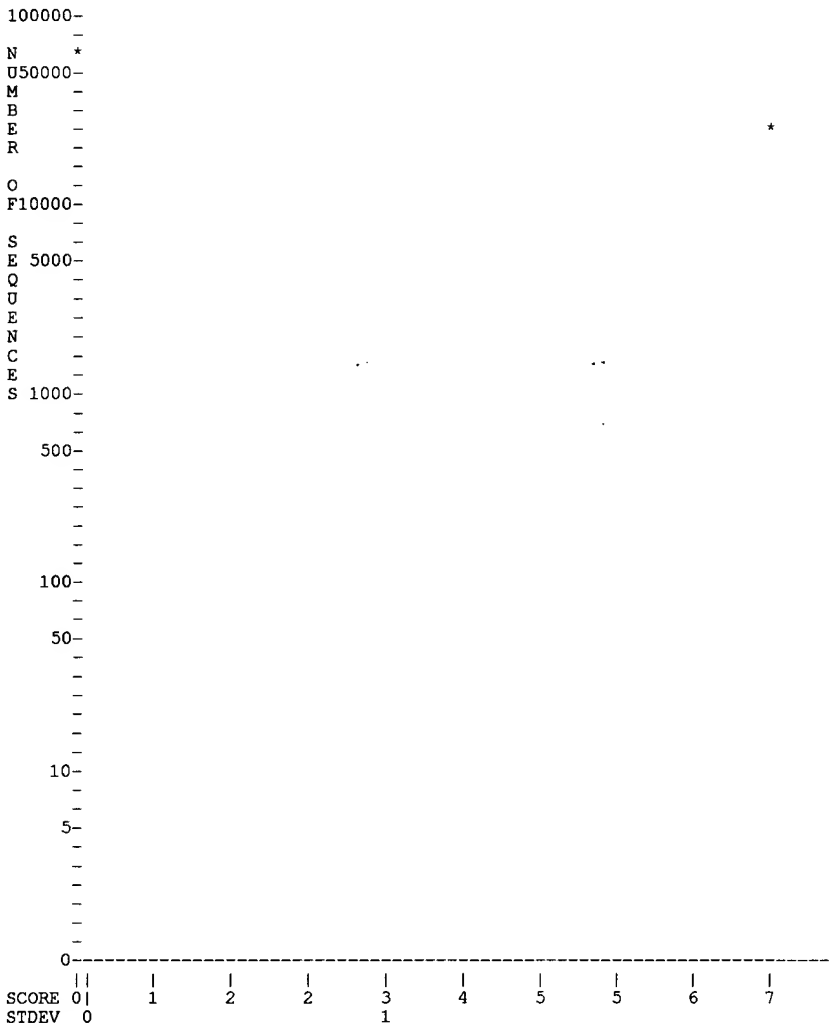
Results of the initial comparison of US-08-121-713B-7 (1-7) with:
Data bank : PIR 43, all entries



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	1	3.26

Times:	CPU	Total Elapsed
	00:01:11.00	00:01:11.00

Number of residues: 22468834
Number of sequences searched: 75511
Number of scores above cutoff: 4262

Cut-off raised to 1.
Cut-off raised to 2.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.
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Cut-off raised to 7.
Cut-off raised to 7.
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Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

4262 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. A46105	polyprotein(NS1, NS3, NS5, NS	3415	7	7	1.53	0
2. B49132	faf=fat facets gene (alternat	2747	7	7	1.53	0
3. A49132	faf=fat facets gene (alternat	2711	7	7	1.53	0
4. S17796	inositol-trisphosphate recept	2701	7	7	1.53	0
5. S18188	notch protein homolog - rat	2531	7	7	1.53	0
6. S30446	fatty-acid synthase (EC 2.3.1	2505	7	7	1.53	0
7. A46299	disabled product (alternative	2411	7	7	1.53	0
8. S14568	microtubule-associated protei	1828	7	7	1.53	0

9. S13507	microtubule-associated protei	1825	7	7	1.53	0
10. A48298	sodium channel homolog - jell	1739	7	7	1.53	0
11. A37491	orf1 putative helicase/polyme	1737	7	7	1.53	0
12. A48613	polyprotein=gag(CA, IN, MA, N	1603	7	7	1.53	0
13. A46221	160K abdominal segment format	1533	7	7	1.53	0
14. S45323	hypothetical protein - wheat	1470	7	7	1.53	0
15. S47423	virus envelope protein - tran	1449	7	7	1.53	0
16. S36126	neural cell adhesion molecule	1259	7	7	1.53	0
17. S28764	neurocan - rat	1257	7	7	1.53	0
18. S17655	neural cell adhesion molecule	1255	7	7	1.53	0
19. S16948	hypothetical protein IRS-1 -	1235	7	7	1.53	0
20. A46194	high-molecular-weight neurofi	1200	7	7	1.53	0
21. S15362	glutamate receptor, metabotro	1199	7	7	1.53	0
22. A43963	envelope glycoprotein G(envel	1148	7	7	1.53	0
23. S38253	nitric-oxide synthase (EC 1.1	1147	7	7	1.53	0
24. S40126	nitric-oxide synthase - rat	1147	7	7	1.53	0
25. A36968	P1-like adhesin precursor - M	1144	7	7	1.53	0
26. S23600	integrin alpha chain - rat (f	1106	7	7	1.53	0
27. S38783	integrin alpha chain - rat (f	1106	7	7	1.53	0
28. B47521	putative RNA-dependent RNA po	1057	7	7	1.53	0
29. A46284	Ca(2+)-ATPase, LCA1 - Lycoper	1048	7	7	1.53	0
30. JC2314	chitin synthase (EC 2.4.1.16)	1013	7	7	1.53	0
31. A48821	intercellular signaling prote	1004	7	7	1.53	0
32. JQ1165	Env protein - Visna virus (st	992	7	7	1.53	0
33. S16385	CSF-1 receptor - rat	978	7	7	1.53	0
34. JH0312	glutamate receptor GluR5-1 ch	920	7	7	1.53	0
35. JC2315	chitin synthase (EC 2.4.1.16)	916	7	7	1.53	0
36. A44884	sex-specific germline RNA-bin	915	7	7	1.53	0
37. G48613	pol polyprotein - myeloblasto	896	7	7	1.53	0
38. E48613	pol polyprotein - myeloblasto	896	7	7	1.53	0
39. A47521	putative capsid protein - gia	890	7	7	1.53	0
40. JH0311	glutamate receptor K3 chain p	888	7	7	1.53	0
41. S13677	glutamate receptor chain K2 p	883	7	7	1.53	0
42. JH0310	glutamate receptor K2 chain p	883	7	7	1.53	0
43. PC2219	polypeptide - Hepatitis C vir	876	7	7	1.53	0
44. S22338	glycogen phosphorylase (EC 2.	850	7	7	1.53	0
45. S47410	DNA polymerase - human hepati	845	7	7	1.53	0

1. US-08-121-713B-7 (1-7)
   A46105 polyprotein(NS1, NS3, NS5, NS2A, NS2B, NS4A, NS4B,

```
ENTRY            A46105     #type complete
TITLE            polyprotein(NS1, NS3, NS5, NS2A, NS2B, NS4A, NS4B, C=small
                   capsid protein, E=large envelope protein,
                   (pr)M=membrane-anchored protein precursor) - Powassan virus
ORGANISM         #formal_name Powassan virus
DATE             07-Apr-1994; #sequence_revision 07-Apr-1994; #text_change
                   07-Apr-1994
ACCESSIONS       A46105
REFERENCE        A46105
   #authors      Mandl, C.W.; Holzmann, H.; Kunz, C.; Heinz, F.X.
   #journal      Virology (1993) 194:173-184
   #title        Complete genomic sequence of Powassan virus: evaluation of
                   genetic elements in tick-borne versus mosquito-borne
                   flaviviruses.
   #cross-references MUID:93242744
   #accession    A46105
      ##status       preliminary
      ##molecule_type genomic RNA
```



```
      ##residues      1-3415 ##label MAN
      ##cross-references NCBIN:130654; NCBIP:130655
      ##note          sequence extracted from NCBI backbone
SUMMARY          #length 3415  #molecular-weight 378568  #checksum 9967
SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XXXXPXX
                   |
   KLKVTANKSRPATSPMPKGFVLSRMLG
      20     X  30 X      40
```

2. US-08-121-713B-7 (1-7)
   B49132 faf=fat facets gene (alternatively spliced, transc

```
ENTRY            B49132     #type complete
TITLE            faf=fat facets gene (alternatively spliced, transcript 1) -
                   Drosophila
ORGANISM         #formal_name Drosophila
DATE             19-Dec-1993; #sequence_revision 19-Dec-1993; #text_change
                   16-Nov-1994
ACCESSIONS       B49132
REFERENCE        A49132
   #authors      Fischer-Vize, J.A.; Rubin, G.M.; Lehmann, R.
   #journal      Development (1992) 116:985-1000
   #title        The fat facets gene is required for Drosophila eye and embryo
                   development.
   #cross-references MUID:93202020
   #contents     isogenic st
   #accession    B49132
      ##status       preliminary
      ##molecule_type nucleic acid
      ##residues      1-2747 ##label FIS
      ##cross-references NCBIN:127836; NCBIN:129008; NCBIP:127839
      ##note          sequence inconsistent with the nucleotide translation
      ##note          sequence extracted from NCBI backbone
SUMMARY          #length 2747  #molecular-weight 307955  #checksum 2752
SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XXXXPXX
                   |
   AYFSHRSQPLPHCMPEDEMDWLTADRM
  440       450    X  460
```

3. US-08-121-713B-7 (1-7)
   A49132 faf=fat facets gene (alternatively spliced, transc

```
ENTRY            A49132     #type complete
TITLE            faf=fat facets gene (alternatively spliced, transcript 2) -
```

```
                  Drosophila
 ORGANISM         #formal_name Drosophila
 DATE             19-Dec-1993; #sequence_revision 19-Dec-1993; #text_change
                    19-Dec-1993
 ACCESSIONS       A49132
 REFERENCE        A49132
    #authors      Fischer-Vize, J.A.; Rubin, G.M.; Lehmann, R.
    #journal      Development (1992) 116:985-1000
    #title        The fat facets gene is required for Drosophila eye and embryo
                    development.
    #cross-references MUID:93202020
    #contents     isogenic st
    #accession    A49132
       ##status        preliminary
       ##molecule_type nucleic acid
       ##residues      1-2711 ##label FIS
       ##cross-references NCBIN:127836; NCBIN:129008; NCBIP:129029
       ##note          sequence extracted from NCBI backbone
 SUMMARY          #length 2711  #molecular-weight 304063  #checksum 2362
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =      6
Gaps             =      0  Conservative Substitutions               =      0

             X     X
             XXXXPXX
                   |
   AYFSHRSQPLPHCMPEDEMDWLTADRM
  440       450    X  460


4. US-08-121-713B-7 (1-7)
   S17796       inositol-trisphosphate receptor type 2 - rat

 ENTRY            S17796     #type complete
 TITLE            inositol-trisphosphate receptor type 2 - rat
 ORGANISM         #formal_name Rattus norvegicus #common_name Norway rat
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S17796
 REFERENCE        S17796
    #authors      Suedhof, T.C.; Newton, C.L.; Archer III, B.T.; Ushkaryov,
                    Y.A.; Mignery, G.A.
    #journal      EMBO J. (1991) 10:3199-3206
    #title        Structure of a novel InsP(3) receptor.
    #cross-references MUID:92007769
    #accession    S17796
       ##status        preliminary
       ##residues      1-2701 ##label SUE
       ##cross-references EMBL:X61677
 SUMMARY          #length 2701  #molecular-weight 307056  #checksum 2707
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =      6
Gaps             =      0  Conservative Substitutions               =      0

             X     X
             XXXXPXX
```



```
                   |
   EGDNIVVGDKVVLMPVNAGQPLHASNV
        180 X     190


5. US-08-121-713B-7 (1-7)
   S18188       notch protein homolog - rat

 ENTRY            S18188     #type complete
 TITLE            notch protein homolog - rat
 ORGANISM         #formal_name Rattus norvegicus #common_name Norway rat
 DATE             19-Feb-1994; #sequence_revision 19-Feb-1994; #text_change
                    19-Feb-1994
 ACCESSIONS       S18188
 REFERENCE        S18188
    #authors      Weinmaster, G.; Roberts, V.J.; Lemke, G.
    #journal      Development (1991) 113:199-205
    #title        A homolog of Drosophila Notch expressed during mammalian
                    development.
    #cross-references MUID:92111383
    #accession    S18188
       ##status        preliminary
       ##residues      1-2531 ##label WEI
       ##cross-references EMBL:X57405
 SUMMARY          #length 2531  #molecular-weight 270907  #checksum 2705
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =      6
Gaps             =      0  Conservative Substitutions               =      0

             X     X
             XXXXPXX
                   |
   GQYCTEDVDECQLMPNACQNAGTCHNS
  290       300    X  310


6. US-08-121-713B-7 (1-7)
   S30446       fatty-acid synthase (EC 2.3.1.85) - rat

 ENTRY            S30446     #type complete
 TITLE            fatty-acid synthase (EC 2.3.1.85) - rat
 ORGANISM         #formal_name Rattus norvegicus #common_name Norway rat
 DATE             08-Jun-1994; #sequence_revision 08-Jun-1994; #text_change
                    08-Jun-1994
 ACCESSIONS       S30446
 REFERENCE        S30446
    #authors      Beck, K.F.; Schreglmann, R.; Stathopulos, I.; Klein, H.;
                    Hoch, J.; Schweizer, M.
    #journal      DNA Seq. (1992) 2:359-386
    #title        The fatty acid synthase (FAS) gene and its promoter in Rattus
                    norvegicus.
    #accession    S30446
       ##status        preliminary
       ##residues      1-2505 ##label BEC
       ##cross-references EMBL:X62888
 SUMMARY          #length 2505  #molecular-weight 272647  #checksum 9219
 SEQUENCE
```

```
Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                  |
    SMLNDIAATPTAAMPFRGYTVLGVEGH
          460 X     470
```

7. US-08-121-713B-7 (1-7)
   A46299 disabled product (alternatively spliced) - Drosoph

```
 ENTRY            A46299     #type complete
 TITLE            disabled product (alternatively spliced) - Drosophila
 ORGANISM         #formal_name Drosophila
 DATE             22-Sep-1993; #sequence_revision 22-Sep-1993; #text_change
                    17-Nov-1994
 ACCESSIONS       A46299
 REFERENCE        A46299
    #authors      Gertler, F.B.; Hill, K.K.; Clark, M.J.; Hoffmann, F.M.
    #journal      Genes Dev. (1993) 7:441-453
    #title        Dosage-sensitive modifiers of Drosophila abl tyrosine kinase
                    function: prospero, a regulator of axonal outgrowth, and
                    disabled, a novel tyrosine kinase substrate.
    #cross-references MUID:93194063
    #accession    A46299
       ##status         preliminary
       ##molecule_type nucleic acid
       ##residues       1-2411 ##label GER
       ##cross-references NCBIP:127163
       ##note           sequence extracted from NCBI backbone
       ##note           sequence not compared to nucleotide translation
 SUMMARY          #length 2411  #molecular-weight 264046  #checksum 83
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                  |
    TFVANFANFNDAPTPMPTVSPVVATVP
       1110   X  1120      1130
```

8. US-08-121-713B-7 (1-7)
   S14568 microtubule-associated protein MAP2 - rat

```
 ENTRY            S14568     #type complete
 TITLE            microtubule-associated protein MAP2 - rat
 ORGANISM         #formal_name Rattus norvegicus #common_name Norway rat
 DATE             21-Nov-1993; #sequence_revision 21-Nov-1993; #text_change
                    21-Nov-1993
 ACCESSIONS       S14568
 REFERENCE        S14568
    #authors      Matus, A.; Doll, T.
    #submission   submitted to the EMBL Data Library, May 1990
```



```
    #accession    S14568
       ##status        preliminary
       ##residues      1-1828 ##label MAT
       ##cross-references EMBL:X53455
 SUMMARY          #length 1828  #molecular-weight 198982  #checksum 5694
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                  |
    PLAPKDQKDWFIEMPVESKKDEWGLAA
      260     X 270 X     280
```

9. US-08-121-713B-7 (1-7)
   S13507 microtubule-associated protein MAP2 - rat

```
 ENTRY            S13507     #type complete
 TITLE            microtubule-associated protein MAP2 - rat
 ORGANISM         #formal_name Rattus norvegicus #common_name Norway rat
 DATE             21-Nov-1993; #sequence_revision 21-Nov-1993; #text_change
                    21-Nov-1993
 ACCESSIONS       S13507
 REFERENCE        S13507
    #authors      Marechal, D.; Delapierre, D.; Dresse, A.
    #journal      Arch. Int. Physiol. Biochim. (1988) 96:231-236
    #title        Cloning and partial sequencing of a new rat brain specific
                    cDNA.
    #cross-references MUID:89334524
    #accession    S13507
       ##status        preliminary
       ##residues      1-1825 ##label MAR
       ##cross-references EMBL:X54100
 SUMMARY          #length 1825  #molecular-weight 198565  #checksum 5960
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                  |
    PLAPKDQKDWFIEMPVESKKDEWGLAA
          260 X     270
```

10. US-08-121-713B-7 (1-7)
    A48298 sodium channel homolog - jellyfish (Cyanea capilla

```
 ENTRY            A48298     #type complete
 TITLE            sodium channel homolog - jellyfish (Cyanea capillata)
 ORGANISM         #formal_name Cyanea capillata
 DATE             03-Jun-1994; #sequence_revision 03-Jun-1994; #text_change
                    03-Jun-1994
 ACCESSIONS       A48298
```

```
 REFERENCE        A48298
    #authors      Anderson, P.A.V.; Holman, M.A.; Greenberg, R.M.
    #journal      Proc. Natl. Acad. Sci. U.S.A. (1993) 90:7419-7423
    #title        Deduced amino acid sequence of a putative sodium channel from
                    the scyphozoan jellyfish Cyanea capillata.
    #accession    A48298
       ##status        preliminary
       ##residues      1-1739 ##label AND
       ##cross-references GB:L15445
 SUMMARY          #length 1739  #molecular-weight 197832  #checksum 3088
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                   |
    ASTAWNCPPNYLCMPGAGSNPKNGYVS
         330  X    340
```

```
11. US-08-121-713B-7 (1-7)
    A37491       orf1 putative helicase/polymerase polyprotein - So

 ENTRY            A37491     #type complete
 TITLE            orf1 putative helicase/polymerase polyprotein - Southampton
                    virus
 ORGANISM         #common_name Southampton virus
 DATE             03-Mar-1994; #sequence_revision 03-Mar-1994; #text_change
                    17-Nov-1994
 ACCESSIONS       A37491
 REFERENCE        A37491
    #authors      Lambden, P.R.; Caul, E.O.; Ashley, C.R.; Clarke, I.N.
    #journal      Science (1993) 259:516-519
    #title        Sequence and genome organization of a human small
                    round-structured (Norwalk-like) virus.
    #cross-references MUID:93142023
    #contents     small round-structured virus, SRSV, Norwalk virus,
                    Norwalk-like virus, serotype 3
    #accession    A37491
       ##status        preliminary
       ##molecule_type genomic RNA
       ##residues      1-1737 ##label LAM
       ##cross-references NCBIP:123456
       ##note          sequence extracted from NCBI backbone
       ##note          sequence not compared to nucleotide translation
 SUMMARY          #length 1737  #molecular-weight 193342  #checksum 6745
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                   |
    KEWFDAGGLGPCTMPPTYERVKDDSPP
    70        80    X   90
```



```
12. US-08-121-713B-7 (1-7)
    A48613       polyprotein=gag(CA, IN, MA, NC, PR, GAG, POL, p10)

 ENTRY            A48613     #type complete
 TITLE            polyprotein=gag(CA, IN, MA, NC, PR, GAG, POL, p10) -
                    myeloblastosis-associated virus MAV
 ORGANISM         #formal_name myeloblastosis-associated virus, MAV
 DATE             21-Jan-1994; #sequence_revision 21-Jan-1994; #text_change
                    21-Jan-1994
 ACCESSIONS       A48613
 REFERENCE        A48613
    #authors      Joliot, V.; Boroughs, K.; Lasserre, F.; Crochet, J.;
                    Dambrine, G.; Smith, R.E.; Perbal, B.
    #journal      Virology (1993) 195:812-819
    #title        Pathogenic potential of myeloblastosis-associated virus:
                    implication of env proteins for osteopetrosis induction.
    #cross-references MUID:93331743
    #contents     MAV2(O)/2
    #accession    A48613
       ##status        preliminary
       ##molecule_type nucleic acid
       ##residues      1-1603 ##label JOL
       ##cross-references NCBIN:135486; NCBIP:135487
       ##note          sequence extracted from NCBI backbone
 SUMMARY          #length 1603  #molecular-weight 173689  #checksum 1201
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                   |
    REELASTGPPVVAMPVVIKTEGPAWTP
      230     X 240 X     250
```

```
13. US-08-121-713B-7 (1-7)
    A46221       160K abdominal segment formation protein Pumilio -

 ENTRY            A46221     #type complete
 TITLE            160K abdominal segment formation protein Pumilio - Drosophila
 ORGANISM         #formal_name Drosophila
 DATE             21-Sep-1993; #sequence_revision 21-Sep-1993; #text_change
                    17-Nov-1994
 ACCESSIONS       A46221
 REFERENCE        A46221
    #authors      Barker, D.D.; Wang, C.; Moore, J.; Dickinson, L.K.; Lehmann,
                    R.
    #journal      Genes Dev. (1992) 6:2312-2326
    #title        Pumilio is essential for function but not for distribution of
                    the Drosophila abdominal determinant Nanos.
    #cross-references MUID:93093466
    #contents     embryo
    #accession    A46221
       ##status        preliminary
       ##molecule_type nucleic acid
```

```
       ##residues      1-1533 ##label BAR
       ##cross-references NCBIN:120203; NCBIP:120204
       ##note          sequence extracted from NCBI backbone
 SUMMARY          #length 1533  #molecular-weight 157453  #checksum 5038
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                   |
    HHGGAMHPGMNGGMPKQQPLGPPGAGG
      310     X 320 X     330


14. US-08-121-713B-7 (1-7)
    S45323       hypothetical protein - wheat spindle streak mosaic

 ENTRY            S45323     #type complete
 TITLE            hypothetical protein - wheat spindle streak mosaic virus
 ORGANISM         #formal_name wheat spindle streak mosaic virus
 DATE             20-Oct-1994; #sequence_revision 20-Oct-1994; #text_change
                    20-Oct-1994
 ACCESSIONS       S45323
 REFERENCE        S45323
    #authors      Sohn, A.; Schenk, P.; Signoret, P.A.; Schmitz, G.; Schell,
                    J.; Steinbiss, H.H.
    #journal      Arch. Virol. (1994) 135:279-292
    #title        Sequence analysis of the 3'-terminal half of RNA 1 of wheat
                    spindle streak mosaic virus.
    #accession    S45323
       ##status       preliminary
       ##residues     1-1470 ##label SOH
       ##cross-references EMBL:X73883
 SUMMARY          #length 1470  #molecular-weight 163878  #checksum 2907
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                   |
    KSSLNSSDELSNTMPVSEGEGILKEVM
    180       190   X   200


15. US-08-121-713B-7 (1-7)
    S47423       virus envelope protein - transmissible gastroenter

 ENTRY            S47423     #type complete
 TITLE            virus envelope protein - transmissible gastroenteritis virus
 ORGANISM         #formal_name transmissible gastroenteritis virus
 DATE             23-Nov-1994; #sequence_revision 23-Nov-1994; #text_change
                    23-Nov-1994
 ACCESSIONS       S47423
 REFERENCE        S47422
```



```
    #authors      Chen, C.; Cavanagh, D.; Britton, P.
    #submission   submitted to the EMBL Data Library, August 1994
    #accession    S47423
       ##status       preliminary
       ##residues     1-1449 ##label CHE
       ##cross-references EMBL:Z35758
 SUMMARY          #length 1449  #molecular-weight 160118  #checksum 3476
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  1.53
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                   |
    NSDVVLGDYFPTVQPWFNCIRNNSNDL
   50        60     X  70
> O <
O| |O  IntelliGenetics
> O <

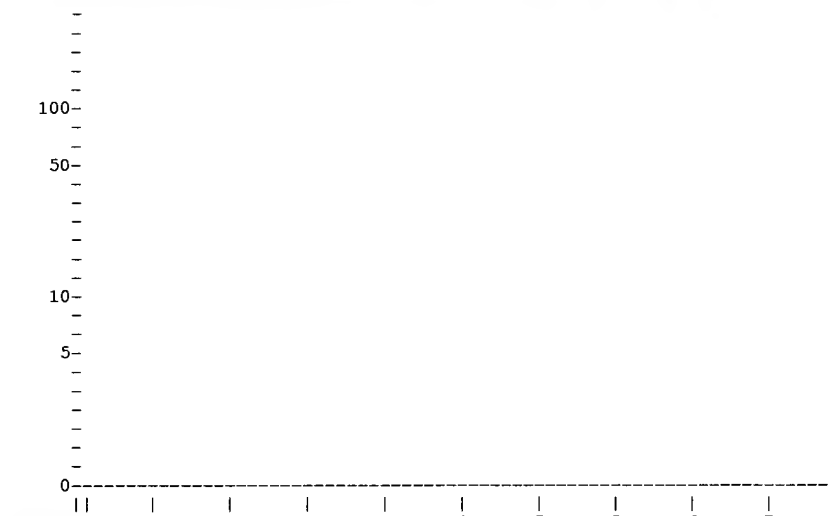
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq7spt.res made by  on Fri 19 May 95 8:55:49-PDT.


Query sequence being compared:US-08-121-713B-7 (1-7)
Number of sequences searched:                43470
Number of scores above cutoff:                4963

      Results of the initial comparison of US-08-121-713B-7 (1-7) with:
   Data bank : Swiss-Prot 31, all entries

100000-
      -
N     -
U50000-
M     -
B     *
E     -
R     -                                                              *
      -
O     -
F10000-
      -
S     -
E 5000-
Q     -
U     -
E     -
N     -
C     -
E     -
S 1000-
      -
      -
   500-
      -
```



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	1	3.38

Times:	CPU	Total Elapsed
	00:00:44.04	00:00:45.00

Number of residues: 15335248
Number of sequences searched: 43470
Number of scores above cutoff: 4963

Cut-off raised to 1.
Cut-off raised to 2.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.

Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.
Cut-off raised to 7.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

4963 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. YHP9_YEAST	HYPOTHETICAL 433.2 KD PROTEIN	3744	7	7	1.48	0
2. ZFH2_DROME	ZINC-FINGER PROTEIN 2 (ZINC-F	3005	7	7	1.48	0
3. ZEP1_HUMAN	ZINC FINGER PROTEIN 40 (HUMAN	2717	7	7	1.48	0
4. YLJ6_CAEEL	HYPOTHETICAL 272.0 KD PROTEIN	2329	7	7	1.48	0
5. YNJ1_CAEEL	HYPOTHETICAL 223.8 KD PROTEIN	2027	7	7	1.48	0
6. YHD0_YEAST	HYPOTHETICAL 210.4 KD PROTEIN	1868	7	7	1.48	0
7. ZEP2_HUMAN	HUMAN IMMUNODEFICIENCY VIRUS	1833	7	7	1.48	0
8. YM68_CAEEL	HYPOTHETICAL 208.3 KD PROTEIN	1822	7	7	1.48	0
9. YO25_CAEEL	HYPOTHETICAL 202.6 KD PROTEIN	1799	7	7	1.48	0
10. YKB4_YEAST	HYPOTHETICAL 203.3 KD PROTEIN	1764	7	7	1.48	0
11. YIR7_YEAST	HYPOTHETICAL 197.5 KD PROTEIN	1758	7	7	1.48	0
12. YEW2_YEAST	HYPOTHETICAL 195.4 KD PROTEIN	1753	7	7	1.48	0
13. YK11_YEAST	HYPOTHETICAL 195.2 KD PROTEIN	1683	7	7	1.48	0
14. YL54_CAEEL	HYPOTHETICAL 176.0 KD PROTEIN	1609	7	7	1.48	0
15. YIR3_YEAST	PUTATIVE MEMBRANE GLYCOPROTEI	1549	7	7	1.48	0
16. YJ64_YEAST	PUTATIVE MEMBRANE GLYCOPROTEI	1549	7	7	1.48	0
17. YHY6_YEAST	HYPOTHETICAL 175.8 KD PROTEIN	1541	7	7	1.48	0
18. YHW4_YEAST	HYPOTHETICAL 171.7 KD PROTEIN	1522	7	7	1.48	0
19. YEZ4_YEAST	HYPOTHETICAL 168.2 KD PROTEIN	1468	7	7	1.48	0
20. YEC2_YEAST	HYPOTHETICAL 165.7 KD PROTEIN	1459	7	7	1.48	0
21. YN81_CAEEL	HYPOTHETICAL 155.8 KD PROTEIN	1439	7	7	1.48	0
22. YIB3_YEAST	PROBABLE ATP-DEPENDENT PERMEA	1411	7	7	1.48	0
23. YMS5_CAEEL	HYPOTHETICAL 161.8 KD PROTEIN	1409	7	7	1.48	0
24. YIP9_YEAST	HYPOTHETICAL 156.9 KD PROTEIN	1375	7	7	1.48	0
25. YHO0_YEAST	HYPOTHETICAL 149.7 KD PROTEIN	1345	7	7	1.48	0
26. YKM9_YEAST	MYOSIN HEAVY CHAIN HOMOLOG YK	1271	7	7	1.48	0
27. YNCA_CAEEL	HYPOTHETICAL 142.5 KD PROTEIN	1254	7	7	1.48	0
28. YMF6_CAEEL	HYPOTHETICAL 139.9 KD PROTEIN	1247	7	7	1.48	0
29. YOQ5_CAEEL	HYPOTHETICAL 134.9 KD PROTEIN	1232	7	7	1.48	0
30. YCX1_YEAST	HYPOTHETICAL 143.8 KD PROTEIN	1226	7	7	1.48	0
31. YMA1_CAEEL	PROBABLE INTEGRIN ALPHA CHAIN	1226	7	7	1.48	0
32. YSY2_YEAST	HYPOTHETICAL 137.7 KD PROTEIN	1224	7	7	1.48	0
33. YMH5_CAEEL	HYPOTHETICAL 136.3 KD PROTEIN	1222	7	7	1.48	0
34. YK83_YEAST	PROBABLE ATP-DEPENDENT PERMEA	1218	7	7	1.48	0
35. YED1_YEAST	PROBABLE E1-E2 ATPASE YEL031W	1215	7	7	1.48	0
36. YNX5_CAEEL	HYPOTHETICAL 139.4 KD PROTEIN	1213	7	7	1.48	0
37. YEHI_ECOLI	HYPOTHETICAL 138.1 KD PROTEIN	1210	7	7	1.48	0
38. YLU8_CAEEL	HYPOTHETICAL 138.6 KD PROTEIN	1207	7	7	1.48	0
39. YK76_YEAST	HYPOTHETICAL 137.5 KD PROTEIN	1195	7	7	1.48	0
40. ZN91_HUMAN	ZINC FINGER PROTEIN 91 (ZINC	1191	7	7	1.48	0
41. YKD8_YEAST	PUTATIVE 128.2 KD TRANSCRIPTI	1170	7	7	1.48	0
42. YK82_YEAST	HYPOTHETICAL 122.2 KD PROTEIN	1169	7	7	1.48	0
43. YK62_YEAST	HYPOTHETICAL 133.3 KD PROTEIN	1157	7	7	1.48	0
44. YIE8_YEAST	PROBABLE E1-E2 ATPASE YIL048W	1151	7	7	1.48	0

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   45. YHC3_YEAST   HYPOTHETICAL 130.0 KD PROTEIN   1146     7     7  1.48   0


1. US-08-121-713B-7 (1-7)
   YHP9_YEAST   HYPOTHETICAL 433.2 KD PROTEIN IN HXT5-CDC12 INTERG

 ID   YHP9_YEAST     STANDARD;      PRT;  3744 AA.
 AC   P38811;
 DT   01-FEB-1995 (REL. 31, CREATED)
 DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE   HYPOTHETICAL 433.2 KD PROTEIN IN HXT5-CDC12 INTERGENIC REGION.
 GN   YHR099W.
 OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=S288C / AB972;
 RM   94378003
 RA   JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
 RA   DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,
 RA   KUCABA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,
 RA   LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER L.,
 RA   NHAN M., RIFKIN L., RILES L., ST.PETER H., TREVASKIS E., VAUGHAN K.,
 RA   VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
 RA   VAUDIN M.;
 RL   SCIENCE 265:2077-2082(1994).
 DR   EMBL; U00060; SCH9332.
 DR   PIR; S46715; S46715.
 KW   HYPOTHETICAL PROTEIN.
 SQ   SEQUENCE   3744 AA;  433171 MW;  20943107 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions             =     0

             X     X
             XXXXPXX
                   |
    MRKVLEPSDDDHLMPQPKKEDINDSPD
    520       530   X   540


2. US-08-121-713B-7 (1-7)
   ZFH2_DROME   ZINC-FINGER PROTEIN 2 (ZINC-FINGER HOMEODOMAIN PRO

 ID   ZFH2_DROME     STANDARD;      PRT;  3005 AA.
 AC   P28167;
 DT   01-OCT-1994 (REL. 30, CREATED)
 DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE   ZINC-FINGER PROTEIN 2 (ZINC-FINGER HOMEODOMAIN PROTEIN 2).
 GN   ZFH-2.
 OS   DROSOPHILA MELANOGASTER (FRUIT FLY).
 OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RM   92001539
 RA   FORTINI M.E., LAI Z., RUBIN G.M.;
 RL   MECH. DEV. 34:113-122(1991).
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 CC   -!- FUNCTION: INVOLVED IN THE DEVELOPMENT OF THE EMBRYONIC CENTRAL
 CC       NERVOUS SYSTEM.
 CC   -!- TISSUE SPECIFICITY: LARGELY RESTRICTED TO THE CNS OF LATE EMBRYO.
 CC   -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
 CC   -!- SIMILARITY: CONTAINS THREE HOMEOBOX DOMAINS.
 DR   EMBL; M63450; DMZFH2.
 DR   PIR; S27817; S27817.
 DR   PIR; S33642; S33642.
 DR   HSSP; P02836; 1HDD.
 DR   FLYBASE; FBGN0004607; ZFH2.
 KW   ZINC-FINGER; METAL-BINDING; DNA-BINDING; HOMEOBOX; NUCLEAR PROTEIN;
 KW   REPEAT.
 FT   ZN_FING     133    156       C2H2-TYPE.
 FT   ZN_FING     559    582       C2H2-TYPE.
 FT   ZN_FING     614    638       C2H2-TYPE.
 FT   ZN_FING     732    756       C2H2-TYPE.
 FT   ZN_FING     897    916       C2H2-TYPE (DEGENERATE).
 FT   ZN_FING     940    964       C2H2-TYPE.
 FT   ZN_FING     999   1023       C2H2-TYPE.
 FT   ZN_FING    1074   1098       C2H2-TYPE.
 FT   ZN_FING    1210   1233       C2H2-TYPE.
 FT   ZN_FING    1341   1365       C2H2-TYPE.
 FT   ZN_FING    1438   1462       C2H2-TYPE.
 FT   ZN_FING    1477   1500       C2H2-TYPE (DEGENERATE).
 FT   ZN_FING    1513   1535       C2H2-TYPE.
 FT   ZN_FING    1541   1564       C2H2-TYPE.
 FT   DNA_BIND   1797   1856       HOMEOBOX 1.
 FT   DNA_BIND   2154   2213       HOMEOBOX 2.
 FT   ZN_FING    2234   2256       C2H2-TYPE.
 FT   ZN_FING    2371   2393       C2H2-TYPE.
 FT   DNA_BIND   2760   2819       HOMEOBOX 3.
 SQ   SEQUENCE   3005 AA;  332056 MW;  22430417 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions             =     0

             X     X
             XXXXPXX
                   |
    GTGNIASHSSGSFMPEVALADLAYNQA
        790   X    800


3. US-08-121-713B-7 (1-7)
   ZEP1_HUMAN   ZINC FINGER PROTEIN 40 (HUMAN IMMUNODEFICIENCY VIR

 ID   ZEP1_HUMAN     STANDARD;      PRT;  2717 AA.
 AC   P15822;
 DT   01-APR-1990 (REL. 14, CREATED)
 DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE   ZINC FINGER PROTEIN 40 (HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-
 DE   BINDING PROTEIN 1) (HIV-EP1) (MAJOR HISTOCOMPATIBILITY COMPLEX BINDING
 DE   PROTEIN 1) (MBP-1) (POSITIVE REGULATORY DOMAIN II BINDING FACTOR 1)
 DE   (PRDII-BF1).
 GN   HIVEP1 OR ZNF40.
 OS   HOMO SAPIENS (HUMAN).
 OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC   EUTHERIA; PRIMATES.
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RN   [1]
RP   SEQUENCE FROM N.A.
RM   90169514
RA   FAN C.M., MANIATIS T.;
RL   GENES DEV. 4:29-42(1990).
RN   [2]
RP   STRUCTURE BY NMR OF 2113-2142.
RM   91064333
RA   OMICHINSKI J.G., CLORE G.M., APPELLA E., SAKAGUCHI K.,
RA   GRONENBORN A.M.;
RL   BIOCHEMISTRY 29:9324-9334(1990).
RN   [3]
RP   STRUCTURE BY NMR OF 2087-2142.
RM   92232684
RA   OMICHINSKI J.G., CLORE G.M., ROBIEN M., SAKAGUCHI K., APPELLA E.,
RA   GRONENBORN A.M.;
RL   BIOCHEMISTRY 31:3907-3917(1992).
CC   -!- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE
CC       5'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF
CC       NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1.
CC       IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS
CC       OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I
CC       MHC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT
CC       IN T-CELL ACTIVATION.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPARATED
CC       AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH ZINC-FINGER
CC       IN-BETWEEN.
CC   -!- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
CC   -!- SIMILARITY: 70% BETWEEN THE TWO ZINC-FINGER DOMAINS.
CC   -!- SIMILARITY: STRONG, TO HIV-EP2.
DR   EMBL; X51435; HSZFPBF1.
DR   PIR; A34203; A34203.
DR   PDB; 3ZNF; 15-JAN-92.
DR   PDB; 4ZNF; 15-JAN-92.
DR   PDB; 1BBO; 31-OCT-93.
DR   TRANSFAC; T00497; -.
DR   MIM; 194540; 11TH EDITION.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2.
KW   TRANSCRIPTION REGULATION; ZINC-FINGER; METAL-BINDING; DNA-BINDING;
KW   NUCLEAR PROTEIN; 3D-STRUCTURE.
FT   DOMAIN      406    456       ZINC-FINGERS.
FT   ZN_FING     406    428       C2H2-TYPE.
FT   ZN_FING     434    456       C2H2-TYPE.
FT   ZN_FING     955    981       CC-X(13)-HC MOTIF (POTENTIAL).
FT   DOMAIN     2087   2139       ZINC-FINGERS.
FT   ZN_FING    2087   2109       C2H2-TYPE.
FT   ZN_FING    2115   2139       C2H2-TYPE.
FT   STRAND     2088   2088
FT   TURN       2090   2092
FT   STRAND     2095   2095
FT   HELIX      2099   2108
FT   TURN       2109   2109
FT   STRAND     2115   2116
FT   STRAND     2123   2124
FT   HELIX      2127   2135
SQ   SEQUENCE   2717 AA;  297217 MW;  19898490 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    25%  Matches          =      1  Mismatches   =      3
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Gaps             =      0  Conservative Substitutions             =      0

      X  X
    XXXXPXX
      |
    MPRTKQIHPRNLRD
    X  X    10


4. US-08-121-713B-7 (1-7)
   YLJ6_CAEEL   HYPOTHETICAL 272.0 KD PROTEIN C50C3.6 IN CHROMOSOM

ID   YLJ6_CAEEL     STANDARD;      PRT;  2329 AA.
AC   P34369;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 272.0 KD PROTEIN C50C3.6 IN CHROMOSOME III.
GN   C50C3.6.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RM   94150718
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA   FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA   JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
RA   LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA   SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA   WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA   WOHLDMAN P.;
RL   NATURE 368:32-38(1994).
DR   EMBL; L14433; CEC50C3.
DR   PIR; S44625; S44625.
DR   WORMPEP; C50C3.6; CE00122.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   2329 AA;  272025 MW;  19536537 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =      6
Gaps             =      0  Conservative Substitutions             =      0

            X     X
            XXXXPXX
              |
   KKKFGMSDTQKEEMPPEHVRKVIRDHG
    40        50   X    60


5. US-08-121-713B-7 (1-7)
   YNJ1_CAEEL   HYPOTHETICAL 223.8 KD PROTEIN R10E11.1 IN CHROMOSO

ID   YNJ1_CAEEL     STANDARD;      PRT;  2027 AA.
AC   P34545;
DT   01-FEB-1994 (REL. 28, CREATED)
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DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 223.8 KD PROTEIN R10E11.1 IN CHROMOSOME III.
GN   R10E11.1.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RM   94150718
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA   FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA   JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
RA   LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA   SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA   WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA   WOHLDMAN P.;
RL   NATURE 368:32-38(1994).
CC   -!- SIMILARITY: CONTAINS A COPY OF THE BROMODOMAIN.
DR   EMBL; Z29095; CER10E11.
DR   PIR; S40713; S40713.
DR   HSSP; P19999; 1CLG.
DR   WORMPEP; R10E11.1; CE01049.
DR   PROSITE; PS00633; BROMODOMAIN.
KW   HYPOTHETICAL PROTEIN; BROMODOMAIN.
FT   DOMAIN      886    948       BROMODOMAIN.
SQ   SEQUENCE   2027 AA;  223840 MW;  18596053 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0

            X     X
            XXXXPXX
                  |
    GQPMGRGAMMNGAMPRSGPMPTQGRPG
  230       240    X  250
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6. US-08-121-713B-7 (1-7)
   YHD0_YEAST   HYPOTHETICAL 210.4 KD PROTEIN IN GUT1-RIM1 INTERGE

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ID   YHD0_YEAST     STANDARD;      PRT;  1868 AA.
AC   P38737;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 210.4 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION.
GN   YHL030W.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RM   94378003
RA   JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
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RA   DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,
RA   KUCABA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,
RA   LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER L.,
RA   NHAN M., RIFKIN L., RILES L., ST.PETER H., TREVASKIS E., VAUGHAN K.,
RA   VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
RA   VAUDIN M.;
RL   SCIENCE 265:2077-2082(1994).
DR   EMBL; U11583; SCH9196.
DR   PIR; S48938; S48938.
KW   HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
FT   TRANSMEM    695    715       POTENTIAL.
FT   TRANSMEM    747    767       POTENTIAL.
SQ   SEQUENCE   1868 AA;  210430 MW;  17651645 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0

            X     X
            XXXXPXX
                  |
    TNLSDDAAQFMKRFPMPYENEEFITFL
        280  X    290
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7. US-08-121-713B-7 (1-7)
   ZEP2_HUMAN   HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDI

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ID   ZEP2_HUMAN     STANDARD;      PRT;  1833 AA.
AC   P31629;
DT   01-JUL-1993 (REL. 26, CREATED)
DT   01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2
DE   (HIV-EP2).
GN   HIVEP2.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   91217105
RA   NOMURA N., ZHAO M.-J., NAGASE T., MAEKAWA T., ISHIZAKI R., TABATA S.,
RA   ISHII S.;
RL   J. BIOL. CHEM. 266:8590-8594(1991).
CC   -!- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE
CC       5'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF
CC       NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1.
CC       IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS
CC       OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I
CC       MHC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT
CC       IN T-CELL ACTIVATION.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
CC   -!- SIMILARITY: TO THE HIV-EP1.
DR   EMBL; M60119; HSEP2AA.
DR   PIR; A39829; WMHUE2.
DR   HSSP; P15822; 1BBO.
DR   TRANSFAC; T00939; -.
DR   MIM; 143054; 11TH EDITION.
```

```
DR   PROSITE; PS00028; ZINC_FINGER_C2H2.
KW   TRANSCRIPTION REGULATION; ZINC-FINGER; METAL-BINDING; DNA-BINDING;
KW   NUCLEAR PROTEIN.
FT   DOMAIN      324    330       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DOMAIN      337    369       SER-RICH.
FT   DOMAIN     1286   1310       ASP/GLU-RICH (ACIDIC).
FT   ZN_FING    1186   1208       C2H2-TYPE.
FT   ZN_FING    1214   1238       C2H2-TYPE.
SQ   SEQUENCE   1833 AA;  202128 MW;  17625550 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                  |
    QYPTVCMVHLPAQQPPWWQAHFPHPFA
      600     X 610 X     620
```

8. US-08-121-713B-7 (1-7)
   YM68_CAEEL HYPOTHETICAL 208.3 KD PROTEIN K12H4.8 IN CHROMOSOM

```
ID   YM68_CAEEL     STANDARD;      PRT;  1822 AA.
AC   P34529;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 208.3 KD PROTEIN K12H4.8 IN CHROMOSOME III.
GN   K12H4.8.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RM   94150718
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA   FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA   JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
RA   LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA   SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA   WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA   WOHLDMAN P.;
RL   NATURE 368:32-38(1994).
CC   -!- SIMILARITY: TO EUKARYOTIC INITIATION FACTOR-4A AND RIBONUCLEASE
CC       III.
DR   EMBL; L14331; CEK12H4.
DR   PIR; S44849; S44849.
DR   WORMPEP; K12H4.8; CE00273.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   1822 AA;  208291 MW;  15724531 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0
```



```
             X     X
             XXXXPXX
                  |
    DSLKTTRAVFRQLGPWAAWRTAQVWEK
    280       290   X   300
```

9. US-08-121-713B-7 (1-7)
   YO25_CAEEL HYPOTHETICAL 202.6 KD PROTEIN ZK688.5 IN CHROMOSOM

```
ID   YO25_CAEEL     STANDARD;      PRT;  1799 AA.
AC   P34675;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 202.6 KD PROTEIN ZK688.5 IN CHROMOSOME III.
GN   ZK688.5.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RM   94150718
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA   FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA   JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
RA   LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA   SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA   WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA   WOHLDMAN P.;
RL   NATURE 368:32-38(1994).
DR   EMBL; L16621; CEZK688.
DR   PIR; S44920; S44920.
DR   WORMPEP; ZK688.5; CE00463.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   1799 AA;  202641 MW;  15440747 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XXXXPXX
                  |
    DRGPSGENDRPNVMPDRVAGPRIINAI
          100       110
```

10. US-08-121-713B-7 (1-7)
    YKB4_YEAST HYPOTHETICAL 203.3 KD PROTEIN IN PUT3-CCE1 INTERGE

```
ID   YKB4_YEAST     STANDARD;      PRT;  1764 AA.
AC   P34241; P34242;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
```

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DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 203.3 KD PROTEIN IN PUT3-CCE1 INTERGENIC REGION.
GN   YKL014C.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   94205264
RA   WIEMANN S., VOSS H., SCHWAGER C., RUPP T., STEGEMANN J.,
RA   ZIMMERMANN J., GROTHUES D., SENSEN C., ERFLE H., HEWITT N.,
RA   BANREVI A., ANSORGE W.;
RL   YEAST 9:1343-1348(1993).
RN   [2]
RP   REVISIONS.
RA   WIEMANN S., VOSS H., SCHWAGER C., RUPP T., STEGEMANN J.,
RA   ZIMMERMANN J., GROTHUES D., SENSEN C., ERFLE H., HEWITT N.,
RA   BANREVI A., ANSORGE W.;
RL   SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; X74152; SCPUKGA.
DR   EMBL; Z28014; SCYKL014C.
DR   PIR; S37827; S37827.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   1764 AA;  203286 MW;  16178809 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XXXXPXX
                   |
    IHNKLLFNTLRLFKPWEDTLQLGTLIK
          340 X     350
```

11. US-08-121-713B-7 (1-7)
    YIR7_YEAST   HYPOTHETICAL 197.5 KD PROTEIN IN SUC2 5'REGION.

```
ID   YIR7_YEAST     STANDARD;      PRT;  1758 AA.
AC   P40434;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 197.5 KD PROTEIN IN SUC2 5'REGION.
GN   YIL177C.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RA   BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,
RA   CHURCHER C.M., CONNOR R., COPSEY T., DEAR S., DEVLIN K., FRASER A.,
RA   GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES M.,
RA   LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D.,
RA   RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
RA   WALSH S.V., WHITEHEAD S.;
RL   SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SIMILARITY: TO HYPOTHETICAL PROTEIN IN SUBTELOMERIC Y'REPEAT
CC       (Z46921).
DR   EMBL; Z47047; SCCHRIX.
```



```
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   1758 AA;  197511 MW;  15509879 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XXXXPXX
                   |
    ICALGNSYDAFNHDPWMDVVGFEDPNQ
      450     X 460 X     470
```

12. US-08-121-713B-7 (1-7)
    YEW2_YEAST   HYPOTHETICAL 195.4 KD PROTEIN IN RPS26B-GLC7 INTER

```
ID   YEW2_YEAST     STANDARD;      PRT;  1753 AA.
AC   P32634;
DT   01-OCT-1993 (REL. 27, CREATED)
DT   01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 195.4 KD PROTEIN IN RPS26B-GLC7 INTERGENIC REGION.
GN   YER132C OR SYGP-ORF50.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   MULLIGAN J.T., DIETRICH F.S., HENNESSEY K.M., SEHL P., KOMP C.,
RA   WEI Y., TAYLOR P., NAKAHARA K., ROBERTS D., DAVIS R.W.;
RL   SUBMITTED (FEB-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RA   DIETRICH F.S., MULLIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R.,
RA   AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M.,
RA   CHUNG E., DUNCAN M., GUZMAN E., HARTZELL G., HUNICKE-SMITH S.,
RA   HYMAN R., KAYSER A., KOMP C., LASHKARI D., LEW H., LIN D.,
RA   MOSEDALE D., NAKAHARA K., NAMATH A., NORGREN R., OEFNER P., OH C.,
RA   PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN T., SMITH V.,
RA   TAYLOR P., WEI Y., YELTON M., BOTSTEIN D., DAVIS R.W.;
RL   SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SIMILARITY: TO S.POMBE RAL2.
DR   EMBL; L11120; SCSYGP4.
DR   EMBL; U18916; U18916.
DR   PIR; S30855; S30855.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   1753 AA;  195382 MW;  16043187 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XXXXPXX
                   |
    SKGSSKILVNIDGMPISLSHDSNFSVL
      250     X  260       270
```

13. US-08-121-713B-7 (1-7)
YK11_YEAST HYPOTHETICAL 195.2 KD PROTEIN IN GCN3-DAL80 INTERG

```
 ID   YK11_YEAST     STANDARD;      PRT;  1683 AA.
 AC   P36126;
 DT   01-JUN-1994 (REL. 29, CREATED)
 DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE   HYPOTHETICAL 195.2 KD PROTEIN IN GCN3-DAL80 INTERGENIC REGION.
 GN   YKR031C.
 OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RA   URRESTARAZU L.A., JAUNIAUX J.-C.;
 RL   SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
 DR   EMBL; Z28256; SCYKR031C.
 DR   PIR; S38103; S38103.
 KW   HYPOTHETICAL PROTEIN.
 SQ   SEQUENCE   1683 AA;  195203 MW;  14046134 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            XXXXPXX
                  |
   KQWMSSIIKMSTSTPWSKPNRFGSFAP
          660       670
```

14. US-08-121-713B-7 (1-7)
YL54_CAEEL HYPOTHETICAL 176.0 KD PROTEIN F44E2.4 IN CHROMOSOM

```
 ID   YL54_CAEEL     STANDARD;      PRT;  1609 AA.
 AC   P34434;
 DT   01-FEB-1994 (REL. 28, CREATED)
 DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE   HYPOTHETICAL 176.0 KD PROTEIN F44E2.4 IN CHROMOSOME III.
 GN   F44E2.4.
 OS   CAENORHABDITIS ELEGANS.
 OC   EUKARYOTA; METAZOA; ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=BRISTOL N2;
 RM   94150718
 RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
 RA   FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
 RA   JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
 RA   LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
 RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA   SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
 RA   SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
 RA   WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
 RA   WOHLDMAN P.;
 RL   NATURE 368:32-38(1994).
```



```
 DR   EMBL; L23646; CEF44E2.
 DR   PIR; S44821; S44821.
 DR   WORMPEP; F44E2.4; CE00182.
 KW   HYPOTHETICAL PROTEIN.
 SQ   SEQUENCE   1609 AA;  175966 MW;  13272801 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            XXXXPXX
                  |
   TTYQECVGNQKGCMPDEGVHSWGEVEV
 120       130    X  140
```

15. US-08-121-713B-7 (1-7)
YIR3_YEAST PUTATIVE MEMBRANE GLYCOPROTEIN IN SUC2 5'REGION PR

```
 ID   YIR3_YEAST     STANDARD;      PRT;  1549 AA.
 AC   P40438;
 DT   01-FEB-1995 (REL. 31, CREATED)
 DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE   PUTATIVE MEMBRANE GLYCOPROTEIN IN SUC2 5'REGION PRECURSOR.
 GN   YIL173W.
 OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=S288C / AB972;
 RA   BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,
 RA   CHURCHER C.M., CONNOR R., COPSEY T., DEAR S., DEVLIN K., FRASER A.,
 RA   GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES M.,
 RA   LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D.,
 RA   RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
 RA   WALSH S.V., WHITEHEAD S.;
 RL   SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
 CC   -!- SIMILARITY: ALMOST IDENTICAL TO YEAST HRC1549. ALSO STRONG, TO
 CC       YEAST PEP1.
 DR   EMBL; Z47047; SCCHRIX.
 KW   HYPOTHETICAL PROTEIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT   SIGNAL        1     21       POTENTIAL.
 FT   CHAIN        22   1549       MEMBRANE GLYCOPROTEIN YIL173W.
 FT   TRANSMEM   1370   1390       POTENTIAL.
 FT   CARBOHYD    479    479       POTENTIAL.
 FT   CARBOHYD    769    769       POTENTIAL.
 FT   CARBOHYD    986    986       POTENTIAL.
 FT   CARBOHYD   1418   1418       POTENTIAL.
 SQ   SEQUENCE   1549 AA;  174426 MW;  12283501 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  1.48
Residue Identity =    14%  Matches          =      1  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            XXXXPXX
                  |
   FMIAKLPEARQLGMPLDFSAKAQDTFI
```

800 810

maryh@stic **stdin**

NeWSprinter20

Fri May 19 11:01:15 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

Salata 121713

SEQ 12

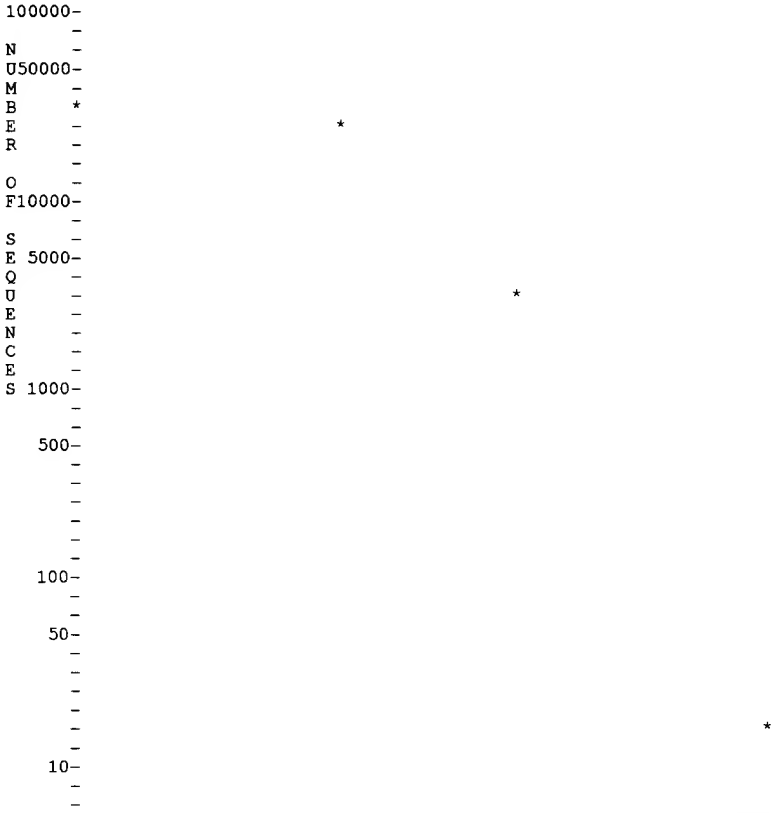
```
> O <
O| |O  IntelliGenetics
> O <

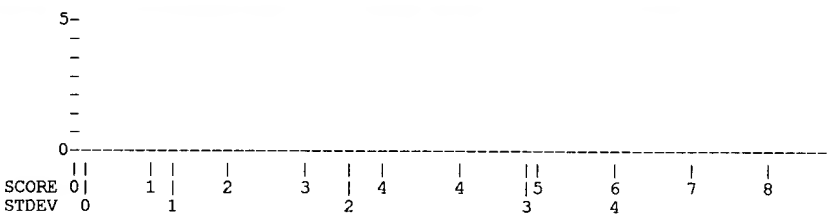
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq12asq.res made by  on Fri 19 May 95 8:40:34-PDT.


Query sequence being compared:US-08-121-713B-12 (1-8)
Number of sequences searched:                53402
Number of scores above cutoff:                4582

     Results of the initial comparison of US-08-121-713B-12 (1-8) with:
   Data bank : A-GeneSeq 18, all entries
```





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	1	1.67

Times:	CPU	Total Elapsed
	00:00:30.03	00:00:30.00

Number of residues: 6354270
Number of sequences searched: 53402
Number of scores above cutoff: 4582

Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

13 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. R12609	Versican.	2409	8	8	4.20	0
2. R42839	Urea amidolyase.	1835	8	8	4.20	0
3. R41732	High molecular weight protein	1529	8	8	4.20	0
4. P81854	Sequence encoded by LAV EL I	1022	8	8	4.20	0
5. R08060	HIV-1 pol protein of HIVMAL.	1003	8	8	4.20	0
6. R08061	HIV-1 pol protein of HIVELI.	1003	8	8	4.20	0
7. P81861	Sequence encoded by LAV MA L	1002	8	8	4.20	0
8. R09301	Sequence deduced from pol gen	982	8	8	4.20	0
9. R54631	Fragment of mannuronan C-5-ep	872	8	8	4.20	0
10. R44470	Eleusine indica alpha-1-tubul	451	8	8	4.20	0

11.	R44469	Eleusine indica alpha-1-tubul	451	8	8	4.20	0
12.	R53465	Glutamate-1-semialdehyde amin	441	8	8	4.20	0
13.	R27872	Odorant receptor clone I7.	327	8	8	4.20	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 2 standard deviations above mean ****					
14. R38905	Diuretic hormone binding pept	6	5	5	2.40	0
15. R51613	Mimotope nonapeptide #19 from	9	5	5	2.40	0
16. R55669	30-36 kD glial growth factor	10	5	5	2.40	0
17. R46862	Cell proliferation inhibitor.	10	5	5	2.40	0
18. R43629	Peptide derived from insulin-	10	5	5	2.40	0
19. R36885	Insulin-like growth factor-II	10	5	5	2.40	0
20. R28519	Novel peptide GGF-I 13.	10	5	5	2.40	0
21. R28626	Alpha-1 collagen chain derive	10	5	5	2.40	0
22. P60730	Block unit.	10	5	5	2.40	0
23. R37523	22(D)3-(2'napthyl)-alanine29A	11	5	5	2.40	0
24. R37522	22(D)3-(2'napthyl)-alanine29A	11	5	5	2.40	0
25. R37521	27Tyr, 28Pro, 29Arg, 32Thr, 3	11	5	5	2.40	0
26. R37002	22(D)3-(2'Napthyl)-ala 29Ala,	11	5	5	2.40	0
27. R34658	Heparinase tryptic fragment t	11	5	5	2.40	0
28. R27985	Tryptic peptide fragment #3.	11	5	5	2.40	0
29. R49866	Sequence of tryptic digest pe	12	5	5	2.40	0
30. R12491	Lys(342)-alpa-1-antitrypsin d	12	5	5	2.40	0
31. R11088	Human beta-lipotropic derived	12	5	5	2.40	0
32. R54967	SorhI grass pollen allergen T	13	5	5	2.40	0
33. P81289	Atrial natriuretic polypeptid	13	5	5	2.40	0
34. R54139	CHA255 light chain variable r	14	5	8	2.40	0
35. R36559	Thrombin inhibitor protein pa	14	5	5	2.40	0
36. R34532	Beta-hexosaminidase active pe	14	5	5	2.40	0
37. R32168	Soluble Kit Ligand M1.	14	5	5	2.40	0
38. R22078	Peptide for diagnosis of dise	14	5	5	2.40	0
39. R58349	Porcine parvovirus peptide 13	15	5	5	2.40	0
40. R58347	Porcine parvovirus peptide 8L	15	5	5	2.40	0
41. R58346	Porcine parvovirus peptide 7L	15	5	5	2.40	0
42. R33260	Sj23-like protein fragment.	15	5	5	2.40	0
43. P50768	Synthetic interleukin-2 antig	15	5	5	2.40	0
44. R58348	Porcine parvovirus peptide 10	16	5	5	2.40	0
45. R45248	HCV NS5 region (2422-2437).	16	5	5	2.40	0

1. US-08-121-713B-12 (1-8)
   R12609 Versican.

```
ID   R12609 standard; Protein; 2409 AA.
AC   R12609;
DT   11-SEP-1991  (first entry)
DE   Versican.
KW   Fibroblast proteoglycan; hyaluronic acid binding;
KW   tissue reconstruction.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT   /label= signal peptide
FT   Protein         21..2409
FT   /label= versican
FT   Modified -site  34..35
```



```
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  37..38
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  507..508
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  525..526
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  561..562
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  644..646
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  654..656
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  849..851
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  948..949
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  971..973
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1023..1025
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1047..1048
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1094..1095
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1267..1268
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1270..1272
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1336..1339
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1441..1442
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1444..1446
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1531..1532
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1651.1652
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1780..1781
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1814..1816
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1846..1847
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1851..1852
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1868..1869
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  1954..1955
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  2133..2134
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  2255..2256
FT   /label= glycosaminoglycan attachment site
FT   Modified -site  57
FT   /label= N-glycosylation site
FT   Modified -site  330
FT   /label= N-glycosylation site
FT   Modified -site  411
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```
FT   /label= N-glycosylation site
FT   Modified -site  455
FT   /label= N-glycosylation site
FT   Modified -site  481
FT   /label= N-glycosylation site
FT   Modified -site  676
FT   /label= N-glycosylation site
FT   Modified -site  911
FT   /label= N-glycosylation site
FT   Modified -site  1192
FT   /label= N-glycosylation site
FT   Modified -site  1285
FT   /label= N-glycosylation site
FT   Modified -site  1293
FT   /label= N-glycosylation site
FT   Modified -site  1373
FT   /label= N-glycosylation site
FT   Modified -site  1398
FT   /label= N-glycosylation site
FT   Modified -site  1405
FT   /label= N-glycosylation site
FT   Modified -site  1509
FT   /label= N-glycosylation site
FT   Modified -site  1641
FT   /label= N-glycosylation site
FT   Modified -site  1947
FT   /label= N-glycosylation site
FT   Modified -site  2080
FT   /label= N-glycosylation site
FT   Modified -site  2367
FT   /label= N-glycosylation site
FT   Modified -site  2382
FT   /label= N-glycosylation site
FT   Modified -site  2392
FT   /label= N-glycosylation site
FT   Modified -site  416..419
FT   /label= O-glycosylation site
FT   Modified -site  590..592
FT   /label= O-glycosylation site
FT   Modified -site  646..648
FT   /label= O-glycosylation site
FT   Modified -site  729..732
FT   /label= O-glycosylation site
FT   Modified -site  755..757
FT   /label= O-glycosylation site
FT   Modified -site  859..861
FT   /label= O-glycosylation site
FT   Modified -site  1008..1010
FT   /label= O-glycosylation site
FT   Modified -site  1018..1020
FT   /label= O-glycosylation site
FT   Modified -site  1032..1034
FT   /label= O-glycosylation site
FT   Modified -site  1127..1129
FT   /label= O-glycosylation site
FT   Modified -site  1205..1208
FT   /label= O-glycosylation site
FT   Modified -site  1341..1344
FT   /label= O-glycosylation site
FT   Modified -site  1399..1401
```



```
FT   /label= O-glycosylation site
FT   Modified -site  1407..1412
FT   /label= O-glycosylation site
FT   Modified -site  1468..1471
FT   /label= O-glycosylation site
FT   Modified -site  1735..1737
FT   /label= O-glycosylation site
FT   Modified -site  1990..1992
FT   /label= O-glycosylation site
FT   Modified -site  2018..2020
FT   /label= O-glycosylation site
FT   Region          400..408
FT   /label= unusual cluster of Glu residues
PN   WO9108230-A.
PD   13-JUN-1991.
PF   27-NOV-1990; U06897.
PR   27-NOV-1989; US-441179.
PA   (JOLL-) LA JOLLA CANCER RES.
PI   Ruoslahti E;
DR   WPI; 91-193156/26.
PT   Versican proteoglycan and nucleic acid - having hyaluronic acid
PT   binding region and used in e.g.. tissue reconstruction
PS   Claim 1; Fig 1; 27pp; English.
CC   The new fibroblast proteoglycan comprises a signal peptide,
CC   N-terminal hyaluronic acid domain, C-terminal EGF-like domain,
CC   lectin-like sequence and complement regulatory protein-like domain.
CC   Recombinant protein can be used to determine the presence of hyal-
CC   uronic acid, and as a vehicle to bring other molecules into contact
CC   with hyaluronic acid.  Antibodies can be prepared against the N-
CC   terminal or glycosaminoglycan attachment domain.  The protein is
CC   rich in glutamic acid and is highly negatively charged with a pI of
CC   4.2.  There are a total of 34 cysteine residues located exclusively
CC   in the N- and C-terminal domains.  On the C-terminal side of the
CC   link protein-like sequence is a 200 AA sequence contg. two
CC   cysteines and an unusual cluster of glutamic acid residues. The
CC   glycosaminoglycan attachment sites have a consensus sequence of
CC   E/DGSGE/D and the site of attachment is the Ser residue.
SQ   Sequence   2409 AA;
SQ   146A; 79 R; 73 N; 141D; 0  B; 35 C; 94 Q; 258E; 0  Z; 133G; 57 H;
SQ   114I; 139L; 96 K; 37 M; 95 F; 155P; 253S; 259T; 24 W; 62 Y; 159V;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.20
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    SVTSTTLIEILSDTGAEGPTVAPLPFST
  1340      1350      1360


2. US-08-121-713B-12 (1-8)
   R42839       Urea amidolyase.

 ID   R42839 standard; Protein; 1835 AA.
 AC   R42839;
 DT   10-MAY-1994  (first entry)
 DE   Urea amidolyase.
 KW   Urea amidolyase; URL; yeast; recombinant plasmid.
```

```
OS   Saccharomyces cerevisiae.
PN   J05244959-A.
PD   24-SEP-1993.
PF   05-MAR-1992; 084531.
PR   05-MAR-1992; JP-084531.
PA   (TOYM ) TOYOBO KK.
DR   WPI; 93-338925/43.
DR   N-PSDB; Q49460.
PT   DNA having the genetic information of urea amidolyase originated
PT   from Saccharomyces yeast - can be used to prepare high purity
PT   urea amidolyase by culturing the transformant comprising the DNA
PS   Claim 2; Page 10-17; 17pp; Japanese.
CC   This sequence represents a protein which has urea amidolyase (URL)-
CC   activity and is derived from yeast.  The DNA encoding this protein
CC   may be used within a recombinant plasmid for the production of highly
CC   pure URL.
SQ   Sequence   1835 AA;
SQ   127A; 74 R; 82 N; 97 D; 0  B; 31 C; 60 Q; 126E; 0  Z; 145G; 23 H;
SQ   127I; 156L; 117K; 26 M; 72 F; 102P; 144S; 95 T; 22 W; 65 Y; 144V;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.20
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    PVLFSNAVENLSRTGANVIEIDFEPLLE
  280       290       300
```

3. US-08-121-713B-12 (1-8)
   R41732 High molecular weight protein 4 (HMW4).

```
ID   R41732 standard; Protein; 1529 AA.
AC   R41732;
DT   26-APR-1994  (first entry)
DE   High molecular weight protein 4 (HMW4).
KW   HMW; high molecular weight protein; virus; vaccine; influenza;
KW   epitope; immunity; haemophilus influenzae.
OS   Haemophilus influenzae.
PN   WO9319090-A.
PD   30-SEP-1993.
PF   16-MAR-1993; U02166.
PR   16-MAR-1992; GB-005704.
PA   (BARE/) BARENKAMP S J.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PI   Barenkamp SJ;
DR   WPI; 93-320683/40.
DR   N-PSDB; Q49511.
PT   High molecular weight surface proteins - of non-typeable
PT   haemophilus which exhibit immunogenic properties
PS   Claim 6; Figure 10; 100pp; English.
CC   The isolation and purification of the high molecular weight protein
CC   enables the identification of the major protective epitopes of the
CC   protein by conventional epitope mapping.  These epitopes can then be
CC   synthesised using standard techniques and incorporated into fully
CC   synthetic or recombinant vaccines.
SQ   Sequence   1529 AA;
SQ   117A; 30 R; 176N; 80 D; 0  B; 2  C; 44 Q; 65 E; 0  Z; 168G; 13 H;
```



```
SQ   139I; 88 L; 110K; 6  M; 35 F; 12 P; 148S; 183T; 6  W; 10 Y; 97 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.20
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    TLGNISVEGNLSLTGANANIVGNLSIAE
  810       820   X   830
```

4. US-08-121-713B-12 (1-8)
   P81854 Sequence encoded by LAV EL I POL gene

```
ID   P81854 standard; protein; 1022 AA.
AC   P81854;
DT   16-DEC-1990  (first entry)
DE   Sequence encoded by LAV EL I POL gene
KW   HIV; HTLV III; AIDS; diagnosis; vaccine; probe; hybridisation.
OS   Lymphadenopathy associated virus EL I.
PN   WO8707906-A.
PD   30-DEC-1987.
PF   22-JUN-1987; E00326.
PR   23-JUN-1986; EP-401380.
PA   (INSP) Inst Pasteur.
PI   Alizon M, Sonigo P, Wain-Hobson S, Montagnier L;
DR   WPI; 88-014396/02.
DR   N-PSDB; N80436.
PT   New variants of lymphadenopathy associated virus (LAV) -
PT   used for prodn. of DNA, antigens and antibodies used in
PT   diagnosis of AIDS and pre-AIDS
PS   Claim 8; Fig 7A-7J; 72pp; English.
CC   LAV EL I (N80436) and LAV MA L (N80437) were isolated from the peripheral
CC   blood lymphocytes of patients. Different AIDS virus isolates concerned
CC   are designated by 3 letters of the patients name. Stable probes including
CC   the DNA sequences can be used for detection of the new LAV viruses or
CC   related viruses or DNA proviruses in e.g. biological samples. Proteins
CC   or peptides can be used for detection of antibodies induced in vivo and
CC   present in biological fluids. The DNA can also be used for the expression
CC   of LAV viral antigens for the prodn. of a vaccine against LAV. The
CC   polypeptides can also be used for the prodn. of antibodies for the
CC   detection of proteins related to the LAV viruses, partic. for diagnosis
CC   of AIDS or pre-AIDS.
SQ   Sequence   1022 AA;
SQ   61 A;  50 R;  37 N;  50 D; 0 B;  10 C;  65 Q;  76 E;  0 Z;  74 G;  19 H;
SQ   80 I;  80 L;  94 K;  14 M;30 F;  58 P;  39 S;  56 T; 30 W;  30 Y;  69 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.20
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    ELRVWGRDNPLSKTGAERQGTVSFNFPQ
  30        40      X 50
```

5. US-08-121-713B-12 (1-8)
R08060 HIV-1 pol protein of HIVMAL.

```
 ID   R08060 standard; protein; 1003 AA.
 AC   R08060;
 DT   18-JAN-1991  (first entry)
 DE   HIV-1 pol protein of HIVMAL.
 KW   HIV diagnosis; HIV-pol; vaccine; HIVMAL;
 KW   protein processing; reverse transcriptase; RNAse; integrase.
 OS   Human immunodeficiency virus - 1.
 PN   WO9010230-A.
 PD   07-SEP-1990.
 PF   23-FEB-1990; CA0062.
 PR   18-APR-1989; GB-008725.
 PA   (UYOT-) UNIV OF OTTAWA.
 PI   Kang CY;
 DR   WPI; 90-290460/38.
 PT   Improved polypeptide reagent for HIV diagnosis and vaccine -
 PT   comprises portions of all 4 enzymes encoded by HIV-pol gene
 PS   Disclosure; Page 11-23; 37pp; English.
 CC   Several strains of HIV-1 were cloned and the corresponding amino
 CC   acid sequence derived from the determined DNA sequences.
 CC   An improved polypeptide reagent comprises portions of all of the
 CC   4 enzymes, and is used in a diagnostic test for HIV infection.
 CC   The peptide is also used in vaccines.
 CC   See also R08053-63.
 SQ   Sequence   1003 AA;
 SQ   61 A; 35 R; 36 N; 49 D; 0  B; 10 C; 65 Q; 75 E; 0  Z; 75 G; 17 H;
 SQ   85 I; 71 L; 97 K; 14 M; 29 F; 55 P; 41 S; 58 T; 30 W; 31 Y; 69 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.20
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   ELRVWGGDKTLSETGAERQGIVSFSFPQ
          40        50
```

6. US-08-121-713B-12 (1-8)
R08061 HIV-1 pol protein of HIVELI.

```
 ID   R08061 standard; protein; 1003 AA.
 AC   R08061;
 DT   18-JAN-1991  (first entry)
 DE   HIV-1 pol protein of HIVELI.
 KW   HIV diagnosis; HIV-pol; vaccine; HIVELI;
 KW   protein processing; reverse transcriptase; RNAse; integrase.
 OS   Human immunodeficiency virus - 1.
 PN   WO9010230-A.
 PD   07-SEP-1990.
 PF   23-FEB-1990; CA0062.
 PR   18-APR-1989; GB-008725.
 PA   (UYOT-) UNIV OF OTTAWA.
 PI   Kang CY;
 DR   WPI; 90-290460/38.
 PT   Improved polypeptide reagent for HIV diagnosis and vaccine -
 PT   comprises portions of all 4 enzymes encoded by HIV-pol gene
```



```
 PS   Disclosure; Page 11-23; 37pp; English.
 CC   Several strains of HIV-1 were cloned and the corresponding amino
 CC   acid sequence derived from the determined DNA sequences.
 CC   An improved polypeptide reagent comprises portions of all of the
 CC   4 enzymes, and is used in a diagnostic test for HIV infection.
 CC   The peptide is also used in vaccines.
 CC   See also R08053-63.
 SQ   Sequence   1003 AA;
 SQ   61 A; 44 R; 38 N; 48 D; 0  B; 10 C; 63 Q; 75 E; 0  Z; 73 G; 17 H;
 SQ   81 I; 78 L; 92 K; 15 M; 29 F; 57 P; 39 S; 55 T; 30 W; 30 Y; 68 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.20
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   ELRVWGRDNPLSKTGAERQGTVSFNFPQ
          40        50
```

7. US-08-121-713B-12 (1-8)
P81861 Sequence encoded by LAV MA L POL gene

```
 ID   P81861 standard; protein; 1002 AA.
 AC   P81861;
 DT   16-DEC-1990  (first entry)
 DE   Sequence encoded by LAV MA L POL gene
 KW   HIV; HTLV III; AIDS; diagnosis; vaccine; probe; hybridisation.
 OS   Lymphadenopathy associated virus MA L.
 PN   WO8707906-A.
 PD   30-DEC-1987.
 PF   22-JUN-1987; E00326.
 PR   23-JUN-1986; EP-401380.
 PA   (INSP) Inst Pasteur.
 PI   Alizon M, Sonigo P, Wain-Hobson S, Montagnier L;
 DR   WPI; 88-014396/02.
 DR   N-PSDB; N80437.
 PT   New variants of lymphadenopathy associated virus (LAV) -
 PT   used for prodn. of DNA, antigens and antibodies used in
 PT   diagnosis of AIDS and pre-AIDS
 PS   Claim 8; Fig 8A-8I; 72pp; English.
 CC   LAV EL I (N80436) and LAV MA L (N80437) were isolated from the peripheral
 CC   blood lymphocytes of patients. Different AIDS virus isolates concerned
 CC   are designated by 3 letters of the patients name. Stable probes including
 CC   the DNA sequences can be used for detection of the new LAV viruses or
 CC   related viruses or DNA proviruses in eg. biological samples. The proteins
 CC   or peptides can be used for detection of antibodies induced in vivo and
 CC   present in biological fluids. The DNA can also be used for the expression
 CC   of LAV viral antigens for the prodn. of a vaccine against LAV. The
 CC   polypeptides can also be used for the prodn. of antibodies for the
 CC   detection of proteins related to the LAV viruses, partic. for diagnosis
 CC   of AIDS or pre-AIDS.
 SQ   Sequence   1002 AA;
 SQ   61 A;  38 R;  36 N;  49 D;  0 B;  10 C;  65 Q;  75 E;  0 Z;  75 G;  17 H;
 SQ   84 I;  71 L;  95 K;  13 M; 29 F;  56 P;  40 S;  58 T; 29 W;  31 Y;  70 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.20
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
```

```
Gaps              =      0  Conservative Substitutions              =     0

              X      X
              XSXTXAXX
               | | |
    ELRVWGGDKTLSETGAERQGIVSFSFPQ
   30         40      X 50
```

8. US-08-121-713B-12 (1-8)
R09301 Sequence deduced from pol gene of HIV 1-NDK.

```
 ID   R09301 standard; protein; 982 AA.
 AC   R09301;
 DT   27-FEB-1991  (first entry)
 DE   Sequence deduced from pol gene of HIV 1-NDK.
 KW   Human immunodeficiency virus; AIDS.
 OS   HIV 1-NDK.
 PN   WO9013630-A.
 PD   15-NOV-1990.
 PF   02-MAY-1990; F00312.
 PR   03-MAY-1989; FR-005914.
 PA   (INRM ) INSERM INST NAT SANTE.
 PI   Barre-Sinnoussi F, Chermann JC, Devaux C, Rey F, Sire J;
 PI   Spire B;
 DR   WPI; 90-361470/48.
 DR   N-PSDB; Q06635.
 PT   New HIV-NDK retrovirus and protein component - used in vaccines
 PT   against immuno-deficiency disorders and in raising MAbs for
 PT   retro-virus detection in vivo.
 PS   Disclosure; Fig 2; 37pp; French.
 CC   The HIV NDK virus was isolated from peripheral blood lymphocytes of
 CC   an AIDS patient. A genomic library was prepd. from DNA extracted
 CC   from CEM cells infected with the virus. The library was screened
 CC   with a pBT1 probe corresp. to a fragment from HIV 1.  The virus is
 CC   more cytopathic than other strains and is not inhibited by OKT4A.
 CC   It has been deposited as CNCM I-857.  The sequence can be used to
 CC   express proteins useful for diagnosing the presence of NDK and
 CC   related viruses and in vaccines against immunodeficiency diseases.
 CC   See also R09301-5.
 SQ   Sequence   982 AA;
 SQ   58 A; 39 R; 34 N; 47 D; 0  B; 10 C; 62 Q; 77 E; 0  Z; 74 G; 16 H;
 SQ   79 I; 75 L; 89 K; 12 M; 31 F; 54 P; 39 S; 58 T; 28 W; 31 Y; 69 V;
```

```
Initial Score     =      8  Optimized Score  =      8  Significance =  4.20
Residue Identity  =     37%  Matches          =      3  Mismatches   =     5
Gaps              =      0  Conservative Substitutions               =     0

              X      X
              XSXTXAXX
               | | |
    ELRVWGGDNPLSETGAERQGTVSFSFPQ
   30         40      X 50
```

9. US-08-121-713B-12 (1-8)
R54631 Fragment of mannuronan C-5-epimerase (epimerase 3)

```
 ID   R54631 standard; Protein; 872 AA.
 AC   R54631;
```



```
 DT   04-JAN-1995  (first entry)
 DE   Fragment of mannuronan C-5-epimerase (epimerase 3).
 KW   Mannuronan; epimerase; alginates; immunostimulant;
 KW   cell immobilisation; Azotobacter vinelandii; guluronic acid;
 KW   mannuronic acid.
 OS   Azotobacter vinelandii strain E.
 PN   WO9409124-A.
 PD   28-APR-1994.
 PF   08-OCT-1993; NO0151.
 PR   08-OCT-1992; GB-021163.
 PA   (NOBI-) NOBIPOL NOBIPOLS FORSKNINGSSTIFTELSE.
 PA   (PRON-) PRONOVA BIOPOLYMER AS.
 PI   Ertesvag H,  Larsen B,  Valla S,  Skjak-braek G;
 DR   WPI; 94-151310/18.
 DR   N-PSDB; Q63293.
 PT   New nucleic acid encoding mannuronan C-5-epimerase - and derived
 PT   vectors and polypeptide, for prodn. of alginate of controlled G
 PT   or M content, useful e.g. as immunostimulants or for cell
 PT   immobilisation.
 PS   Claim 14; Page 42-45; 78pp; English.
 CC   The epimerase enzymes (See R54628-R54631) can be used for the
 CC   microbial production of alginates, esp. those of G (guluronic acid)
 CC   block content 75-98% or those with a specific M (mannuronic acid)/G
 CC   block content.  Inactivation of specific enzyme activities allows
 CC   prodn. of pure poly-M alginates or those of G block content below
 CC   25%.  Alginates of high M content are powerful, nontoxic
 CC   immunostimulants while those of high G content can be used for cell
 CC   immobilisation.
 SQ   Sequence   872 AA;
 SQ   86 A; 35 R; 55 N; 97 D; 0  B; 0  C; 32 Q; 35 E; 0  Z; 138G; 9  H;
 SQ   32 I; 76 L; 9  K; 7  M; 37 F; 12 P; 54 S; 67 T; 3  W; 37 Y; 51 V;
```

```
Initial Score     =      8  Optimized Score  =      8  Significance =  4.20
Residue Identity  =     37%  Matches          =      3  Mismatches   =     5
Gaps              =      0  Conservative Substitutions               =     0

              X      X
              XSXTXAXX
               | | |
    TLEGTAGNDVLSGTGAHELILGLAGNDR
      390     X  400 X      410
```

10. US-08-121-713B-12 (1-8)
R44470 Eleusine indica alpha-1-tubulin.

```
 ID   R44470 standard; Protein; 451 AA.
 AC   R44470;
 DT   29-JUN-1994  (first entry)
 DE   Eleusine indica alpha-1-tubulin.
 KW   Alpha-1-tubulin; dinitroaniline; phosphorothioamidate;
 KW   herbicide resistance; pesticide resistance; crop improvement;
 KW   transgenic plant; maize; sugarbeet; ss.
 OS   Eleusine indica.
 FH   Key             Location/Qualifiers
 FT   Modified_site   239..239
 FT   /note= "amino acid substitution from Thr"
 PN   WO9324637-A.
 PD   09-DEC-1993.
 PF   26-MAY-1993; G01085.
```

```
PR   26-MAY-1992; GB-011130.
PA   (ELLI/) ELLIS R R.
PA   (ZENE ) ZENECA LTD.
PI   Cronin KE,  Hussey PJ,  Ray JA,  Waldin TR;
DR   WPI; 93-405828/50.
DR   N-PSDB; Q53405.
PT   Modified tubulin conferring resistance to anti-tubulin agents,
PT   pref. in maize - enables use of di:nitroaniline and
PT   phosphoro:thio:amidate herbicide during maize growth for weed
PT   control
PS   Disclosure; Table 6; 53pp; English.
CC   Alpha-1-tubulin isotype protein found in the dinitroaniline-
CC   susceptible (S) biotype of E. indica.  The protein may be modified
CC   via amino acid substitution at position 239 from Thr to Ile to
CC   resulting in a modified alpha-1-tubulin resistant to dinitroaniline and
CC   phosphorothioamidate herbicides.  The modified protein may be
CC   expressed in transgenic maize (Zea mays) or sugarbeet (Beta
CC   vulgaris) in order to confer resistance to dinitroaniline and
CC   phosphorothioamidate.  The modified resistant alpha-1-tublin
CC   protein sequence is given in R44469.
SQ   Sequence   451 AA;
SQ   33 A; 21 R; 17 N; 29 D; 0  B; 12 C; 14 Q; 35 E; 0  Z; 39 G; 12 H;
SQ   23 I; 35 L; 19 K; 10 M; 20 F; 17 P; 32 S; 23 T; 3  W; 18 Y; 39 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.20
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   GGGDDAFNTFFSETGAGKHVPRAVFVDL
         50  X     60        70
```

11. US-08-121-713B-12 (1-8)
    R44469 Eleusine indica alpha-1-tubulin (modified).

```
ID   R44469 standard; Protein; 451 AA.
AC   R44469;
DT   30-AUG-1994  (first entry)
DE   Eleusine indica alpha-1-tubulin (modified).
KW   Alpha-1-tubulin; dinitroaniline; phosphorothioamidate;
KW   herbicide resistance; pesticide resistance; crop improvement;
KW   transgenic plant; maize; sugarbeet; goosegrass.
OS   Eleusine indica.
PN   WO9324637-A.
PD   09-DEC-1993.
PF   26-MAY-1993; G01085.
PR   26-MAY-1992; GB-011130.
PA   (ELLI/) ELLIS R R.
PA   (ZENE ) ZENECA LTD.
PI   Cronin KE,  Ellis JR,  Hussey PJ,  Ray JA,  Waldin TR;
DR   WPI; 93-405828/50.
DR   N-PSDB; Q53404.
PT   Modified tubulin conferring resistance to anti-tubulin agents,
PT   pref. in maize - enables use of di:nitroaniline and
PT   phosphoro:thio:amidate herbicide during maize growth for weed
PT   control
PS   Disclosure; Table 3; 53pp; English.
```



```
CC   DNA encoding an alpha-1-tubulin isotype is found in the dinitroaniline-
CC   susceptible (S) biotype of E. indica.  The protein generated from
CC   this sequence may be modified via amino acid substitution to
CC   generate a modified alpha-1-tubulin resistant to dinitroaniline and
CC   phosphorothioamidate herbicides.  The modified DNA sequence of this
CC   resistant isotype is given in Q53404.
SQ   Sequence   451 AA;
SQ   33 A; 21 R; 16 N; 30 D; 0  B; 12 C; 14 Q; 35 E; 0  Z; 39 G; 12 H;
SQ   25 I; 35 L; 20 K; 10 M; 20 F; 18 P; 31 S; 21 T; 3  W; 18 Y; 38 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.20
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   GGGDDAFNTFFSETGAGKHVPRAVFVDL
         50  X     60        70
```

12. US-08-121-713B-12 (1-8)
    R53465 Glutamate-1-semialdehyde aminotransferase.

```
ID   R53465 standard; Protein; 441 AA.
AC   R53465;
DT   18-JAN-1995  (first entry)
DE   Glutamate-1-semialdehyde aminotransferase.
KW   Glutamate-1-semialdehyde aminotransferase; Xanthomonas phaseoli;
KW   expression; transformation; fermentation; production.
OS   Propionibacterium freudenreichii.
PN   J06113861-A.
PD   26-APR-1994.
PF   07-OCT-1992; 268655.
PR   07-OCT-1992; JP-268655.
PA   (MAZN ) COSMO OIL CO LTD.
PA   (COSM-) COSMO SOGO KENKYUSHO KK.
DR   WPI; 94-172754/21.
DR   N-PSDB; Q63612.
PT   DNA fragment coding glutamate-1 semi-aldehyde amino transferase -
PT   used for production of alanine and vitamin=B12.
PS   Claim 2; Page 5; 9pp; Japanese.
CC   The sequence encoding the glutamate-1-semialdehyde aminotransferase
CC   (Q63612) was used in the construction of expression vectors which
CC   were used, in turn, to transform competent E. coli.  Culturing the
CC   transformed cells allows the production of large amounts of
CC   glutamate-1-semialdehyde aminotransferase having high activity.
SQ   Sequence   441 AA;
SQ   68 A; 22 R; 5  N; 31 D; 0  B; 5  C; 10 Q; 19 E; 0  Z; 45 G; 11 H;
SQ   12 I; 41 L; 13 K; 11 M; 19 F; 23 P; 32 S; 19 T; 5  W; 7  Y; 43 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.20
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   IQDEVLTGFRLSPTGAWGLQGAKEGWTP
     240     X 250  X    260
```

13. US-08-121-713B-12 (1-8)
R27872 Odorant receptor clone I7.

```
 ID   R27872 standard; Protein; 327 AA.
 AC   R27872;
 DT   15-MAR-1993  (first entry)
 DE   Odorant receptor clone I7.
 KW   Odorant receptor; insect; vertebrate; fish; mammal; neurotransmitter;
 KW   hormone; G-protein; surface receptor; olfactory epithelium; PCR;
 KW   Sprague-Dawley rat; amplify; primer; polymerase chain reaction;
 KW   multigene family; ligand binding domain.
 OS   Ratus ratus.
 FH   Key             Location/Qualifiers
 FT   Misc_difference 35
 FT   /label= VAL, ALA, ASP, GLY
 PN   WO9217585-A.
 PD   15-OCT-1992.
 PF   06-APR-1992; U02741.
 PR   05-APR-1991; US-681880.
 PA   (UYCO ) UNIV COLUMBIA NEW YORK.
 PI   Axel R, Buck LB;
 DR   WPI; 92-366257/44.
 DR   N-PSDB; Q29860.
 PT   Nucleic acid encoding an odorant receptor - can be used to
 PT   control insect populations or for detecting odours e.g. alcohol,
 PT   explosives, natural gas etc.
 PS   Claim 41; Fig 14; 195pp; English.
 CC   The sequences given in R27867-89 are encoded by odorant receptor
 CC   clones derived from an insect, a vertebrate, a fish or a mammal.
 CC   These clones form a family of neurotransmitters and hormone receptors
 CC   which transduce intracellular signals by activation of specific G-
 CC   proteins.  Each of these receptors is a member of a superfamily of
 CC   surface receptors which traverse the membrane seven times.  These
 CC   clones are only expressed in the olfactory epithelium.  These clones
 CC   were isolated using probes derived from RNA prepared from the
 CC   olfactory epithelia of Sprague-Dawley rats.  Isolated cDNA's were
 CC   amplified using primers which correspond to transmembrane domain 2
 CC   and 7.  PCR products of the appropriate size were isolated and
 CC   sequenced.  The deduced protein sequences of these cDNA's defined a
 CC   new multigene family which shared sequence and structural properties
 CC   with the superfamily of neurotransmitter and hormone receptors which
 CC   traverse the membrane seven times.  This novel family, however
 CC   exhibits features different from any other member of the superfamily
 CC   identified so far.  There is a striking divergence within the third,
 CC   fourth and fifth transmembrane domains between the olfactory proteins.
 CC   This divergence in the potential ligand binding domain is consistent
 CC   with the idea that the family of molecules cloned is capable of
 CC   asssociating with a large number of odorant of diverse molecular
 CC   structure.
 SQ   Sequence   327 AA;
 SQ   30 A; 15 R; 13 N; 7  D; 0  B; 10 C; 7  Q; 8  E; 0  Z; 18 G; 10 H;
 SQ   25 I; 43 L; 10 K; 12 M; 21 F; 15 P; 24 S; 17 T; 2  W; 13 Y; 26 V;
 SQ   1 Others;
```

Initial Score	=	8	Optimized Score	=	8	Significance	= 4.20
Residue Identity	=	37%	Matches	=	3	Mismatches	= 5
Gaps	=	0	Conservative Substitutions				= 0


```
            X      X
            XSXTXAXX
             | | |
VLAIFILLGPLSVTGASYMAITGAVMRI
  210     X 220  X    230
```

14. US-08-121-713B-12 (1-8)
R38905 Diuretic hormone binding peptide #2.

```
 ID   R38905 standard; peptide; 6 AA.
 AC   R38905;
 DT   10-NOV-1993  (first entry)
 DE   Diuretic hormone binding peptide #2.
 KW   Diuretic hormone; pharmaceuticals; diagnosis; reagent; detection;
 KW   precursor; drug; activation; modification.
 OS   Synthetic.
 PN   J05140187-A.
 PD   08-JUN-1993.
 PF   12-NOV-1991; 295719.
 PR   12-NOV-1991; JP-295719.
 PA   (HITB ) HITACHI CHEM CO LTD.
 DR   WPI; 93-216808/27.
 PT   Peptide which can combine with diuretic hormone - is useful as
 PT   reagent for detecting diuretic hormone and as treatment drug
 PS   Claim 1; Page 2; 7pp; Japanese.
 CC   The sequences given in R38904-05 are peptides fragments which bind
 CC   to diuretic hormone.  These peptides may be incorporated into a
 CC   larger peptide which can be used in pharmaceuticals, diagnostics, or
 CC   for the preparation of living body substances.  It may also be used
 CC   as a reagent for the detection of diuretic hormone or precursors and
 CC   as a treating drug for activation or modification of diuretic
 CC   hormone function.
 SQ   Sequence   6 AA;
 SQ   1  A; 0  R; 0  N; 0  D; 0  B; 0  C; 1  Q; 2  E; 0  Z; 1  G; 0  H;
 SQ   0  I; 0  L; 0  K; 0  M; 0  F; 0  P; 0  S; 1  T; 0  W; 0  Y; 0  V;
```

Initial Score	=	5	Optimized Score	=	5	Significance	= 2.40
Residue Identity	=	33%	Matches	=	2	Mismatches	= 4
Gaps	=	0	Conservative Substitutions				= 0

```
    X    X
   XSXTXAXX
     | |
    EQTGAE
    X    X
```

15. US-08-121-713B-12 (1-8)
R51613 Mimotope nonapeptide #19 from panel of maximally d

```
 ID   R51613 standard; peptide; 9 AA.
 AC   R51613;
 DT   19-OCT-1994  (first entry)
 DE   Mimotope nonapeptide #19 from panel of maximally diverse mimotopes.
 KW   mimotope panel; rational drug design; candidate drug;
 KW   screening assay; hydrophobicity; antibody repertoire.
 OS   Synthetic.
 FH   Key             Location/Qualifiers
 FT   Modified_site   9
```

```
FT   /note= "amidated"
PN   US5300425-A.
PD   05-APR-1994.
PF   13-OCT-1987; 108130.
PR   13-OCT-1987; US-108130.
PR   11-OCT-1988; US-255906.
PR   06-DEC-1989; US-447009.
PA   (TERR-) TERRAPIN TECHNOLOGIES INC.
PI   Kauvar LM;
DR   WPI; 94-109390/13.
PT   Screening of candidate drugs for binding to receptor - by
PT   comparing inverse image antibody profile of drug with
PT   mimotype-binding profile of receptor
PS   Example 5; Fig 7; 29pp; English.
CC   A panel of 24 nonapeptides (R51595-R51618) was designed to show
CC   high diversity in hydrophobic moment and hydrophobic index, as well
CC   as charge distribution and size. Sixteen of these peptides were
CC   tested for ability to bind the murine antibody MAb 33-6,
CC   arbitrarily chosen. Results of a dot-blot showed that 3 of the 16
CC   peptides tested successfully bound MAb 33-6. Thus a small number of
CC   diverse mimotopes is able to contain a suitable peptide for binding
CC   to a selected antibody.
SQ   Sequence   9 AA;
SQ   2  A; 1  R; 0  N; 1  D; 0  B; 0  C; 0  Q; 0  E; 0  Z; 2  G; 0  H;
SQ   1  I; 0  L; 1  K; 0  M; 0  F; 0  P; 0  S; 1  T; 0  W; 0  Y; 0  V;

Initial Score    =      5  Optimized Score  =      5  Significance =  2.40
Residue Identity =    25%  Matches          =      2  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

     X      X
     XSXTXAXX
       | |
    GKAITGARD
     X      X
> O <
O| |O  IntelliGenetics
> O <

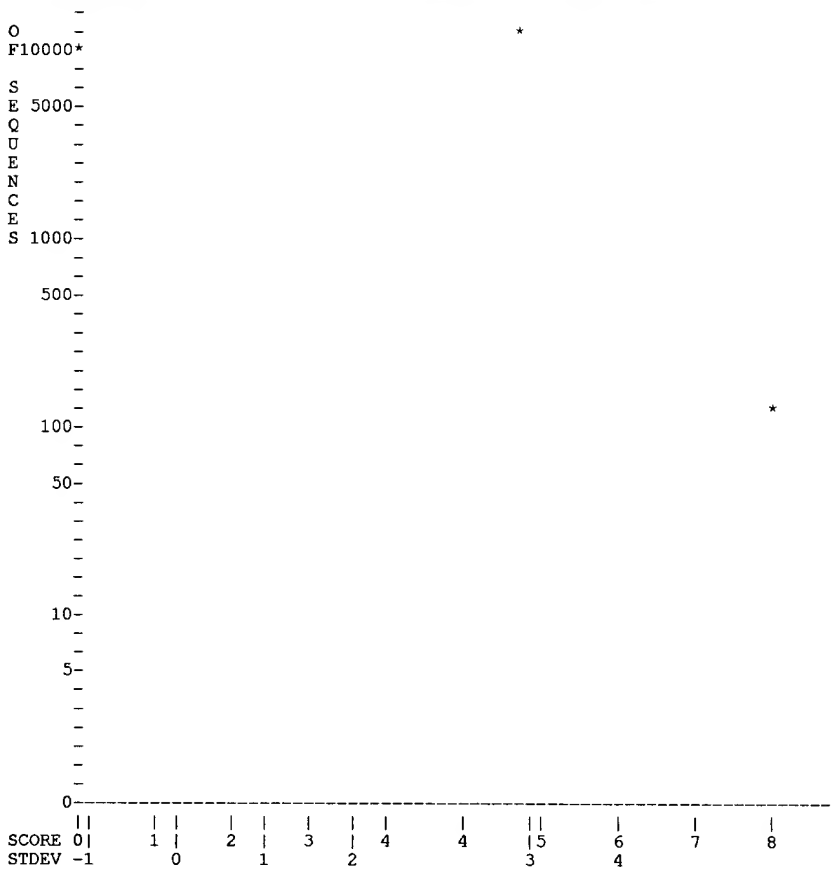
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq12pir.res made by maryh on Fri 19 May 95 10:44:33-PDT.


Query sequence being compared:US-08-121-713B-12 (1-8)
Number of sequences searched:                75511
Number of scores above cutoff:                3810

      Results of the initial comparison of US-08-121-713B-12 (1-8) with:
   Data bank : PIR 43, all entries

100000-
      -
N     -                    *
U50000-
M     -
B     -
E     -
R     -
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation

	2	4	1.31

Times:

CPU	Total Elapsed
00:01:14.99	00:01:16.00

Number of residues: 22468834
Number of sequences searched: 75511
Number of scores above cutoff: 3810

The scores below are sorted by initial score.
Significance is calculated based on initial score.

111 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. S17653	dynein beta heavy chain, cili	4466	8	8	4.59	0
2. S28916	dystrophin - mouse	3678	8	8	4.59	0
3. S18268	delta-(L-alpha-aminoadipyl)-L	3649	8	8	4.59	0
4. A60979	proteoglycan 24K core protein	2409	8	8	4.59	0
5. S46082	urea carboxylase (EC 6.3.4.6)	1835	8	8	4.59	0
6. JN0896	crystalline surface layer pro	1645	8	8	4.59	0
7. RRWGNV	RNA-directed RNA polymerase (	1643	8	8	4.59	0
8. JH0675	restrictin precursor - chicke	1353	8	8	4.59	0
9. A53824	pore membrane protein POM152	1337	8	8	4.59	0
10. S26650	DNA-binding protein 5 - human	1203	8	8	4.59	0
11. S31301	DNA repair protein RAD5 - yea	1169	8	8	4.59	0
12. A36096	Ca2+-transporting ATPase (EC	1037	8	8	4.59	0
13. S04111	collagen alpha 2(VI) chain pr	1022	8	8	4.59	0
14. S23378	collagen alpha 2(VI) chain lo	1022	8	8	4.59	0
15. GNLJND	pol polyprotein - human immun	1002	8	8	4.59	0
16. S33121	Clox protein - dog (fragment)	975	8	8	4.59	0
17. S23377	collagen alpha 2(VI) chain sh	918	8	8	4.59	0
18. DEEC	alcohol dehydrogenase (EC 1.1	891	8	8	4.59	0
19. S14809	alcohol dehydrogenase (EC 1.1	891	8	8	4.59	0
20. A35797	probable DNA-binding protein	790	8	8	4.59	0
21. A49398	cycloartenol synthase (EC 5.4	759	8	8	4.59	0
22. A31806	collagen alpha 2(VI) chain -	720	8	8	4.59	0
23. BVECUB	uvrB protein - Escherichia co	673	8	8	4.59	0
24. S32991	hypothetical protein - human	657	8	8	4.59	0
25. A43317	germ cell-less protein gcl -	569	8	8	4.59	0
26. S36363	pyruvate decarboxylase (EC 4.	564	8	8	4.59	0
27. DCBYP	pyruvate decarboxylase (EC 4.	563	8	8	4.59	0
28. A37293	pyruvate decarboxylase (EC 4.	563	8	8	4.59	0
29. S24344	glucose transport protein Glu	528	8	8	4.59	0
30. S05319	glucose transport protein, he	523	8	8	4.59	0
31. S06920	glucose transport protein, he	523	8	8	4.59	0
32. A31556	glucose transport protein, he	522	8	8	4.59	0
33. A45566	variable surface glycoprotein	512	8	8	4.59	0
34. S36339	pherophorin II - Volvox carte	484	8	8	4.59	0
35. S30057	dihydrolipoamide dehydrogenas	479	8	8	4.59	0
36. A28914	tubulin alpha chain - Naegler	453	8	8	4.59	0
37. S07459	tubulin alpha-I chain - Plasm	453	8	8	4.59	0
38. S47484	alpha-tubulin - Naegleria gru	453	8	8	4.59	0
39. S16339	tubulin alpha chain - Toxopla	453	8	8	4.59	0
40. A60671	tubulin alpha chain - sea urc	452	8	8	4.59	0
41. S42033	alpha tubulin - common limpet	452	8	8	4.59	0

42. S45070	tubulin 2 alpha chain - commo	452	8	8	4.59	0
43. S11207	tubulin alpha chain - sea urc	452	8	8	4.59	0
44. S37933	aspartate transaminase (EC 2.	451	8	8	4.59	0
45. S15773	tubulin alpha-1 chain - maize	451	8	8	4.59	0

1. US-08-121-713B-12 (1-8)
   S17653 dynein beta heavy chain, ciliary - sea urchin (Tri

```
ENTRY            S17653     #type complete
TITLE            dynein beta heavy chain, ciliary - sea urchin (Tripneustes
                   gratilla)
CONTAINS         dynein ATPase (EC 3.6.1.33)
ORGANISM         #formal_name Tripneustes gratilla
DATE             04-Dec-1992 #sequence_revision 02-May-1994 #text_change
                   08-Dec-1994
ACCESSIONS       S17653; S24628
REFERENCE        S17653
   #authors      Gibbons, I.R.; Gibbons, B.H.; Mocz, G.; Asai, D.J.
   #journal      Nature (1991) 352:640-643
   #title        Multiple nucleotide-binding sites in the sequence of dynein
                   beta heavy chain.
   #cross-references MUID:91326103
   #accession    S17653
      ##molecule_type mRNA
      ##residues      1-4466 ##label GIB1
      ##cross-references EMBL:X59603
      ##note          the nucleotide sequence is not given in this paper
   #accession    S24628
      ##molecule_type protein
      ##residues      162-172;1193-1204;3240-3259;3325-3339 ##label GIB2
CLASSIFICATION   #superfamily dynein heavy chain, ciliary
KEYWORDS         ATP; heterotetramer; hydrolase; microtubule binding
FEATURE
   154-161           #region nucleotide-binding motif A (P-loop)\
   1852-1859         #region nucleotide-binding motif A (P-loop)\
   2133-2140         #region nucleotide-binding motif A (P-loop)\
   2460-2467         #region nucleotide-binding motif A (P-loop)\
   2805-2812         #region nucleotide-binding motif A (P-loop)\
   1858              #binding_site ATP (Lys) #status predicted\
   2139              #binding_site ATP (Lys) #status predicted\
   2466              #binding_site ATP (Lys) #status predicted\
   2811              #binding_site ATP (Lys) #status predicted
SUMMARY          #length 4466  #molecular-weight 511778  #checksum 9337
SEQUENCE
```

Initial Score = 8 Optimized Score = 8 Significance = 4.59
Residue Identity = 37% Matches = 3 Mismatches = 5
Gaps = 0 Conservative Substitutions = 0

```
            X      X
            XSXTXAXX
             | | |
   YKSCGNIYKGLSQTGAWGCFDEFNRISV
      1890   X  1900      1910
```

2. US-08-121-713B-12 (1-8)
   S28916 dystrophin - mouse

```
ENTRY            S28916     #type complete
TITLE            dystrophin - mouse
ORGANISM         #formal_name Mus musculus #common_name house mouse
DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                   22-Nov-1993
ACCESSIONS       S28916
REFERENCE        S28916
   #authors      Bies, R.D.; Phelps, S.F.; Cortez, M.D.; Roberts, R.; Caskey,
                   C.T.; Chamberlain, J.S.
   #journal      Nucleic Acids Res. (1992) 20:1725-1731
   #title        Human and murine dystrophin mRNA transcripts are
                   differentially expressed during skeletal muscle, heart, and
                   brain development.
   #accession    S28916
      ##status        preliminary
      ##residues      1-3678 ##label BIE
      ##cross-references EMBL:M68859
SUMMARY          #length 3678  #molecular-weight 425815  #checksum 2460
SEQUENCE
```

```
Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   RTKQPDRAPGLSTTGASASQTVTLVTQS
      2420   X  2430      2440
```

```
3. US-08-121-713B-12 (1-8)
   S18268       delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine s

ENTRY            S18268     #type complete
TITLE            delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase -
                   Streptomyces lactamdurans
ORGANISM         #formal_name Streptomyces lactamdurans
DATE             07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
                   14-Sep-1994
ACCESSIONS       S18268; S15283
REFERENCE        S18268
   #authors      Martin, J.F.
   #submission   submitted to the EMBL Data Library, January 1991
   #accession    S18268
      ##molecule_type DNA
      ##residues      1-3649 ##label MAR
      ##cross-references EMBL:X57310
REFERENCE        S15283
   #authors      Coque, J.J.R.; Martin, J.F.; Calzada, J.G.; Liras, P.
   #journal      Mol. Microbiol. (1991) 5:1125-1133
   #title        The cephamycin biosynthetic genes pcbAB, encoding a large
                   multidomain peptide synthetase, and pcbC of Nocardia
                   lactamdurans are clustered together in an organization
                   different from the same genes in Acremonium chrysogenum and
                   Penicillium chrysogenum.
   #cross-references MUID:92065808
   #accession    S15283
      ##molecule_type DNA
      ##residues      224-940;1319-2010;2373-3307 ##label COQ
```



```
      ##cross-references EMBL:X57310
      ##note          the nucleotide sequence is not given in this paper
      ##note          the source is designated as Nocardia lactamdurans
GENETICS
   #gene         pcbAB
CLASSIFICATION   #superfamily alpha-aminoadipyl-cysteinyl-valine synthetase;
                   acetate--CoA ligase homology; gramicidin S synthetase I
                   repeat homology
KEYWORDS         cephamycin biosynthesis
FEATURE
   236-830           #domain gramicidin S synthetase I repeat homology #label
                       GRS1\
   1331-1906         #domain gramicidin S synthetase I repeat homology #label
                       GRS2\
   2385-2954         #domain gramicidin S synthetase I repeat homology #label
                       GRS3
SUMMARY          #length 3649  #molecular-weight 404084  #checksum 2296
SEQUENCE
```

```
Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   SYPDDRIAFMLSDTGAKLVLAGEAHGSR
      2490  X   2500      2510
```

```
4. US-08-121-713B-12 (1-8)
   A60979       proteoglycan 24K core protein precursor - human

ENTRY            A60979     #type complete
TITLE            proteoglycan 24K core protein precursor - human
ALTERNATE_NAMES  fibroblast-chondroitin sulfate proteoglycan core protein;
                   versican core protein
CONTAINS         glial hyaluronate binding protein
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change
                   28-Oct-1994
ACCESSIONS       S06014; A60979; A30358; A29348; A45131
REFERENCE        S06014
   #authors      Zimmermann, D.R.; Ruoslahti, E.
   #journal      EMBO J. (1989) 8:2975-2981
   #title        Multiple domains of the large fibroblast proteoglycan,
                   versican.
   #cross-references MUID:90059882
   #accession    S06014
      ##molecule_type mRNA
      ##residues      1-2409 ##label ZIM
      ##cross-references GB:X15998
REFERENCE        A60979
   #authors      Bignami, A.; Lane, W.S.; Andrews, D.; Dahl, D.
   #journal      Brain Res. Bull. (1989) 22:67-70
   #title        Structural similarity of hyaluronate binding proteins in
                   brain and cartilage.
   #accession    A60979
      ##molecule_type protein
      ##residues      289-303;171-210 ##label BIG
```

```
REFERENCE        A30358
   #authors      Perides, G.; Lane, W.S.; Andrews, D.; Dahl, D.; Bignami, A.
   #journal      J. Biol. Chem. (1989) 264:5981-5987
   #title        Isolation and partial characterization of a glial
                   hyaluronate-binding protein.
   #cross-references MUID:89174663
   #accession    A30358
      ##molecule_type protein
      ##residues      24-43;40-50;80-87,'D',89-90;80,'E',82-87,'D',89-119;
                       128-155;167-176,178-180;171-218;229-259,'IR',261-268;
                       277-283,'G',285-305;328-329,'X',331-340 ##label PER
REFERENCE        A29348
   #authors      Krusius, T.; Gehlsen, K.R.; Ruoslahti, E.
   #journal      J. Biol. Chem. (1987) 262:13120-13125
   #title        A fibroblast chondroitin sulfate proteoglycan core protein
                   contains lectin-like and growth factor-like sequences.
   #cross-references MUID:88007514
   #accession    A29348
      ##molecule_type mRNA
      ##residues      1725,'V',1727-2409 ##label KRU
      ##cross-references GB:J02814
REFERENCE        A45131
   #authors      Perides, G.; Rahemtulla, F.; Lane, W.S.; Asher, R.A.;
                   Bignami, A.
   #journal      J. Biol. Chem. (1992) 267:23883-23887
   #title        Isolation of a large aggregating proteoglycan from human
                   brain.
   #cross-references MUID:93054750
   #contents     brain
   #accession    A45131
      ##molecule_type protein
      ##residues      21-22,'X',24-37 ##label PE2
      ##cross-references NCBIP:118884
      ##note          sequence extracted from NCBI backbone
CLASSIFICATION   #superfamily EGF homology; complement factor H repeat
                   homology; C-type lectin homology
FEATURE
   1-20              #domain signal sequence #status experimental #label SIG\
   36-348            #domain link protein-like #label LNK\
   559-1654          #domain glycosaminoglycan-binding #label GAG\
   2106-2137         #domain EGF homology #label EGF1\
   2144-2175         #domain EGF homology #label EGF2\
   2182-2302         #domain C-type lectin homology #label LCH\
   2309-2365         #domain complement factor H repeat homology #label FHD
SUMMARY          #length 2409  #molecular-weight 265048  #checksum 1473
SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

            X      X
            XSXTXAXX
             | | |
   SVTSTTLIEILSDTGAEGPTVAPLPFST
 1340      1350      1360


5. US-08-121-713B-12 (1-8)
   S46082       urea carboxylase (EC 6.3.4.6) - yeast (Saccharomyc
```



```
ENTRY            S46082     #type complete
TITLE            urea carboxylase (EC 6.3.4.6) - yeast (Saccharomyces
                   cerevisiae)
ALTERNATE_NAMES  protein YBR1449; protein YBR208c; urea amidolyase
ORGANISM         #formal_name Saccharomyces cerevisiae
DATE             26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change
                   08-Dec-1994
ACCESSIONS       S46082; S46081; S46080; S31341; S34930; S34033
REFERENCE        S45734
   #authors      Rieger, M.
   #submission   submitted to the Protein Sequence Database, August 1994
   #accession    S46082
      ##molecule_type DNA
      ##residues      1-893 ##label RIE
      ##cross-references EMBL:Z36077
REFERENCE        S45927
   #authors      Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
   #submission   submitted to the Protein Sequence Database, August 1994
   #accession    S46081
      ##molecule_type DNA
      ##residues      873-1835 ##label FEL
      ##cross-references EMBL:Z36077
REFERENCE        S46054
   #authors      Bussereau, F.; Demolis, N.; Jacquet, M.; Mallet, L.
   #submission   submitted to the Protein Sequence Database, August 1994
   #accession    S46080
      ##molecule_type DNA
      ##residues      1487-1835 ##label BUS
      ##cross-references EMBL:Z36077
REFERENCE        S31341
   #authors      Genbauffe, F.S.; Cooper, T.G.
   #journal      DNA Seq. (1991) 2:19-32
   #title        The urea amidolyase (DUR1,2) gene of Saccharomyces
                   cerevisiae.
   #accession    S31341
      ##molecule_type DNA
      ##residues      1-95,'R',97-255,257-258,'N',259-458,'M',460-829,'K',
                       831-1394,'E',1396-1835 ##label GEN
      ##cross-references EMBL:M64926
REFERENCE        S34925
   #authors      Bussereau, F.; Mallet, L.; Gaillon, L.; Jacquet, M.
   #journal      Yeast (1993) 9:797-806
   #title        Yeast Sequencing Reports. A 12.8 kb segment, on the right arm
                   of chromosome II from Saccharomyces cerevisiae including
                   part of the DUR1,2 gene, contains five putative new genes.
   #accession    S34930
      ##molecule_type DNA
      ##residues      1487-1835 ##label BU2
      ##cross-references EMBL:Z21487
      ##note          translation of nucleotide sequence not given
GENETICS
   #gene         DUR1;2
   #map_position 2R
KEYWORDS         biotin; ligase; membrane protein; P-loop; purine nucleotide
                   binding
FEATURE
   122-129           #region purine nucleotide-binding motif A (P-loop)\
   163-179           #domain transmembrane #status predicted #label TM1\
   209-225           #domain transmembrane #status predicted #label TM2\
```

```
    411-427            #domain transmembrane #status predicted #label TM3\
    1141-1157          #domain transmembrane #status predicted #label TM4\
    1582-1598          #domain transmembrane #status predicted #label TM5\
    1778-1794          #domain transmembrane #status predicted #label TM6\
    128                #binding_site ATP/GTP (Lys) #status predicted\
    1798               #binding_site biotin (Lys) (covalent) #status predicted
 SUMMARY           #length 1835  #molecular-weight 201830  #checksum 7842
 SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    PVLFSNAVENLSRTGANVIEIDFEPLLE
  280       290       300


6. US-08-121-713B-12 (1-8)
   JN0896       crystalline surface layer protein precursor - Rick

 ENTRY            JN0896     #type complete
 TITLE            crystalline surface layer protein precursor - Rickettsia
                    typhi
 ORGANISM         #formal_name Rickettsia typhi
 DATE             19-May-1994 #sequence_revision 19-May-1994 #text_change
                    19-May-1994
 ACCESSIONS       JN0896; PN0686
 REFERENCE        JN0896
    #authors      Hahn, M.J.; Kim, K.K.; Kim, I.; Chang, W.H.
    #journal      Gene (1993) 133:129-133
    #title        Cloning and sequence analysis of the gene encoding the
                    crystalline surface layer protein of Rickettsia typhi.
    #accession    JN0896
       ##molecule_type DNA
       ##residues      1-1645 ##label HAH
    #accession    PN0686
       ##molecule_type protein
       ##residues      1353-1371 ##label HA2
 FEATURE
    1-32              #domain signal sequence #status predicted #label SIG\
    33-1645           #product crystalline surface layer protein #label MAT
 SUMMARY          #length 1645  #molecular-weight 169697  #checksum 9546
 SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    LSNSETADVGGSETGAVSSGDEAIDQVS
       1340   X  1350      1360


7. US-08-121-713B-12 (1-8)
   RRWGNV       RNA-directed RNA polymerase (EC 2.7.7.48) - narcis
```



```
 ENTRY            RRWGNV     #type complete
 TITLE            RNA-directed RNA polymerase (EC 2.7.7.48) - narcissus mosaic
                    virus
 ALTERNATE_NAMES  RNA nucleotidyltransferase (RNA-directed); RNA replicase
 ORGANISM         #formal_name narcissus mosaic virus
 DATE             30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
                    08-Dec-1994
 ACCESSIONS       JT0470
 REFERENCE        JT0470
    #authors      Zuidema, D.; Linthorst, H.J.M.; Huisman, M.J.; Asjes, C.J.;
                    Bol, J.F.
    #journal      J. Gen. Virol. (1989) 70:267-276
    #title        Nucleotide sequence of narcissus mosaic virus RNA.
    #cross-references MUID:89279206
    #accession    JT0470
       ##molecule_type genomic RNA
       ##residues      1-1643 ##label ZUI
       ##cross-references GB:D00405
 CLASSIFICATION   #superfamily eggplant mosaic virus RNA-directed RNA
                    polymerase
 KEYWORDS         ATP; nucleotidyltransferase; RNA replication; RNA synthesis
 FEATURE
    868-875           #region nucleotide-binding motif A (P-loop)\
    931-936           #region nucleotide-binding motif B\
    874               #binding_site ATP (Lys) #status predicted
 SUMMARY          #length 1643  #molecular-weight 186303  #checksum 8014
 SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    CPAAMNANRPLSKTKAMQMLLYCKSVKQ
       290    X  300 X     310


8. US-08-121-713B-12 (1-8)
   JH0675       restrictin precursor - chicken

 ENTRY            JH0675     #type complete
 TITLE            restrictin precursor - chicken
 ORGANISM         #formal_name Gallus gallus #common_name chicken
 DATE             09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change
                    15-Oct-1994
 ACCESSIONS       JH0675; PS0385
 REFERENCE        JH0675
    #authors      Noerenberg, U.; Wille, H.; Wolff, J.M.; Frank, R.; Rathjen,
                    F.G.
    #journal      Neuron (1992) 8:849-863
    #title        The chicken neural extracellular matrix molecule restrictin:
                    similarity with EGF-, fibronectin type III-, and
                    fibrinogen-like motifs.
    #cross-references MUID:92265298
    #contents     brain
    #accession    JH0675
       ##molecule_type mRNA
```

```
      ##residues      1-1353 ##label NOE
      ##cross-references GB:X64649
   #accession    PS0385
      ##molecule_type protein
      ##residues      579-586;827-840 ##label NOE1
COMMENT    This protein is a neural extracellular matrix protein implicated in
             neural cell attachment.
CLASSIFICATION   #superfamily restrictin; EGF homology; fibrinogen beta/gamma
                   homology; fibronectin type III repeat homology
KEYWORDS         calcium binding; cell adhesion; duplication; extracellular
                   matrix; glycoprotein; homotrimer; tandem repeat
FEATURE
   1-33              #domain signal sequence #label SIG\
   34-1353           #product restrictin #status predicted #label MAT\
   203-229           #domain EGF homology #label EG1\
   234-260           #domain EGF homology #label EG2\
   265-291           #domain EGF homology #label EG3\
   296-322           #domain EGF homology #label EG4\
   323-412           #domain fibronectin type III repeat homology #label FN1\
   413-501           #domain fibronectin type III repeat homology #label FN2\
   502-591           #domain fibronectin type III repeat homology #label FN3\
   592-683           #domain fibronectin type III repeat homology #label FN4\
   684-771           #domain fibronectin type III repeat homology #label FN5\
   772-860           #domain fibronectin type III repeat homology #label FN6\
   861-948           #domain fibronectin type III repeat homology #label FN7\
   949-1034          #domain fibronectin type III repeat homology #label FN8\
   1035-1122         #domain fibronectin type III repeat homology #label FN9\
   1130-1338         #domain fibrinogen beta/gamma homology #label FBG\
   1272-1286         #domain calcium-binding #status predicted #label CAL\
   53,197,277,391,469,
   580,734,790,960,
   1031,1041,1256,
   1342              #binding_site carbohydrate (Asn) (covalent) #status
                       predicted
SUMMARY          #length 1353  #molecular-weight 148278  #checksum 975
SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    VTASTETSISLSWTKAMGPIDHYRVTFT
         700  X    710       720


9. US-08-121-713B-12 (1-8)
   A53824        pore membrane protein POM152 - yeast (Saccharomyce

 ENTRY            A53824     #type complete
 TITLE            pore membrane protein POM152 - yeast (Saccharomyces
                    cerevisiae)
 ORGANISM         #formal_name Saccharomyces cerevisiae
 DATE             07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change
                    07-Oct-1994
 ACCESSIONS       A53824
 REFERENCE        A53824
   #authors       Wozniak, R.W.; Blobel, G.; Rout, M.P.
```



```
   #journal       J. Cell Biol. (1994) 125:31-42
   #title         POM152 is an integral protein of the pore membrane domain of
                    the yeast nuclear envelope.
   #accession     A53824
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-1337 ##label WOZ
      ##cross-references GB:Z31592
GENETICS
   #gene          POM152
KEYWORDS          glycoprotein; nucleus; repeat; transmembrane protein
SUMMARY           #length 1337  #molecular-weight 151651  #checksum 61
SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    CVGQVGLNFELSFTGAPPYYYNTKIYKL
    630       640    X  650


10. US-08-121-713B-12 (1-8)
    S26650       DNA-binding protein 5 - human

 ENTRY            S26650     #type complete
 TITLE            DNA-binding protein 5 - human
 ORGANISM         #formal_name Homo sapiens #common_name man
 DATE             25-Feb-1994; #sequence_revision 25-Feb-1994; #text_change
                    25-Feb-1994
 ACCESSIONS       S26650
 REFERENCE        S26650
   #authors       Mattioni, T.; Hume, C.R.; Konigorski, S.; Hayes, P.;
                    Osterweil, Z.; Lee, J.S.
   #journal       Chromosoma (1992) 101:618-624
   #title         A cDNA clone for a novel nuclear protein with DNA binding
                    activity.
   #accession     S26650
      ##status        preliminary
      ##residues      1-1203 ##label MAT
      ##cross-references EMBL:X63071
SUMMARY           #length 1203  #molecular-weight 131866  #checksum 8686
SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    VVPERPVTCMVSETPAMSAEPTVLASEP
       160    X  170 X     180


11. US-08-121-713B-12 (1-8)
    S31301       DNA repair protein RAD5 - yeast (Saccharomyces cer
```

```
ENTRY            S31301     #type complete
TITLE            DNA repair protein RAD5 - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES  REV2 protein
ORGANISM         #formal_name Saccharomyces cerevisiae
DATE             28-May-1993 #sequence_revision 28-May-1993 #text_change
                   02-Jun-1994
ACCESSIONS       S31301; S26983
REFERENCE        S31301
   #authors      Johnson, R.E.; Henderson, S.T.; Petes, T.D.; Prakash, S.;
                   Bankmann, M.; Prakash, L.
   #journal      Mol. Cell. Biol. (1992) 12:3807-3818
   #title        Saccharomyces cerevisiae RAD5-encoded DNA repair protein
                   contains DNA helicase and zinc-binding sequence motifs and
                   affects the stability of simple repetitive sequences in the
                   genome.
   #cross-references MUID:92375048
   #accession    S31301
      ##molecule_type DNA
      ##residues      1-1169 ##label JOH
      ##cross-references EMBL:M96644
REFERENCE        S26983
   #authors      Ahne, F.; Baur, M.; Eckardt-Schupp, F.
   #journal      Curr. Genet. (1992) 22:277-282
   #title        The REV2 gene of Saccharomyces cerevisiae: cloning and DNA
                   sequence.
   #accession    S26983
      ##molecule_type DNA
      ##residues      402-477,'R',479-634,'N',636-845,'S',847-897,'S',899-972,
                       'A',974-1062,'R' ##label AHN
      ##cross-references EMBL:S46103
GENETICS
   #gene         LISTA:RAD5; REV2
   #map_position 12
KEYWORDS         DNA repair; leucine zipper; zinc finger
SUMMARY          #length 1169  #molecular-weight 134001  #checksum 8376
SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   EFAKAASDGEASETGANMINPLWKQFKW
       460   X   470       480


12. US-08-121-713B-12 (1-8)
    A36096       Ca2+-transporting ATPase (EC 3.6.1.38) - fission y

ENTRY            A36096     #type complete
TITLE            Ca2+-transporting ATPase (EC 3.6.1.38) - fission yeast
                   (Schizosaccharomyces pombe)
ORGANISM         #formal_name Schizosaccharomyces pombe
DATE             08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change
                   30-Sep-1993
ACCESSIONS       A36096
REFERENCE        A36096
```



```
   #authors      Ghislain, M.; Goffeau, A.; Halachmi, D.; Eilam, Y.
   #journal      J. Biol. Chem. (1990) 265:18400-18407
   #title        Calcium homeostasis and transport are affected by disruption
                   of cta3, a novel gene encoding CA(2+)-ATPase in
                   Schizosaccharomyces pombe.
   #cross-references MUID:91009335
   #accession    A36096
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-1037 ##label GHI
      ##cross-references GB:J05634
KEYWORDS         hydrolase
SUMMARY          #length 1037  #molecular-weight 115326  #checksum 8079
SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   SIIPESLIAVLSITMAMGQKNMSKRRVI
        330 X     340


13. US-08-121-713B-12 (1-8)
    S04111       collagen alpha 2(VI) chain precursor - chicken

ENTRY            S04111     #type complete
TITLE            collagen alpha 2(VI) chain precursor - chicken
ORGANISM         #formal_name Gallus gallus #common_name chicken
DATE             07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
                   18-Jun-1993
ACCESSIONS       S04111
REFERENCE        S04111
   #authors      Koller, E.; Winterhalter, K.H.; Trueb, B.
   #journal      EMBO J. (1989) 8:1073-1077
   #title        The globular domains of type VI collagen are related to the
                   collagen-binding domains of cartilage matrix protein and
                   von Willebrand factor.
   #cross-references MUID:89305506
   #accession    S04111
      ##molecule_type mRNA
      ##residues      1-1022 ##label KOL
      ##cross-references EMBL:X15041
      ##note          it is uncertain whether Met-1 or Met-8 is the initiator
FEATURE
   1-27             #domain signal sequence #status predicted #label SIG\
   28-1022          #product collagen alpha 2(VI) chain #status predicted
                      #label MAT
SUMMARY          #length 1022  #molecular-weight 109176  #checksum 3489
SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
```

```
              | | |
    SRLGSIAKDPKSETGARVGVVQYSHEGT
         650  X    660       670


14. US-08-121-713B-12 (1-8)
    S23378       collagen alpha 2(VI) chain long form precursor - c

 ENTRY            S23378     #type complete
 TITLE            collagen alpha 2(VI) chain long form precursor - chicken
 ORGANISM         #formal_name Gallus gallus #common_name chicken
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S23378
 REFERENCE        S23377
    #authors      Hayman, A.R.; Koppel, J.; Trueb, B.
    #submission   submitted to the EMBL Data Library, November 1990
    #description  Complete structure of the chicken alpha2(VI) collagen gene.
    #accession    S23378
       ##status        preliminary
       ##residues      1-1022 ##label HAY
       ##cross-references EMBL:X56659
 SUMMARY          #length 1022  #molecular-weight 109176  #checksum 3489
 SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    SRLGSIAKDPKSETGARVGVVQYSHEGT
         650  X    660       670


15. US-08-121-713B-12 (1-8)
    GNLJND       pol polyprotein - human immunodeficiency virus typ

 ENTRY            GNLJND     #type complete
 TITLE            pol polyprotein - human immunodeficiency virus type 1
                    (isolate NDK)
 CONTAINS         endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16);
                    RNA-directed DNA polymerase (EC 2.7.7.49)
 ORGANISM         #formal_name human immunodeficiency virus type 1, HIV-1
    #note         host Homo sapiens (man)
 DATE             30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
                    08-Dec-1994
 ACCESSIONS       JQ0067
 REFERENCE        JQ0065
    #authors      Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.;
                    Galibert, F.; Hampe, A.; Chermann, J.C.
    #journal      Gene (1989) 81:275-284
    #title        Nucleotide sequence of HIV1-NDK: a highly cytopathic strain
                    of the human immunodeficiency virus.
    #cross-references MUID:90034200
    #accession    JQ0067
       ##molecule_type DNA
       ##residues      1-1002 ##label SPI
       ##cross-references GB:M27323
```



```
 COMMENT     Specific enzymatic cleavages may yield mature proteins including
               protease, reverse transcriptase, and endonuclease. However, exact
               cleavage sites are undetermined.
 GENETICS
    #gene          pol
 CLASSIFICATION  #superfamily pol polyprotein
 KEYWORDS        acquired immune deficiency syndrome; aspartic proteinase;
                   endonuclease; nucleotidyltransferase; polyprotein; reverse
                   transcriptase

 FEATURE
    56-154            #product retropepsin #status predicted #label RTP\
    80                #active_site Asp (shared with dimeric partner) #status
                        predicted
 SUMMARY         #length 1002  #molecular-weight 113621  #checksum 9917
 SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  4.59
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    ELRVWGGDNPLSETGAERQGTVSFSFPQ
   30        40       X 50
> o <
o|  |o  IntelliGenetics
> o <

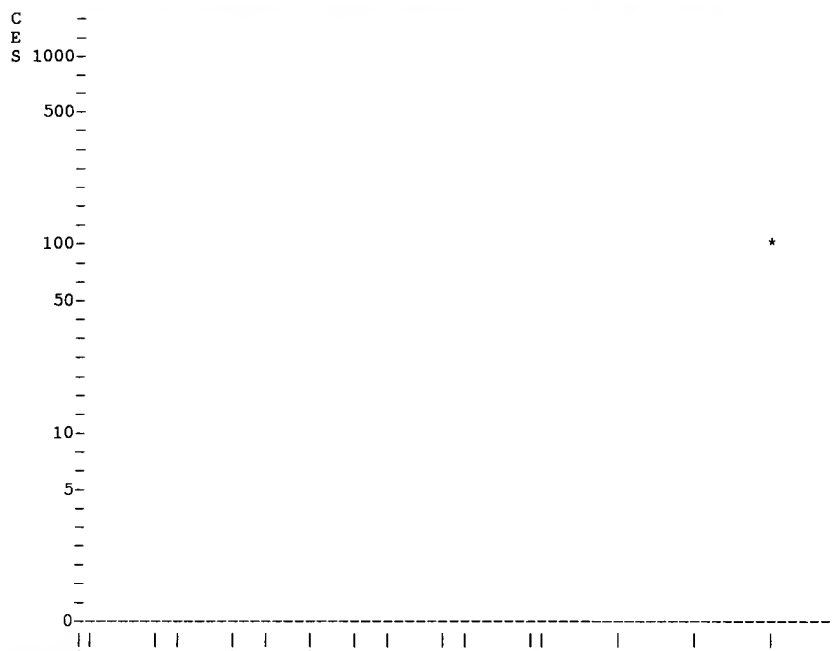
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sql2spt.res made by  on Fri 19 May 95 8:56:51-PDT.


Query sequence being compared:US-08-121-713B-12 (1-8)
Number of sequences searched:                43470
Number of scores above cutoff:                3809

     Results of the initial comparison of US-08-121-713B-12 (1-8) with:
   Data bank : Swiss-Prot 31, all entries

100000-
      -
N     -
U50000-
M     -                        *
B     -
E     -
R     -
      -
O     -
F10000-
      -                                    *
S     -
E 5000-
Q     -
U     *
E     -
N     -
```



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	3	4	1.13

Times:	CPU	Total Elapsed
	00:00:44.04	00:00:44.00

Number of residues: 15335248
Number of sequences searched: 43470

Number of scores above cutoff: 3809

Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.
Cut-off raised to 6.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

90 100% similar sequences to the query sequence were found:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1.	DYHC_TRIGR	DYNEIN BETA CHAIN, CILIARY.	4466	8	8	4.42	0
2.	ACVS_NOCLA	L-(ALPHA-AMINOADIPYL)-L-CYSTE	3649	8	8	4.42	0
3.	PGCS_HUMAN	LARGE FIBROBLAST PROTEOGLYCAN	2409	8	8	4.42	0
4.	DUR1_YEAST	UREA AMIDOLYASE (CONTAINS: UR	1835	8	8	4.42	0
5.	RRPO_NMV	RNA REPLICATION PROTEIN (CONT	1643	8	8	4.42	0
6.	SON_HUMAN	SON PROTEIN (SON3).	1523	8	8	4.42	0
7.	CDP_HUMAN	CCAAT DISPLACEMENT PROTEIN (C	1505	8	8	4.42	0
8.	P152_YEAST	NUCLEAR ENVELOPE PORE MEMBRAN	1337	8	8	4.42	0
9.	RAD5_YEAST	DNA REPAIR PROTEIN RAD5.	1169	8	8	4.42	0
10.	ATC3_SCHPO	CALCIUM-TRANSPORTING ATPASE 3	1037	8	8	4.42	0
11.	CA26_CHICK	COLLAGEN ALPHA 2(VI) CHAIN PR	1022	8	8	4.42	0
12.	POL_HV1EL	POL POLYPROTEIN (PROTEASE (EC	1002	8	8	4.42	0
13.	POL_HV1MA	POL POLYPROTEIN (PROTEASE (EC	1002	8	8	4.42	0
14.	POL_HV1ND	POL POLYPROTEIN (PROTEASE (EC	1002	8	8	4.42	0
15.	POL_HV1Z2	POL POLYPROTEIN (PROTEASE (EC	1002	8	8	4.42	0
16.	CDP_CANFA	CCAAT DISPLACEMENT PROTEIN (H	975	8	8	4.42	0
17.	ADHE_ECOLI	ALCOHOL DEHYDROGENASE (EC 1.1	890	8	8	4.42	0
18.	A20_HUMAN	PUTATIVE DNA BINDING PROTEIN	790	8	8	4.42	0
19.	CAS1_ARATH	CYCLOARTENOL SYNTHASE (EC 5.4	759	8	8	4.42	0
20.	UVRB_ECOLI	EXCINUCLEASE ABC SUBUNIT B.	673	8	8	4.42	0
21.	UL49_EBV	HYPOTHETICAL BFRF2 PROTEIN.	591	8	8	4.42	0
22.	GCL1_DROME	GERM CELL-LESS PROTEIN.	569	8	8	4.42	0
23.	DCP1_KLUMA	PYRUVATE DECARBOXYLASE ISOZYM	564	8	8	4.42	0
24.	DCPY_HANUV	PYRUVATE DECARBOXYLASE (EC 4.	564	8	8	4.42	0
25.	DCP2_YEAST	PYRUVATE DECARBOXYLASE ISOZYM	563	8	8	4.42	0
26.	DCP1_YEAST	PYRUVATE DECARBOXYLASE ISOZYM	562	8	8	4.42	0
27.	GTR7_RAT	GLUCOSE TRANSPORTER TYPE 7, H	528	8	8	4.42	0
28.	GTR2_MOUSE	GLUCOSE TRANSPORTER TYPE 2, L	523	8	8	4.42	0
29.	GTR2_RAT	GLUCOSE TRANSPORTER TYPE 2, L	522	8	8	4.42	0
30.	DLDH_TRYBB	DIHYDROLIPOAMIDE DEHYDROGENAS	479	8	8	4.42	0
31.	TBA_NAEGR	TUBULIN ALPHA CHAIN.	453	8	8	4.42	0
32.	TBA_PLAFK	TUBULIN ALPHA CHAIN.	453	8	8	4.42	0
33.	TBA_TOXGO	TUBULIN ALPHA CHAIN.	453	8	8	4.42	0
34.	TBA1_PARLI	TUBULIN ALPHA-1 CHAIN.	452	8	8	4.42	0
35.	TBA2_MOUSE	TUBULIN ALPHA-2 CHAIN.	451	8	8	4.42	0
36.	TBA1_VOLCA	TUBULIN ALPHA-1 CHAIN.	451	8	8	4.42	0
37.	TBA1_ANEPH	TUBULIN ALPHA-1 CHAIN.	451	8	8	4.42	0
38.	TBA1_CHLRE	TUBULIN ALPHA-1 CHAIN.	451	8	8	4.42	0
39.	TBA1_CRIGR	TUBULIN ALPHA-1 CHAIN.	451	8	8	4.42	0
40.	TBA1_HUMAN	TUBULIN ALPHA-1 CHAIN.	451	8	8	4.42	0
41.	TBA1_MAIZE	TUBULIN ALPHA-1 CHAIN.	451	8	8	4.42	0
42.	TBA_TRYBR	TUBULIN ALPHA CHAIN.	451	8	8	4.42	0
43.	TBA_TORMA	TUBULIN ALPHA CHAIN.	451	8	8	4.42	0
44.	TBA_PIG	TUBULIN ALPHA CHAIN.	451	8	8	4.42	0

45. TBA_EUGGR TUBULIN ALPHA CHAIN. 451 8 8 4.42 0

1. US-08-121-713B-12 (1-8)
DYHC_TRIGR DYNEIN BETA CHAIN, CILIARY.

```
ID   DYHC_TRIGR     STANDARD;      PRT;  4466 AA.
AC   P23098;
DT   01-NOV-1991 (REL. 20, CREATED)
DT   01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   DYNEIN BETA CHAIN, CILIARY.
OS   TRIPNEUSTES GRATILLA (HAWAIAN SEA URCHIN).
OC   EUKARYOTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA;
OC   EUECHINOIDEA.
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=BLASTULA EMBRYO;
RM   91326103
RA   GIBBONS I.R., GIBBONS B.H., MOCZ G., ASAI D.J.;
RL   NATURE 352:640-643(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RM   92020893
RA   GIBBONS I.R., ASAI D.J., CHING N.S., DOLECKI G.J., MOCZ G.,
RA   PHILLIPSON C.A., REN H., TANG W.Y., GIBBONS B.H.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 88:8563-8567(1991).
CC   -!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
CC       FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
CC       DYNEIN HAS ATPASE ACTIVITY.
CC   -!- SUBUNIT: CONSIST OF AT LEAST TWO HEAVY CHAINS (ALPHA AND BETA),
CC       THREE INTERMEDIATE CHAINS AND SEVERAL LIGHT CHAINS.
CC   -!- SIMILARITY: TO OTHER DYNEIN HEAVY CHAINS.
DR   EMBL; X59603; TGDYH2.
DR   PIR; S17653; S17653.
KW   MOTOR PROTEIN; MICROTUBULES; DYNEIN; ATP-BINDING; FLAGELLA;
KW   HEPTAD REPEAT PATTERN.
FT   NP_BIND     154    161       ATP (POTENTIAL).
FT   NP_BIND    1852   1859       ATP (POTENTIAL).
FT   NP_BIND    2133   2140       ATP (POTENTIAL).
FT   NP_BIND    2460   2467       ATP (POTENTIAL).
FT   NP_BIND    2805   2812       ATP (POTENTIAL).
FT   VARIANT     611    615       MISSING.
FT   VARIANT    3356   3358       LPG -> LLTGNFFCCFMTAG.
SQ   SEQUENCE   4466 AA;  511771 MW;  20102986 CN;
```

Initial Score = 8 Optimized Score = 8 Significance = 4.42
Residue Identity = 37% Matches = 3 Mismatches = 5
Gaps = 0 Conservative Substitutions = 0

```
            X      X
            XSXTXAXX
              | | |
   YKSCGNIYKGLSQTGAWGCFDEFNRISV
      1890   X  1900      1910
```

2. US-08-121-713B-12 (1-8)
ACVS_NOCLA L-(ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE SYNTHET


```
ID   ACVS_NOCLA     STANDARD;      PRT;  3649 AA.
AC   P27743;
DT   01-AUG-1992 (REL. 23, CREATED)
DT   01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   L-(ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE SYNTHETASE (EC 6.-.-.-)
DE   (ACV SYNTHETASE) (ACVS).
GN   PCBAB.
OS   NOCARDIA LACTAMDURANS.
OC   PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; NOCARDIOFORM.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VAR LC 411;
RM   92065808
RA   COQUE J.J.R., MARTIN J.F., CALZADA J.G., LIRAS P.;
RL   MOL. MICROBIOL. 5:1125-1133(1991).
CC   -!- FUNCTION: EACH OF THE CONSTITUENT AMINO ACIDS OF ACV ARE ACTIVATED
CC       AS AMIONACYL-ADENYLATES WITH PEPTIDE BONDS FORMED THROUGH THE
CC       PARTICIPATION OF AMINO ACID THIOLESTER INTERMEDIATES.
CC   -!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF PENICILLIN AND
CC       CEPHALOSPORIN.
CC   -!- COFACTOR: CONTAINS THREE COVALENTLY BOUND PHOSPHOPANTETHEINES.
CC   -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
CC       COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
DR   EMBL; X57310; NLPCBABC.
DR   PIR; S18268; S18268.
DR   PROSITE; PS00455; AMP_BINDING.
KW   LIGASE; ANTIBIOTIC BIOSYNTHESIS; MULTIFUNCTIONAL ENZYME;
KW   REPEAT; PHOSPHOPANTETHEINE.
FT   REPEAT      401    861       DOMAIN 1.
FT   REPEAT     1014   1937       DOMAIN 2.
FT   REPEAT     2079   2985       DOMAIN 3.
FT   BINDING     820    820       PHOSPHOPANTETHEINE (BY SIMILARITY).
FT   BINDING    1896   1896       PHOSPHOPANTETHEINE (BY SIMILARITY).
FT   BINDING    2944   2944       PHOSPHOPANTETHEINE (BY SIMILARITY).
SQ   SEQUENCE   3649 AA;  404079 MW;  20196076 CN;
```

Initial Score = 8 Optimized Score = 8 Significance = 4.42
Residue Identity = 37% Matches = 3 Mismatches = 5
Gaps = 0 Conservative Substitutions = 0

```
            X      X
            XSXTXAXX
              | | |
   SYPDDRIAFMLSDTGAKLVLAGEAHGSR
      2490  X   2500      2510
```

3. US-08-121-713B-12 (1-8)
PGCS_HUMAN LARGE FIBROBLAST PROTEOGLYCAN PRECURSOR (VERSICAN)

```
ID   PGCS_HUMAN     STANDARD;      PRT;  2409 AA.
AC   P13611;
DT   01-JAN-1990 (REL. 13, CREATED)
DT   01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT   01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE   LARGE FIBROBLAST PROTEOGLYCAN PRECURSOR (VERSICAN) (CHONDROITIN
DE   SULFATE PROTEOGLYCAN CORE PROTEIN 2).
GN   CSPG2.
OS   HOMO SAPIENS (HUMAN).
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OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RM   90059882
RA   ZIMMERMANN D.R., RUOSLAHTI E.;
RL   EMBO J. 8:2975-2981(1989).
RN   [2]
RP   SEQUENCE OF 1722-2409 FROM N.A.
RC   TISSUE=LUNG FIBROBLAST;
RM   88007514
RA   KRUSIUS T., GEHLSEN K.R., RUOSLAHTI E.;
RL   J. BIOL. CHEM. 262:13120-13125(1987).
CC   -!- FUNCTION: MAY PLAY A ROLE IN INTERCELLULAR SIGNALING.
CC   -!- SIMILARITY: IN THE N-TERMINAL PART THIS PROTEIN IS SIMILAR TO
CC       A GLIAL HYALURONATE-BINDING PROTEIN. IN THE MIDDLE OF THE PROTEIN
CC       THERE ARE GLUCOSAMINOGLUCAN ATTACHMENT SITES. THE C-TERMINAL PART
CC       CONTAINS EPIDERMAL GROWTH FACTOR (EGF)-LIKE REPEATS AND A LECTIN-
CC       LIKE DOMAIN. VERSICAN CONTAINS A DOMAIN STRONGLY HOMOLOGOUS WITH
CC       THE C-TERMINAL CORE PROTEIN DOMAIN OF THE RAT AND CHICKEN LARGE
CC       AGGREGATING CARTILAGE PROTEOGLYCAN. IT ALSO CONTAINS SEQUENCES
CC       HOMOLOGOUS WITH CHICKEN AND MAMMALIAN HEPATIC AND LUNG LECTINS.
CC   -!- SIMILARITY: CONTAINS 2 EGF-LIKE REPEATS.
CC   -!- SIMILARITY: CONTAINS A C-TYPE LECTIN FAMILY DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 SUSHI (SCR) REPEAT.
DR   EMBL; J02814; HSPGC.
DR   PIR; S06014; S06014.
DR   PIR; A29348; A29348.
DR   HSSP; P01132; 1EGF.
DR   MIM; 118661; 11TH EDITION.
DR   PROSITE; PS00022; EGF.
DR   PROSITE; PS00615; C_TYPE_LECTIN.
KW   GLYCOPROTEIN; PROTEOGLYCAN; LECTIN; EXTRACELLULAR MATRIX; SUSHI;
KW   SIGNAL; REPEAT; EGF-LIKE DOMAIN.
FT   SIGNAL        1     20       PROBABLE.
FT   CHAIN        21   2409       VERSICAN.
FT   DOMAIN       36    348       SIMILAR TO HYALURONIC ACID-BINDING
FT                                PROTEINS, LINK-PROTEIN LIKE DOMAIN.
FT   DOMAIN      559   1654       GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN,
FT                                SIMILAR TO CHONDROITIN SULFATE ATTACHMENT
FT                                SITE IN COLLAGEN TYPE IX.
FT   DOMAIN     2103   2178       2 X EGF-LIKE REPEATS.
FT   DOMAIN     2179   2305       C-TYPE LECTIN.
FT   REPEAT     2308   2366       SUSHI.
FT   DISULFID   2309   2352       BY SIMILARITY.
FT   DISULFID   2338   2365       BY SIMILARITY.
FT   CARBOHYD     57     57       POTENTIAL.
FT   CARBOHYD    330    330       POTENTIAL.
FT   CARBOHYD    411    411       POTENTIAL.
FT   CARBOHYD    455    455       POTENTIAL.
FT   CARBOHYD    481    481       POTENTIAL.
FT   CARBOHYD    676    676       POTENTIAL.
FT   CARBOHYD    911    911       POTENTIAL.
FT   CARBOHYD   1192   1192       POTENTIAL.
FT   CARBOHYD   1285   1285       POTENTIAL.
FT   CARBOHYD   1293   1293       POTENTIAL.
FT   CARBOHYD   1373   1373       POTENTIAL.
FT   CARBOHYD   1398   1398       POTENTIAL.
FT   CARBOHYD   1405   1405       POTENTIAL.
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FT   CARBOHYD   1509   1509       POTENTIAL.
FT   CARBOHYD   1641   1641       POTENTIAL.
FT   CARBOHYD   1947   1947       POTENTIAL.
FT   CARBOHYD   2080   2080       POTENTIAL.
FT   CARBOHYD   2382   2382       POTENTIAL.
FT   CARBOHYD   2392   2392       POTENTIAL.
FT   CONFLICT   1722   1726       IKAEA -> EFREV (IN REF. 2).
SQ   SEQUENCE   2409 AA;  265048 MW;  21910895 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    SVTSTTLIEILSDTGAEGPTVAPLPFST
  1340      1350      1360


4. US-08-121-713B-12 (1-8)
   DUR1_YEAST   UREA AMIDOLYASE (CONTAINS: UREA CARBOXYLASE (EC 6.

ID   DUR1_YEAST     STANDARD;      PRT;  1835 AA.
AC   P32528;
DT   01-OCT-1993 (REL. 27, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   UREA AMIDOLYASE (CONTAINS: UREA CARBOXYLASE (EC 6.3.4.6) /
DE   ALLOPHANATE HYDROLASE (EC 3.5.1.54)).
GN   DUR1,2 OR YBR208C OR YBR1448.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92199240
RA   GENBAUFFE F.S., COOPER T.G.;
RL   DNA SEQ. 2:19-32(1991).
RN   [2]
RP   SEQUENCE OF 1-893 FROM N.A.
RC   STRAIN=S288C;
RA   RIEGER M.;
RL   SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [3]
RP   SEQUENCE OF 873-1835 FROM N.A.
RC   STRAIN=S288C;
RA   FELDMANN H., MANNHAUPT G., SCHWARZLOSE C., VETTER I.;
RL   SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [4]
RP   SEQUENCE OF 1487-1835 FROM N.A.
RC   STRAIN=S288C;
RM   93377417
RA   BUSSEREAU F., MALLET L., GAILLON L., JACQUET M.;
RL   YEAST 9:797-806(1993).
CC   -!- FUNCTION:HYDROLYSIS OF UREA TO AMMONIA AND CO2.
CC   -!- CATALYTIC ACTIVITY: ATP + UREA + CO(2) = ADP + ORTHOPHOSPHATE +
CC       UREA-1-CARBOXYLATE.
CC   -!- CATALYTIC ACTIVITY: UREA-1-CARBOXYLATE + H(2)O = 2 CO(2) +
CC       2 NH(3).
CC   -!- PATHWAY: ALLANTOIN AND ARGININE METABOLISM.
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CC   -!- SUBUNIT: MONOMER.
CC   -!- COFACTOR: BIOTIN.
CC   -!- INDUCTION: BY ALLOPHANATE OR ITS NON-METABOLIZED ANALOGUE
CC       OXALURATE. REPRESSED IN THE PRESENCE OF READILY USED NITROGEN
CC       SOURCES.
DR   EMBL; M64926; SCUAMD.
DR   EMBL; Z36077; SCYBR208C.
DR   EMBL; Z21487; SCCHRIIFG.
DR   PIR; S46082; S46082.
DR   PROSITE; PS00188; BIOTIN.
DR   PROSITE; PS00866; CPSASE_1.
DR   PROSITE; PS00867; CPSASE_2.
KW   LIGASE; HYDROLASE; MULTIFUNCTIONAL ENZYME; ARGININE METABOLISM;
KW   BIOTIN; ATP-BINDING.
FT   NP_BIND     122    129       ATP (POTENTIAL).
FT   BINDING    1798   1798       BIOTIN.
FT   SIMILAR    1779   1835       TO OTHER BIOTIN CARBOXYLASES C-TERMINI.
FT   CONFLICT     96     96       P -> R (IN REF. 1).
FT   CONFLICT    256    258       LKK -> KKN (IN REF. 1).
FT   CONFLICT    459    459       I -> M (IN REF. 1).
FT   CONFLICT    830    830       E -> K (IN REF. 1).
FT   CONFLICT   1395   1395       D -> E (IN REF. 1).
SQ   SEQUENCE   1835 AA;  201831 MW;  16646414 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =     37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions                =     0

             X      X
             XSXTXAXX
              | | |
   PVLFSNAVENLSRTGANVIEIDFEPLLE
 280       290       300
```

5. US-08-121-713B-12 (1-8)
   RRPO_NMV RNA REPLICATION PROTEIN (CONTAINS: RNA-DIRECTED RN

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ID   RRPO_NMV       STANDARD;      PRT;  1643 AA.
AC   P15095;
DT   01-APR-1990 (REL. 14, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   RNA REPLICATION PROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE
DE   (EC 2.7.7.48) / PROBABLE HELICASE) (186 KD PROTEIN) (ORF 1).
OS   NARCISSUS MOSAIC VIRUS (NMV).
OC   VIRIDAE; SS-RNA NONENVELOPED VIRUSES; POTEXVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   89279206
RA   ZUIDEMA D., LINTHORST H.J.M., HUISMAN M.J., ASJES C.J., BOL J.F.;
RL   J. GEN. VIROL. 70:267-276(1989).
CC   -!- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
CC       POSSIBLY FUNCTIONS AS A ATP-BINDING HELICASE.
DR   EMBL; D13747; MNCCGAA.
DR   EMBL; D00405; NMV.
DR   PIR; JT0470; RRWGNV.
KW   ATP-BINDING; HELICASE; RNA REPLICATION; RNA-DIRECTED RNA POLYMERASE.
FT   NP_BIND     868    875       ATP (POTENTIAL).
SQ   SEQUENCE   1643 AA;  186304 MW;  13928612 CN;
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Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =     37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions                =     0

             X      X
             XSXTXAXX
              | | |
   CPAAMNANRPLSKTKAMQMLLYCKSVKQ
     290     X  300 X      310
```

6. US-08-121-713B-12 (1-8)
   SON_HUMAN SON PROTEIN (SON3).

```
ID   SON_HUMAN      STANDARD;      PRT;  1523 AA.
AC   P18583;
DT   01-NOV-1990 (REL. 16, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   SON PROTEIN (SON3).
GN   SON.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92049296
RA   CHUMAKOV I.M., BERDICHEVSKII F.B., SOKOLOV N.V., REZNIKOV M.V.,
RA   PRASOLOV V.S.;
RL   MOL. BIOL. (MOSK) 25:731-740(1991).
RN   [2]
RP   SEQUENCE OF 686-1168 FROM N.A.
RA   BERDICHEVSKII F.B., CHUMAKOV I.M., KISELEV L.L.;
RL   MOL. BIOL. (MOSK) 22:639-646(1988).
RN   [3]
RP   ALTERNATIVE SPLICING.
RC   TISSUE=PLACENTA;
RA   BLISKOVSKII V.V., KIRILLOV A.A., ZACHAR'EV V.M., CHUMAKOV I.M.;
RL   MOL. BIOL. (MOSK) 26:547-549(1992).
CC   -!- DOMAIN: THE REPEAT REGION CONTAINS FIVE TYPES OF SEQUENCES LARGELY
CC       HOMOLOGOUS WITH ONE ANOTHER.
DR   EMBL; X63753; HSSONA.
DR   EMBL; M36428; HSSON3A.
DR   PIR; PN0099; PN0099.
DR   MIM; 182465; 11TH EDITION.
KW   REPEAT; DNA-BINDING; ALTERNATIVE SPLICING.
FT   DOMAIN      854   1042       REGION OF REPEATS.
FT   DOMAIN      854    878       2 X APPROXIMATE TANDEM REPEATS, TYPE E.
FT   DOMAIN      880    905       2 X APPROXIMATE TANDEM REPEATS, TYPE D.
FT   REPEAT      917    923       TYPE A REPEAT.
FT   REPEAT      926    944       TYPE B REPEAT.
FT   DOMAIN      945    986       6 X TANDEM REPEATS, TYPE A.
FT   REPEAT      987   1005       TYPE B REPEAT.
FT   DOMAIN     1006   1032       3 X TANDEM REPEATS, TYPE C.
FT   REPEAT     1033   1046       TYPE D REPEAT.
FT   SIMILAR     689    782       TO C-MYC (AA 242-319).
FT   SIMILAR     932    995       TO GALLIN (AA 2-64).
FT   SIMILAR    1046   1105       TO C-MOS (AA 155-213).
FT   CONFLICT    686    686       A -> R (IN REF. 2).
```

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FT   CONFLICT   1083   1083       V -> E (IN REF. 2).
FT   CONFLICT   1141   1141       F -> P (IN REF. 2).
SQ   SEQUENCE   1523 AA;  168281 MW;  12056646 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    VVPERPVTCMVSETPAMSAEPTVLASEP
     270       280   X   290
```

7. US-08-121-713B-12 (1-8)
   CDP_HUMAN CCAAT DISPLACEMENT PROTEIN (CDP).

```
ID   CDP_HUMAN      STANDARD;      PRT;  1505 AA.
AC   P39880;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   CCAAT DISPLACEMENT PROTEIN (CDP).
GN   CUTL1.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=UMBILICAL VEIN;
RA   NEUFELD E.J., SKALNIK D.G., LIEVENS P.M.J., ORKIN S.H.;
RL   NATURE GENET. 1:50-55(1992).
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC   -!- SIMILARITY: TO DROSOPHILA HOMEOBOX PROTEIN CUT.
DR   EMBL; M74099; HSCDP.
DR   MIM; 116896; 11TH EDITION.
KW   HOMEOBOX; DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN;
KW   REPEAT.
FT   DNA_BIND   1244   1303       HOMEOBOX.
SQ   SEQUENCE   1505 AA;  164353 MW;  11395795 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    AESPYSQSSELSLTGASRSETPQNSPLP
       890    X  900 X     910
```

8. US-08-121-713B-12 (1-8)
   P152_YEAST NUCLEAR ENVELOPE PORE MEMBRANE PORTEIN POM152 (P15

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ID   P152_YEAST     STANDARD;      PRT;  1337 AA.
AC   P39685;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
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DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   NUCLEAR ENVELOPE PORE MEMBRANE PORTEIN POM152 (P150).
GN   POM152.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=W303;
RM   94186543
RA   WOZNIAK R.W., BLOBEL G., ROUT M.P.;
RL   J. CELL BIOL. 125:31-42(1994).
CC   -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. NUCLEAR PORE
CC       MEMBRANE.
CC   -!- PTM: THE N-TERMINAL IS BLOCKED.
DR   EMBL; Z31592; SCPOM152.
DR   PIR; A53824; A53824.
DR   LISTA; SC00844; POM152.
KW   NUCLEAR PROTEIN; TRANSMEMBRANE; REPEAT; GLYCOPROTEIN.
FT   DOMAIN        1    175       PORE SIDE (POTENTIAL).
FT   TRANSMEM    176    195       POTENTIAL.
FT   DOMAIN      196   1337       CISTERNAL SIDE (POTENTIAL).
FT   CARBOHYD    280    280
FT   DOMAIN      390   1276       8 X 24 AA APPROXIMATE REPEATS.
FT   REPEAT      390    413       1.
FT   REPEAT      626    650       2.
FT   REPEAT      732    755       3.
FT   REPEAT      836    859       4.
FT   REPEAT      943    966       5.
FT   REPEAT     1058   1077       6.
FT   REPEAT     1157   1178       7.
FT   REPEAT     1253   1276       8.
SQ   SEQUENCE   1337 AA;  151651 MW;  9840385 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
    CVGQVGLNFELSFTGAPPYYYNTKIYKL
    630       640    X  650
```

9. US-08-121-713B-12 (1-8)
   RAD5_YEAST DNA REPAIR PROTEIN RAD5.

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ID   RAD5_YEAST     STANDARD;      PRT;  1169 AA.
AC   P32849;
DT   01-OCT-1993 (REL. 27, CREATED)
DT   01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT   01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE   DNA REPAIR PROTEIN RAD5.
GN   RAD5 OR REV2 OR SNM2.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92375048
RA   JOHNSON R.E., HENDERSON S.T., PETES T.D., PRAKASH S., BANKMANN M.,
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RA   PRAKASH L.;
RL   MOL. CELL. BIOL. 12:3807-3818(1992).
RN   [2]
RP   SEQUENCE OF 402-1063 FROM N.A.
RM   93008350
RA   AHNE F., BAUR M., ECKARDT-SCHUPP F.;
RL   CURR. GENET. 22:277-282(1992).
CC   -!- FUNCTION: PROBABLE HELICASE, FUNCTIONS WITH DNA REPAIR PROTEIN
CC       RAD18 IN ERROR-FREE POSTREPLICATION DNA REPAIR. INVOLVED IN THE
CC       MAINTENANCE OF WILD-TYPE RATES OF INSTABILITY OF SIMPLE
CC       REPETITIVE SEQUENCES SUCH AS POLY(GT) REPEATS.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC   -!- SIMILARITY: TO HELICASES OF THE SNF2/RAD54 FAMILY.
DR   EMBL; M96644; SCRAD5A.
DR   EMBL; S43248; S43248.
DR   EMBL; S46103; S46103.
DR   PIR; S31301; S31301.
DR   PIR; S26983; S26983.
DR   LISTA; SC00924; RAD5.
DR   PROSITE; PS00518; ZINC_FINGER_C3HC4.
KW   DNA DAMAGE; DNA REPAIR; NUCLEAR PROTEIN; ZINC-FINGER; DNA-BINDING;
KW   HELICASE; ATP-BINDING.
FT   DOMAIN       42     60       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      303    315       ARG/LYS-RICH (BASIC).
FT   NP_BIND     532    539       ATP (POTENTIAL).
FT   SITE        681    684       DEGH BOX.
FT   ZN_FING     914    960       C3HC4-TYPE.
FT   CONFLICT    478    478       Q -> R (IN REF. 2).
FT   CONFLICT    635    635       T -> N (IN REF. 2).
FT   CONFLICT    846    846       G -> S (IN REF. 2).
FT   CONFLICT    898    898       R -> S (IN REF. 2).
FT   CONFLICT    973    973       V -> A (IN REF. 2).
FT   CONFLICT   1063   1063       A -> R (IN REF. 2).
SQ   SEQUENCE   1169 AA;  134001 MW;  7092987 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   EFAKAASDGEASETGANMINPLWKQFKW
       460   X   470       480


10. US-08-121-713B-12 (1-8)
    ATC3_SCHPO   CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38).

ID   ATC3_SCHPO     STANDARD;      PRT;  1037 AA.
AC   P22189;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE   CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38).
GN   CTA3.
OS   SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
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RP   SEQUENCE FROM N.A.
RM   91009335
RA   GHISLAIN M., GOFFEAU A., HALACHMI D., EILAM Y.;
RL   J. BIOL. CHEM. 265:18400-18407(1990).
CC   -!- FUNCTION: THIS MAGNESIUM DEPENDENT ENZYME CATALYZES THE
CC       HYDROLYSIS OF ATP COUPLED WITH THE TRANSPORT OF THE CALCIUM.
CC   -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
CC       (E1-E2 ATPASES).
DR   EMBL; J05634; SPCA2AT.
DR   PIR; A36096; A36096.
DR   PROSITE; PS00154; ATPASE_E1_E2.
KW   HYDROLASE; CALCIUM TRANSPORT; TRANSMEMBRANE; PHOSPHORYLATION;
KW   MAGNESIUM; ATP-BINDING.
FT   MOD_RES     368    368       PHOSPHORYLATION (BY SIMILARITY).
SQ   SEQUENCE   1037 AA;  115327 MW;  5734435 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   SIIPESLIAVLSITMAMGQKNMSKRRVI
        330 X     340


11. US-08-121-713B-12 (1-8)
    CA26_CHICK   COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.

ID   CA26_CHICK     STANDARD;      PRT;  1022 AA.
AC   P15008;
DT   01-APR-1990 (REL. 14, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE   COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.
OS   GALLUS GALLUS (CHICKEN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC   GALLIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   89305506
RA   KOLLER E., WINTERHALTER K.H., TRUEB B.;
RL   EMBO J. 8:1073-1077(1989).
RN   [2]
RP   SEQUENCE OF 8-38 FROM N.A.
RC   TISSUE=LIVER;
RM   91187664
RA   KOLLER E., HAYMAN A.R., TRUEB B.;
RL   NUCLEIC ACIDS RES. 19:485-491(1991).
CC   -!- FUNCTION: COLLAGEN VI ACTS AS A CELL-BINDING PROTEIN.
CC   -!- SUBUNIT: TRIMERS COMPOSED OF THREE DIFFERENT CHAINS: ALPHA 1(VI),
CC       ALPHA 2(VI), AND ALPHA 3(VI).
CC   -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC       UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
DR   EMBL; X15041; GDCOL6A2.
DR   EMBL; X56595; GGCOLVIA.
DR   PIR; S04111; S04111.
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DR   PIR; S23378; S23378.
DR   HSSP; P19999; 1CLG.
KW   EXTRACELLULAR MATRIX; CONNECTIVE TISSUE; REPEAT; HYDROXYLATION;
KW   GLYCOPROTEIN; CELL ADHESION; COLLAGEN; SIGNAL.
FT   SIGNAL        1     27
FT   CHAIN        28   1022       COLLAGEN ALPHA 2(VI) CHAIN.
FT   DOMAIN       28    255       NONHELICAL REGION.
FT   DOMAIN      256    590       TRIPLE-HELICAL REGION.
FT   DOMAIN      591   1022       NONHELICAL REGION.
FT   SITE        514    519       INTERUPTION IN COLLAGENOUS REGION.
FT   DOMAIN       44    168       VWF TYPE A-LIKE DOMAIN.
FT   DOMAIN      613    738       VWF TYPE A-LIKE DOMAIN.
FT   DOMAIN      833    957       VWF TYPE A-LIKE DOMAIN.
FT   CARBOHYD    141    141       POTENTIAL.
FT   CARBOHYD    215    215       POTENTIAL.
FT   CARBOHYD    327    327       POTENTIAL.
FT   CARBOHYD    630    630       POTENTIAL.
FT   CARBOHYD    897    897       POTENTIAL.
SQ   SEQUENCE   1022 AA;  109176 MW;  5032827 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =     37%  Matches         =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X      X
             XSXTXAXX
              | | |
    SRLGSIAKDPKSETGARVGVVQYSHEGT
         650  X    660       670
```

12. US-08-121-713B-12 (1-8)
    POL_HV1EL POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE T

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ID   POL_HV1EL      STANDARD;      PRT;  1002 AA.
AC   P04589;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE
DE   (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)).
GN   POL.
OS   HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ELI ISOLATE) (HIV-1).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC   LENTIVIRINAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   86245056
RA   ALIZON M., WAIN-HOBSON S., MONTAGNIER L., SONIGO P.;
RL   CELL 46:63-74(1986).
CC   -!- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
CC       DETERMINED.
DR   EMBL; X04414; HIVELICG.
DR   HSSP; P03366; 1HRH.
DR   HIV; K03454; POL$ELI.
DR   PROSITE; PS00141; ASP_PROTEASE.
KW   AIDS; POLYPROTEIN; HYDROLASE; ASPARTYL PROTEASE; ENDONUCLEASE;
KW   RNA-DIRECTED DNA POLYMERASE.
FT   CHAIN        56    154       PROTEASE.
FT   ACT_SITE     80     80       BY SIMILARITY.
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SQ   SEQUENCE   1002 AA;  114002 MW;  5118813 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =     37%  Matches         =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X      X
             XSXTXAXX
              | | |
    ELRVWGRDNPLSKTGAERQGTVSFNFPQ
  30         40      X 50
```

13. US-08-121-713B-12 (1-8)
    POL_HV1MA POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE T

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ID   POL_HV1MA      STANDARD;      PRT;  1002 AA.
AC   P04588;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE
DE   (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)).
GN   POL.
OS   HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MAL ISOLATE) (HIV-1).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC   LENTIVIRINAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   86245056
RA   ALIZON M., WAIN-HOBSON S., MONTAGNIER L., SONIGO P.;
RL   CELL 46:63-74(1986).
CC   -!- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
CC       DETERMINED.
DR   EMBL; X04415; HIVMALCG.
DR   HSSP; P03366; 1HRH.
DR   HIV; K03456; POL$MAL.
DR   PROSITE; PS00141; ASP_PROTEASE.
KW   AIDS; POLYPROTEIN; HYDROLASE; ASPARTYL PROTEASE; ENDONUCLEASE;
KW   RNA-DIRECTED DNA POLYMERASE.
FT   CHAIN        56    154       PROTEASE.
FT   ACT_SITE     80     80       BY SIMILARITY.
SQ   SEQUENCE   1002 AA;  113537 MW;  5140518 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =     37%  Matches         =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X      X
             XSXTXAXX
              | | |
    ELRVWGGDKTLSETGAERQGIVSFSFPQ
  30         40      X 50
```

14. US-08-121-713B-12 (1-8)
    POL_HV1ND POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE T

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ID   POL_HV1ND      STANDARD;      PRT;  1002 AA.
AC   P18802;
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DT   01-NOV-1990 (REL. 16, CREATED)
DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE
DE   (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)).
GN   POL.
OS   HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC   LENTIVIRINAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   90034200
RA   SPIRE B., SIRE J., ZACHAR V., REY F., BARRE-SINOUSSI F., GALIBERT F.,
RA   HAMPE A., CHERMANN J.C.;
RL   GENE 81:275-284(1989).
CC   -!- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
CC       DETERMINED.
CC   -!- NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH AIDS, AND IS
CC       A HIGHLY CYTOPATHOGENIC STRAIN.
DR   EMBL; M27323; HIVNDK.
DR   PIR; JQ0067; GNLJND.
DR   HSSP; P03366; 1HRH.
DR   HIV; M27323; POL$NDK.
DR   PROSITE; PS00141; ASP_PROTEASE.
KW   AIDS; POLYPROTEIN; HYDROLASE; ASPARTYL PROTEASE; ENDONUCLEASE;
KW   RNA-DIRECTED DNA POLYMERASE.
FT   CHAIN        56    154       PROTEASE.
FT   ACT_SITE     80     80       BY SIMILARITY.
SQ   SEQUENCE   1002 AA;  113621 MW;  5174153 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   ELRVWGGDNPLSETGAERQGTVSFSFPQ
 30        40      X 50
```

15. US-08-121-713B-12 (1-8)
    POL_HV1Z2   POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE T

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ID   POL_HV1Z2      STANDARD;      PRT;  1002 AA.
AC   P12499;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE
DE   (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)).
GN   POL.
OS   HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC   LENTIVIRINAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   THEODORE T., BUCKLER-WHITE A.;
RL   SUBMITTED (NOV-1988) TO THE HIV DATA BANK.
CC   -!- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
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CC       DETERMINED.
DR   EMBL; M22639; REHIVZ2Z.
DR   HSSP; P03366; 1HRH.
DR   HIV; M22639; POL$Z2Z6.
DR   PROSITE; PS00141; ASP_PROTEASE.
KW   AIDS; POLYPROTEIN; HYDROLASE; ASPARTYL PROTEASE; ENDONUCLEASE;
KW   RNA-DIRECTED DNA POLYMERASE.
FT   CHAIN        56    154       PROTEASE.
FT   ACT_SITE     81     81       BY SIMILARITY.
SQ   SEQUENCE   1002 AA;  113724 MW;  5178811 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  4.42
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XSXTXAXX
              | | |
   ELRVWGRDNPLSETGAERQGTVSFNCPQ
 30        40      X 50
```

maryh@stic **stdin**

NeWSprinter20

Fri May 19 10:51:22 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

Salata 12/7/13

SEQ 17

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq17asq.res made by  on Fri 19 May 95 8:40:36-PDT.


Query sequence being compared:US-08-121-713B-17 (1-6)
Number of sequences searched:                53402
Number of scores above cutoff:                3823

      Results of the initial comparison of US-08-121-713B-17 (1-6) with:
   Data bank : A-GeneSeq 18, all entries

100000-
      -
N     -
U50000-
M     -
B     *
E     -
R     -
      -                    *
O     -
F10000-                                  *
      -
S     -
E 5000-
Q     -
U     -
E     -
N     -
C     -
E     -
S 1000-
      -
      -
   500-
      -
      -
      -
      -
      -
      -
   100-                                                          *
      -
      -
    50-
      -
      -
      -
      -
      -
      -                                                          *
    10-
      -
      -
```



```
     5-
      -
      -
      -
      -
      -
      -
     0-----------------------------------------------------------------------
      ||      |     ||      |     | |     |     |     |     |     |
SCORE 0|      1     |1      2     | 2     3     3     4     4     5
STDEV  0           1             2
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	1	1.25

Times:	CPU	Total Elapsed
	00:00:30.96	00:00:31.00

Number of residues:	6354270
Number of sequences searched:	53402
Number of scores above cutoff:	3823

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 3 standard deviations above mean ****					
1. R05171	Natural killer cell stimulato	291	5	5	3.20	0
2. R12493	Cytotoxic lymphocyte maturati	313	5	5	3.20	0
3. R22769	Natural killer cell stimulato	328	5	5	3.20	0
4. R45936	A glycosyltransferase.	365	5	5	3.20	0
5. R13751	GDP-Fuc:beta-D-galactoside al	365	5	5	3.20	0
6. R33744	XR2.	440	5	5	3.20	0
7. R48205	H.tuberosus cytochrome P450 C	505	5	5	3.20	0

8.	R44140	Murine FACC encoded by cDNA c	558	5	5	3.20	0
9.	R51270	Murine FACC encoded by cDNA c	591	5	5	3.20	0
10.	R30497	N-terminal of LH receptor/FSH	757	5	5	3.20	0
11.	R05935	Secreted GPIIb subunit of mul	993	5	5	3.20	0
12.	R44430	eryA region polypeptide modul	3398	5	5	3.20	0
		**** 2 standard deviations above mean ****					
13.	R38556	Sequence of peptide which cor	15	4	5	2.40	0
14.	R41497	TNF inhibitory peptide IX.	21	4	5	2.40	0
15.	R25980	Peptide monomer 18.	23	4	5	2.40	0
16.	R21896	Magainin 2 peptide analogue.	23	4	5	2.40	0
17.	R21788	Magainin 2 peptide analogue.	23	4	5	2.40	0
18.	R40010	Scintigraph imaging agent spe	28	4	5	2.40	0
19.	R42547	Leukocyte-binding peptide whi	29	4	5	2.40	0
20.	R42546	Leukocyte-binding peptide whi	30	4	5	2.40	0
21.	P81566	Human insulin acceptor protei	31	4	5	2.40	0
22.	R29178	Astrovirus serotype A1 clone	92	4	5	2.40	0
23.	R25189	21B4 gene clone product pT#10	108	4	5	2.40	0
24.	R24082	Truncated TNF-alpha 55kD rece	154	4	5	2.40	0
25.	R24081	Truncated TNF-alpha 55kD rece	158	4	5	2.40	0
26.	R24083	Truncated TNF-alpha 55kD rece	159	4	5	2.40	0
27.	R27496	Native 30 kD TNF inhibitor.	161	4	5	2.40	0
28.	R24080	Truncated TNF-alpha 55kD rece	199	4	5	2.40	0
29.	P80436	Recombinant human glutathioni	200	4	5	2.40	0
30.	P80918	Sequence of human glutathione	201	4	5	2.40	0
31.	P80916	Sequence of bovine glutathion	205	4	5	2.40	0
32.	P82488	Sequence of Mycobacterium tub	205	4	5	2.40	0
33.	P70055	Fes/fps proto-oncogene-relate	211	4	5	2.40	0
34.	R57361	Translation from reading fram	220	4	5	2.40	0
35.	R31229	Prepro-thyrotropin releasing	242	4	5	2.40	0
36.	R22390	Antigen ac-1b.	242	4	5	2.40	0
37.	P82592	Polyhedrin protein.	245	4	5	2.40	0
38.	R32546	HaNPV polyhedrin.	246	4	5	2.40	0
39.	R06559	Polyhedrin of Spodoptera litu	249	4	5	2.40	0
40.	P94369	Fusion protein congt. 41kD pr	252	4	5	2.40	0
41.	R06201	O-acetylserine sulphyrylase (	253	4	5	2.40	0
42.	R13274	Petunia extracellular chitina	254	4	5	2.40	0
43.	R22959	Human proteasome component HC	255	4	5	2.40	0
44.	R21516	Polyfunctional protease C8.	255	4	5	2.40	0
45.	R10169	Vaccina virus 35k gene produc	258	4	5	2.40	0

1. US-08-121-713B-17 (1-6)
   R05171 Natural killer cell stimulatory factor (NKSF).

ID R05171 standard; protein; 291 AA.
AC R05171;
DT 11-OCT-1990 (first entry)
DE Natural killer cell stimulatory factor (NKSF).
KW Natural killer cell stimulatory factor; NKSF; cancer;
KW leukopaenia; anaemia; radiation; bone marrow transplantation; ds.
OS Homo sapiens.
PN WO9005147-A.
PD 17-MAY-1990.
PF 9-NOV-1989; 005027.
PR 10-NOV-1988; US-269945.
PA (GENE-) Genetics Inst Inc, (WIST-) Wistar Inst.
PI Trinchieri G, Perussia B, Kobayashi M, Clark SC, Wong GG;
DR WPI; 90-178800/23.
DR N-PSDB; Q04701.
PT New natural killer cell stimulatory factor -

PT useful for treating cancer and eg. leukopenia, bacterial and
PT viral infections, anaemia and B- or T-cell deficiencies.
PS Claim 17; Page 61; 69pp; English.
CC Natural killer cell stimulatory factor (NKSF) is useful in
CC treating cancer and other disease states which respond to NK cell
CC activity. Such states may arise from immune or haematopoietic-cell
CC deficiency following a bone marrow translpantation, exposure to
CC radiation and disease.
SQ Sequence 291 AA;
SQ 12 A; 9 R; 7 N; 19 D; 0 B; 9 C; 12 Q; 23 E; 0 Z; 16 G; 6 H;
SQ 12 I; 26 L; 22 K; 3 M; 10 F; 14 P; 29 S; 20 T; 9 W; 10 Y; 23 V;

Initial Score	=	5	Optimized Score	=	5	Significance	= 3.20
Residue Identity	=	50%	Matches	=	3	Mismatches	= 3
Gaps	=	0	Conservative Substitutions				= 0

```
            X    X
            FXREXA
            | |  |
   KDQKEPKNKTFLRCEAKNYSGRFTCW
   120      130  X    140
```

2. US-08-121-713B-17 (1-6)
   R12493 Cytotoxic lymphocyte maturation factor (40 kD subu

ID R12493 standard; Protein; 313 AA.
AC R12493;
DT 10-SEP-1991 (first entry)
DE Cytotoxic lymphocyte maturation factor (40 kD subunit).
KW Cytotoxic lymphocyte maturation factor; CLMF; probe; antitumour;
KW monoclonal antibodies; T cell.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= sig_peptide
FT Protein 23..313
FT /label= mat_protein
PN EP-433827-A.
PD 26-JUN-1991.
PF 09-DEC-1990; 123670.
PR 22-DEC-1989; US-455708.
PR 09-MAY-1990; US-520935.
PR 27-AUG-1990; US-572284.
PA (HOFF) HOFFMANN-LA ROCHE AG.
PI Chizzonite RA, Gately MK, Gubler UA, Hulmes JD, Pan YCE;
PI Podlaski FJ, Stern AS;
DR WPI; 91-186715/26.
DR N-PSDB; Q12149.
PT New cytotoxic lymphocyte maturation factor - used as antitumour
PT agent and monoclonal antibodies used in transplantation to block
PT proliferation and activation of cytotoxic T cells
PS Disclosure; Fig 25 (a-c); 90pp; English.
CC The natural CLMF protein is a 75 kD heterodimer comprising two
CC polypeptide subunits, a 40 kD and a 35 kD subunit (Q12150).
CC The subunits are bonded together via one or more disulfide bonds.
CC The CLMF can interact with IL-2 to synergistically induce the
CC cytolytic activity of Lymphokine Activated Killer (LAK) cells. It is
CC also capable of stimulating T-cell growth. It can be used for the
CC prepn. of LAK- and T-cell activator and antitumour compsns. and for

```
 CC   stimulating Natural Killer (NK) cells.
 SQ   Sequence   313 AA;
 SQ   15 A; 12 R; 7  N; 21 D; 0  B; 10 C; 13 Q; 23 E; 0  Z; 15 G; 6  H;
 SQ   13 I; 26 L; 26 K; 3  M; 11 F; 14 P; 31 S; 23 T; 9  W; 10 Y; 25 V;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.20
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
             | |  |
    KDQKEPKNKTFLRCEAKNYSGRFTCW
    120      130  X    140
```

3. US-08-121-713B-17 (1-6)
   R22769 Natural killer cell stimulatory factor.

```
 ID   R22769 standard; Protein; 328 AA.
 AC   R22769;
 DT   16-SEP-1992  (first entry)
 DE   Natural killer cell stimulatory factor.
 KW   NKSF; cytokine; gamma interferon; IFN; peripheral blood lymphocytes;
 KW   IL-2; GM-CSF; granulocyte macrophage colony stimulating factor; PBL;
 KW   ds.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   Peptide         23..27
 FT   /label= tryptic peptide 3
 FT   Peptide         75..79
 FT   /label= tryptic fragment 1
 FT   Peptide         219..224
 FT   /label= tryptic fragment 2
 FT   Peptide         303..308
 FT   /label= tryptic fragment 7
 FT   Peptide         127..130
 FT   /label= tryptic fragment 8
 FT   Peptide         231..239
 FT   /label= tryptic fragment 9
 FT   Protein         23..328
 FT   /label= mature 40kD NKSF
 FT   Peptide         1..22
 FT   /label= signal peptide
 PN   WO9205256-A.
 PD   02-APR-1992.
 PF   04-SEP-1991; U06332.
 PR   18-SEP-1990; US-584941.
 PA   (GENE-) GENETICS INST INC.
 PA   (WIST-) WISTAR INST.
 PI   Clark S C, Hewick R, Kobayashi M, Perussia B, Trinchieri G;
 PI   Wong G G;
 DR   WPI; 92-132124/16.
 DR   N-PSDB; Q23586.
 PT   New natural killer cell stimulatory factor - useful as an
 PT   immunostimulant for inducing gamma-interferon and GM-CSF prodn.
 PT   in human peripheral blood lymphocytes
 PS   Claim 12; Page 23; 79pp; English.
 CC   NKSF is capable of inducing the production of gamma interferon in
 CC   human peripheral blood lymphocytes. It has subunits of 40 (R22769)
```



```
 CC   and 30-35 kD (R23729). It is claimed that NKSF is useful in the
 CC   treatment of bacterial and viral  infections e.g. AIDS. It has a
 CC   specific activity of  >1*10power7 dilution units in the gamma-IFN
 CC   induction assay. Additionally it has biological activity in GM-CSF
 CC   inducing assay; biological activity in activating natural killer
 CC   cells to kill leukaemia and tumour derived cells; biological activity
 CC   in a TNF induction assay using PHA activated T-lymphocytes; and co-
 CC   mitogenic activity on PBL. It also synergises with IL-2 in inducing
 CC   gamma IFN production in PBLs and maintaining PBL proliferation.
 SQ   Sequence   328 AA;
 SQ   16 A; 12 R; 7  N; 21 D; 0  B; 11 C; 13 Q; 24 E; 0  Z; 15 G; 6  H;
 SQ   13 I; 26 L; 26 K; 3  M; 11 F; 15 P; 37 S; 23 T; 11 W; 12 Y; 26 V;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.20
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
             | |  |
    KDQKEPKNKTFLRCEAKNYSGRFTCW
    120      130  X    140
```

4. US-08-121-713B-17 (1-6)
   R45936 A glycosyltransferase.

```
 ID   R45936 standard; Protein; 365 AA.
 AC   R45936;
 DT   26-JUL-1994  (first entry)
 DE   A glycosyltransferase.
 KW   Glycosyltransferase; fucosyltransferase; GDP-Fuc; in vitro; cell;
 KW   surface; oligosaccharide.
 OS   Homo sapiens.
 PN   WO9402616-A.
 PD   03-FEB-1994.
 PF   20-JUL-1993; U06703.
 PR   20-JUL-1992; US-914281.
 PA   (UNMI ) UNIV MICHIGAN.
 PI   Lowe JB;
 DR   WPI; 94-048874/06.
 DR   N-PSDB; Q56908.
 PT   DNA fragment encoding a glycosyltransferase - can be used for in
 PT   vitro reactions to modify cell surface oligosaccharide(s) e.g.
 PT   blood gp. determinants, to protect against transplant rejection
 PS   Disclosure; Fig 3; 249pp; English.
 CC   The sequence is that of a human glycosyl transferase.  The enzyme
 CC   may be non glycosylated.  This prevents premature loss of enzyme
 CC   activity.  It can also be used in in vitro reactions to modify cell
 CC   surface oligosaccharide mols. e.g. blood group determinants.
 CC   See also R45933-9.
 SQ   Sequence   365 AA;
 SQ   32 A; 25 R; 9  N; 18 D; 0  B; 8  C; 16 Q; 15 E; 0  Z; 26 G; 14 H;
 SQ   12 I; 44 L; 7  K; 9  M; 24 F; 24 P; 19 S; 22 T; 12 W; 7  Y; 22 V;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.20
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
```

```
              FXREXA
                || |
    QIRREFTLHDHLREEAQSVLGQLRLG
  180       190    X  200
```

5. US-08-121-713B-17 (1-6)
R13751 GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltrans

```
ID   R13751 standard; Protein; 365 AA.
AC   R13751;
DT   07-NOV-1991  (first entry)
DE   GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase.
KW   Glycosyltransferase.
OS   Homo sapiens.
PN   WO9112340-A.
PD   22-AUG-1991.
PF   14-FEB-1991; U00899.
PR   14-FEB-1990; US-480133.
PR   14-FEB-1990; US-479858.
PR   12-DEC-1990; US-627621.
PA   (UNMI ) UNIV OF MICHIGAN.
PI   Lowe JB;.
DR   WPI; 91-267151/36.
DR   P-PSDB; R13751.
PT   Isolation of gene conveying post-translational characteristic -
PT   e.g. the presence of soluble or membrane bound oligo or
PT   polysaccharide or glycosyltransferase.
PS   Disclosure; Fig 3; 155pp; English.
CC   The amino acid sequence codes for a protein capable of functioning
CC   as a GDP- Fuc:{beta-D-Gal alpha(1,2)- fucosyltransferase. The
CC   functional protein is represented by amino acids 33 to 365. The
CC   enzyme produced by the DNA sequence can be used in enzymatic
CC   fucosylation of chain-terminating galactose residues on lactose-
CC   amine or neolacto type beta-D-galactoside to alpha-2-L-fucose
CC   residues. See also R13749-R13752.
SQ   Sequence   365 AA;
SQ   31 A; 25 R; 9  N; 18 D; 0  B; 8  C; 16 Q; 15 E; 0  Z; 26 G; 14 H;
SQ   12 I; 44 L; 7  K; 9  M; 24 F; 25 P; 19 S; 22 T; 12 W; 7  Y; 22 V;
```

Initial Score	=	5	Optimized Score	=	5	Significance =	3.20
Residue Identity	=	50%	Matches	=	3	Mismatches =	3
Gaps	=	0	Conservative Substitutions			=	0

```
              X    X
              FXREXA
                || |
    QIRREFTLHDHLREEAQSVLGQLRLG
  180       190    X  200
```

6. US-08-121-713B-17 (1-6)
R33744 XR2.

```
ID   R33744 standard; Protein; 440 AA.
AC   R33744;
DT   23-JUL-1993  (first entry)
DE   XR2.
KW   Receptor; XR2; DNA binding domain; human; retinoic acid receptor-alpha;
KW   hRAR-alpha; thyroid receptor-beta; hTR-beta; glucocorticoid receptor;
```



```
KW   hGR; retinoid X receptor-alpha; hRXR-alpha; verht3; verhr5; ligand;
KW   transcription-activation; response element.
OS   Homo sapiens.
PN   WO9306215-A.
PD   01-APR-1993.
PF   08-SEP-1992; U07570.
PR   17-SEP-1991; US-761068.
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
PI   Borgmeyer UK,  Evans RM,  Giguere V,  Mangelsdorf DJ;
PI   Ong ES,  Oro AE,  Yao TP;
DR   WPI; 93-117536/14.
DR   N-PSDB; Q39088.
PT   DNA encoding proteins of thyroid-steroid hormone receptor
PT   super-family - useful for screening for agonists-antagonists of
PT   such receptors
PS   Claim 9; Page 40-42; 71pp; English.
CC   This sequence represents the receptor XR2.  This polypeptide has a
CC   DNA binding domain comprising approx. 55% amino acid sequence identity
CC   with the DNA binding domain of human retinoic acid receptor-alpha
CC   (hRAR-alpha), about 56% amino acid sequence identity with the DNA
CC   binding domain of human thyroid receptor-beta (hTR-beta), about 50%
CC   amino acid sequence identity with the DNA binding domain of human
CC   glucocorticoid receptor (hGR) and about 52% amino acid sequence
CC   identity with the DNA binding domain of human retinoid X receptor-
CC   alpha (hRXR-alpha).  XR2 receptor can be used for testing a compound
CC   for its ability to regulate transcription-activating effects of a
CC   receptor polypeptide, identifying compounds which act as ligands for
CC   the receptor polypeptides and for identifying response elements for
CC   the receptor polypeptides.
SQ   Sequence   440 AA;
SQ   36 A; 33 R; 9  N; 18 D; 0  B; 12 C; 29 Q; 35 E; 0  Z; 19 G; 15 H;
SQ   20 I; 46 L; 21 K; 13 M; 18 F; 33 P; 37 S; 14 T; 4  W; 7  Y; 21 V;
```

Initial Score	=	5	Optimized Score	=	5	Significance =	3.20
Residue Identity	=	50%	Matches	=	3	Mismatches =	3
Gaps	=	0	Conservative Substitutions			=	0

```
              X    X
              FXREXA
                || |
    SSQAQGGSSCILREEATMPHSAGGTA
    30        40   X    50
```

7. US-08-121-713B-17 (1-6)
R48205 H.tuberosus cytochrome P450 Cinnamate 4-hydroxylas

```
ID   R48205 standard; Protein; 505 AA.
AC   R48205;
DT   12-JUL-1994  (first entry)
DE   H.tuberosus cytochrome P450 Cinnamate 4-hydroxylase.
KW   Cinnamate 4-hydroxylase; Jerusalem artichoke; common white variety;
KW   CA4H; EC.1.14.13.1; cytochrome P450; mono oxidation; hydroxylation;
KW   NADPH-cytochrome P450 reductase.
OS   Helianthus tuberosus.
PN   WO9401564-A.
PD   20-JAN-1994.
PF   02-JUL-1993; F00676.
PR   03-JUL-1992; FR-008254.
PA   (ORSA-) ORSAN.
```

```
PI   Kazmaier M,  Mignotte VC,  Pompon D,  Renaud M,  Teutsch H;
PI   Werck-Reichart D,  Mignotte Vieux C,  Werkreichart D;
DR   WPI; 94-035069/04.
DR   N-PSDB; Q55607.
PT   New yeast strain expressing plant cytochrome P450 mono:oxygenase
PT   - and simultaneously NADPH cytochrome reductase, with gene
PT   integrated, useful for bio conversion, esp. specific
PT   hydroxylation of cinnamate to coumarate
PS   Example 1; Fig 1; 71pp; French.
CC   The cytochrome P450 cinnamate 4-hydroxylase R48205 catalyses the
CC   hydroxylation of trans-cinnamate in the Jerusalem artichoke.
CC   The CA4H gene can be used in the production of yeast strains able
CC   to co-express mono-oxygenase (i.e. hydroxylation) activity of a
CC   plant-derived cytochrome P450 as well as NADPH cytochrome 450
CC   reductase activity.
SQ   Sequence   505 AA;
SQ   31 A; 33 R; 27 N; 26 D; 0  B; 3  C; 18 Q; 37 E; 0  Z; 32 G; 10 H;
SQ   38 I; 58 L; 38 K; 12 M; 27 F; 28 P; 15 S; 18 T; 8  W; 11 Y; 35 V;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.20
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
             |  | |
   KKPEEFRPERFLEEEAKVEANGNDFR
         420     X 430
```

8. US-08-121-713B-17 (1-6)
   R44140 Murine FACC encoded by cDNA clone pmfac2.

```
ID   R44140 standard; Protein; 558 AA.
AC   R44140;
DT   20-MAY-1994  (first entry)
DE   Murine FACC encoded by cDNA clone pmfac2.
KW   Fanconi Anemia Group C; FACC;  complementing cDNA; varient; diagnosis;
KW   open reading frame; Fanconi anemia; gene therapy.
OS   Mus musculus.
PN   WO9322435-A.
PD   11-NOV-1993.
PF   27-APR-1993; CA0178.
PR   29-APR-1992; US-876285.
PR   21-JUL-1992; US-918313.
PR   15-JAN-1993; US-003963.
PA   (HOSP-) HOSPITAL FOR SICK CHILDREN.
PA   (UNME-) UNITED MEDICAL & DENTAL SCHOOL GUYS.
PI   Buchwald M,  Mathew CG,  Strathdee CA,  Wevrick R;
DR   WPI; 93-368794/46.
DR   N-PSDB; Q51455.
PT   Human cDNA which complements Fanconi Anaemia gp. C - used to
PT   develop prods. for use in diagnosis, study and therapy of Fanconi
PT   Anaemia
PS   Claim 1; Fig 11; 137pp; English.
CC   The sequences given in R44140 and R51270 are encoded by murine cDNA
CC   varients from the Fanconi Anemia Group C Complementing (FACC) cDNA.
CC   These two cDNA molecules are cellular varients of a single cDNA
CC   transcribed from the same gene.  The second cDNA contains an additional
CC   exon which was isolated in the clone pmfac7.  The FACC proteins encoded
```



```
CC   by these two clones may be used for the diagnosis and study of Fanconi
CC   anemia and the cDNAs may be used in gene therapy.
SQ   Sequence   558 AA;
SQ   45 A; 29 R; 9  N; 18 D; 0  B; 17 C; 29 Q; 50 E; 0  Z; 20 G; 17 H;
SQ   21 I; 89 L; 20 K; 15 M; 25 F; 31 P; 47 S; 20 T; 11 W; 11 Y; 34 V;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.20
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
               || |
    GWVDLAVAELLLREEAEPPAGLLWLL
        410  X    420
```

9. US-08-121-713B-17 (1-6)
   R51270 Murine FACC encoded by cDNA clone pmfac7.

```
ID   R51270 standard; Protein; 591 AA.
AC   R51270;
DT   20-MAY-1994  (first entry)
DE   Murine FACC encoded by cDNA clone pmfac7.
KW   Fanconi Anemia Group C; FACC;  complementing cDNA; varient; diagnosis;
KW   open reading frame; Fanconi anemia; gene therapy.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   Peptide         514..546
FT   /note= "Encoded by the additional exon"
PN   WO9322435-A.
PD   11-NOV-1993.
PF   27-APR-1993; CA0178.
PR   29-APR-1992; US-876285.
PR   21-JUL-1992; US-918313.
PR   15-JAN-1993; US-003963.
PA   (HOSP-) HOSPITAL FOR SICK CHILDREN.
PA   (UNME-) UNITED MEDICAL & DENTAL SCHOOL GUYS.
PI   Buchwald M,  Mathew CG,  Strathdee CA,  Wevrick R;
DR   WPI; 93-368794/46.
DR   N-PSDB; Q51456.
PT   Human cDNA which complements Fanconi Anaemia gp. C - used to
PT   develop prods. for use in diagnosis, study and therapy of Fanconi
PT   Anaemia
PS   Claim 1; Fig 12; 137pp; English.
CC   The sequences given in R44140 and R51270 are encoded by murine cDNA
CC   varients from the Fanconi Anemia Group C Complementing (FACC) cDNA.
CC   These two cDNA molecules are cellular varients of a single cDNA
CC   transcribed from the same gene.  The second cDNA contains an additional
CC   exon which was isolated in the clone pmfac7.  The FACC proteins encoded
CC   by these two clones may be used for the diagnosis and study of Fanconi
CC   anemia and the cDNAs may be used in gene therapy.
SQ   Sequence   591 AA;
SQ   46 A; 33 R; 9  N; 18 D; 0  B; 21 C; 30 Q; 52 E; 0  Z; 23 G; 19 H;
SQ   23 I; 90 L; 21 K; 15 M; 26 F; 36 P; 48 S; 24 T; 12 W; 11 Y; 34 V;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.20
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0
```

```
            X    X
            FXREXA
              || |
   GWVDLAVAELLLREEAEPPAGLLWLL
       410  X    420
```

10. US-08-121-713B-17 (1-6)
    R30497 N-terminal of LH receptor/FSH receptor chimaera #6

```
 ID   R30497 standard; protein; 757 AA.
 AC   R30497;
 DT   10-MAY-1993  (first entry)
 DE   N-terminal of LH receptor/FSH receptor chimaera #6.
 KW   Follicle stimulating hormone receptor; luteinising hormone receptor;
 KW   human chorionic gonadotrophin; glycoprotein hormone receptor;
 KW   chimaera; chimera.
 OS   Chimaeric; homo sapiens.
 PN   WO9222667-A.
 PD   23-DEC-1992.
 PF   12-JUN-1992; U04987.
 PR   14-JUN-1991; US-715911.
 PA   (UYNE-) UNIV NEW JERSEY.
 PI   Bernard M,  Moyle WR,  Myers R;
 DR   WPI; 93-018150/02.
 PT   Glyco:protein hormone receptor analogues - having binding
 PT   affinity to human chorionic gonadotrophin, luteinising and
 PT   follicle stimulating hormones, useful in bio:immunoassays
 PS   Examples; Fig 12; 103pp; English.
 CC   This sequence represents the N-terminal of a novel protein having a
 CC   binding affinity for human chorionic gonadotrophin (hCG), luteinising
 CC   hormone (LH), and follicle stimulating hormone (FSH). The protein
 CC   itself is a chimaera having residues from both  thew FSH receptor,
 CC   and LH receptor. The receptor analogues can be used in bioimmunoassays
 CC   for the simultaneous detection of both LH  (or hCG) and FSH as
 CC   well as their ratio of biological activities. The analogues can also
 CC   be used for raising, purifying and assaying antibodies to the
 CC   analogues. Coding sequence for the chimaera was produced by two step
 CC   PCR.
 SQ   Sequence   757 AA;
 SQ   47 A; 31 R; 40 N; 26 D; 0  B; 27 C; 30 Q; 43 E; 0  Z; 43 G; 13 H;
 SQ   50 I; 88 L; 36 K; 15 M; 42 F; 35 P; 70 S; 41 T; 9  W; 25 Y; 46 V;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.20
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            FXREXA
            | |  |
   NPCEDIMGYAFLRDEAWVVGMAILMS
      360    X  370       380
```

11. US-08-121-713B-17 (1-6)
    R05935 Secreted GPIIb subunit of multiple subunit polypep

```
 ID   R05935 standard; protein; 993 AA.
 AC   R05935;
 DT   22-NOV-1990  (first entry)
```



```
 DE   Secreted GPIIb subunit of multiple subunit polypeptide (MSP)
 DE   GPIIb-IIIa.
 KW   GPIIb; GPIIIa; MSP GPIIb-IIIa; anti-coagulant; anti-inflamatory;
 KW   immunosuppressant; ds.
 OS   Homo sapiens.
 PN   WO9006953-A.
 PD   28-JUN-1990.
 PF   20-DEC-1989; U05743.
 PR   22-DEC-1988; US-290224.
 PR   01-DEC-1989; US-444490.
 PA   (GETH ) GENENTECH INC.
 PI   BODARY SC, GORMAN CM, NAPIER MA, MCLEAN JW;
 DR   WPI; 90-224496/29.
 DR   N-PSDB; Q05271.
 PT   Soluble analogues of multi-sub-unit polypeptide prodn. - by
 PT   transforming host cells with nucleic acid modified to prevent
 PT   membrane attachment, useful in diagnosis and ligand purificn.
 PS   Disclosure; 47pp; English.
 CC   Peptide product is analogous to MSP with better stability, it is
 CC   not membrane bound and so may be collected as a cell secretion from
 CC   a transformed host. The product is useful as a diagnostic reagent
 CC   eg. immunoassay of MSP; in purification of ligands and matrix
 CC   proteins; and therapeutically as agonists or antagonists of the
 CC   corresponding membrane bound receptor.
 SQ   Sequence   993 AA;
 SQ   81 A;  52 R;  36 N;  49 D;  0 B;  20 C;  62 Q;  54 E;  0 Z;  87 G;  23 H;
 SQ   26 I; 122 L;  22 K;  12 M; 33 F;  73 P;  75 S;  36 T; 17 W;  28 Y;  85 V;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.20
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            FXREXA
            | |  |
   HSPICHTTMAFLRDEADFRDKLSPIV
        580 X     590
```

12. US-08-121-713B-17 (1-6)
    R44430 eryA region polypeptide module #1.

```
 ID   R44430 standard; Protein; 3398 AA.
 AC   R44430;
 DT   22-DEC-1993  (first entry)
 DE   eryA region polypeptide module #1.
 KW   Saccarapolyspora erythraea; eryA; biosynthesis; polyketide; module;
 KW   erythromycin; condensation; elongation; acyl chain growth;
 KW   gene replacement.
 OS   Saccarapolyspora erythraea.
 PN   WO9313663-A.
 PD   22-JUL-1993.
 PF   17-JAN-1992; U00427.
 PR   17-JAN-1992; WO-U00427.
 PA   (ABBO ) ABBOTT LAB.
 PI   Donadio S,  Katz L,  McAlpine JB;
 DR   WPI; 93-242804/30.
 DR   N-PSDB; Q46806.
 PT   Biosynthesis of specific polyketide analogues esp. erythromycin
 PT   cpds. - by introducing altered biosynthetic gene-contg. DNA into
```

```
 PT   microorganisms
 PS   Disclosure; Fig 2; 133pp; English.
 CC   The sequences given in R44430-32 are encoded by the eryA fragment of
 CC   the Saccarapolyspora erythraea genome.  These polypeptides are
 CC   involved in the biosynthesis of the polyketide segment of erythromycin.
 CC   eryA is organised in modules and each module takes care of one
 CC   condensation step.  The precise succession of elongation steps is
 CC   dictated by the genetic order of the modules.  The DNA encoding
 CC   these polypeptides may be specifically altered such that novel
 CC   polyketide molecules of desired structure are produced.  Three types
 CC   of alteration may be produced; those inactivating a single function in
 CC   a module which does not arrest acyl chain growth; those inactivating a
 CC   single function in a module which does affect chain growth; and those
 CC   affecting an entire module.  The mutations may be introduced by gene
 CC   replacement.
 SQ   Sequence   3398 AA;
 SQ   554A; 288R; 39 N; 201D; 0  B; 29 C; 81 Q; 239E; 0  Z; 349G; 66 H;
 SQ   72 I; 331L; 22 K; 44 M; 89 F; 193P; 208S; 171T; 56 W; 34 Y; 332V;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.20
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
             | |  |
    EPHLDFEVIPFLRAEAARREQDAALS
        980   X   990
```

13. US-08-121-713B-17 (1-6)
    R38556 Sequence of peptide which corresponds to ragweed p

```
 ID   R38556 standard; peptide; 15 AA.
 AC   R38556;
 DT   08-NOV-1993  (first entry)
 DE   Sequence of peptide which corresponds to ragweed pollen antigen3
 DE   Ra3.
 KW   Allergen epitope; ragweed pollen; allergy; graft rejection.
 OS   Synthetic.
 PN   WO9312145-A.
 PD   24-JUN-1993.
 PF   18-DEC-1992; U11238.
 PR   19-DEC-1991; US-811050.
 PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
 PI   Ashizawa T,  Atassi MZ;
 DR   WPI; 93-214099/26.
 PT   Immune disorders treatment reagent prodn. for ragweed pollen
 PT   allergy - by forming peptide contg. allergen epitope with polymer
 PT   e.g. polyethylene glycol, deriving aminoacid, de-protecting,
 PT   cleaving, and purifying for Graves disease
 PS   Claim 4; Figure 1 no.2; 76pp; English.
 CC   The peptides of the invention are allergen epitopes bonded to a
 CC   tolerogenic polymer(TP) such as monomethoxypolyethylene glycol(mPEG)
 CC   or polyvinyl alcohol(PVA). Pref.the peptide is attached to the
 CC   resin at the C-terminus and TP attached to the N-terminus. It is
 CC   used for treating a patient having, or likely to develop, ragweed
 CC   allergy.
 SQ   Sequence   15 AA;
 SQ   2  A; 1  R; 0  N; 2  D; 0  B; 1  C; 0  Q; 3  E; 0  Z; 0  G; 1  H;
```



```
 SQ   1  I; 0  L; 1  K; 0  M; 0  F; 0  P; 0  S; 0  T; 1  W; 1  Y; 1  V;

Initial Score    =      4  Optimized Score  =      5  Significance =  2.40
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

     X    X
     FXREXA
      || |
    EVWREEAYHACDIKD
     X    X 10
```

14. US-08-121-713B-17 (1-6)
    R41497 TNF inhibitory peptide IX.

```
 ID   R41497 standard; peptide; 21 AA.
 AC   R41497;
 DT   23-FEB-1994  (first entry)
 DE   TNF inhibitory peptide IX.
 KW   Tumour necrosis factor; TNF; inhibition; solid phase synthesis; ss.
 OS   Synthetic.
 PN   J05194594-A.
 PD   03-AUG-1993.
 PF   21-JAN-1992; 029044.
 PR   21-JAN-1992; JP-029044.
 PA   (SAGA ) SAGAMI CHEM RES CENTRE.
 DR   WPI; 93-282916/36.
 PT   TNF inhibitory novel peptide(s) - include N-terminal amino Gp.
 PT   which is opt. modified with acetyl, T-butoxy-carbonyl or
 PT   benzyl-oxy-carbonyl Gp. and C-terminal carboxy Gp. is opt.
 PT   amidated
 PS   Claim 1; Page 6; 8pp; Japanese.
 CC   The sequences given in R41489-99 are tumour necrosis factor (TNF)
 CC   inhibitory peptides.  They may optionally be modified at the N-
 CC   terminal with an acetyl, t-butoxycarbonyl or benzyloxycarbonyl, and
 CC   at the C-terminal they are optionally amidated.  These peptides are
 CC   produced by solid phase synthesis methods and may be produced at low
 CC   cost.
 SQ   Sequence   21 AA;
 SQ   3  A; 1  R; 2  N; 0  D; 0  B; 0  C; 2  Q; 3  E; 0  Z; 2  G; 1  H;
 SQ   0  I; 1  L; 1  K; 0  M; 2  F; 0  P; 0  S; 2  T; 0  W; 0  Y; 1  V;

Initial Score    =      4  Optimized Score  =      5  Significance =  2.40
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
             | ||
    NTVATAHAGFFLRENEG
        10    X   20
```

15. US-08-121-713B-17 (1-6)
    R25980 Peptide monomer 18.

```
 ID   R25980 standard; Protein; 23 AA.
 AC   R25980;
 DT   21-JAN-1993  (first entry)
```

```
DE   Peptide monomer 18.
KW   Reverse peptide; microbial pathogen; phytotoxicity; head-to-tail;
KW   proteolytic degradation; dimer; peptide bond; bridging group;
KW   omega loop.
OS   Synthetic.
PN   EP-497366-A.
PD   05-AUG-1992.
PF   31-JAN-1992; 101616.
PR   01-FEB-1991; US-649784.
PA   (DONG ) IST DONEGANI SPA GUIDO.
PI   Bascomb NF, Dugas de Robertis C, Everett NP, Mapelli C;
PI   Stahl GF, Swerdloff MD, Williams JI;
DR   WPI; 92-260816/32.
PT   Reverse antimicrobial peptide(s) and oligopeptide(s) - useful for
PT   protecting plants from pathogens and for determining
PT   phytotoxicity
PS   Disclosure; Fig 1; 79pp; English.
CC   The sequences given in R25963-83 are a collection of natural and
CC   reverse peptides which are active against at least one microbial
CC   pathogen and, preferably, at least one plant pathogen.  It has been
CC   found that acceptable activity and acceptable levels of protection
CC   against at least one microbial pathogen and at least one microbial
CC   plant pathogen may be obtained by reversing the sequence of amino
CC   acids contained within naturally occuring antimicrobial peptides
CC   while maintaining the directionality of the peptide bonds.  These
CC   peptides possess relatively low phytotoxicity and/or low susceptibility
CC   to proteolytic degradation.  The oligopeptides may be used as dimers
CC   composed of two peptide units with or without an intervening bridge.
CC   The simplest structure taken by these dimers is the "head-to-tail"
CC   configuration.  This comprises at least one first peptide monomer and
CC   at least one second peptide monomer.  Each peptide monomer has an N-
CC   and C-terminus, both of which are capable of forming peptide bonds.
CC   In the head-to-tail configuration the C-terminal amino acid of the
CC   first monomer peptide is directly bound to the N-terminus of the
CC   second monomer peptide, by a peptide bond, without an intervening
CC   bridging group.  In other peptide dimers bridging groups may be used
CC   and may be as few as one amino acid but may be as large as 100 amino
CC   acids in length and form omega loops or other secondary structures.
SQ   Sequence   23 AA;
SQ   2  A; 1  R; 0  N; 0  D; 0  B; 0  C; 0  Q; 2  E; 0  Z; 5  G; 0  H;
SQ   2  I; 1  L; 4  K; 1  M; 3  F; 1  P; 0  S; 0  T; 0  W; 0  Y; 1  V;

Initial Score    =      4  Optimized Score  =      5  Significance =  2.40
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

        X    X
        FXREXA
        | ||
    GIGKFLREAGKFGKAFVGEI
       X   10        20
> O <
O| |O  IntelliGenetics
> O <

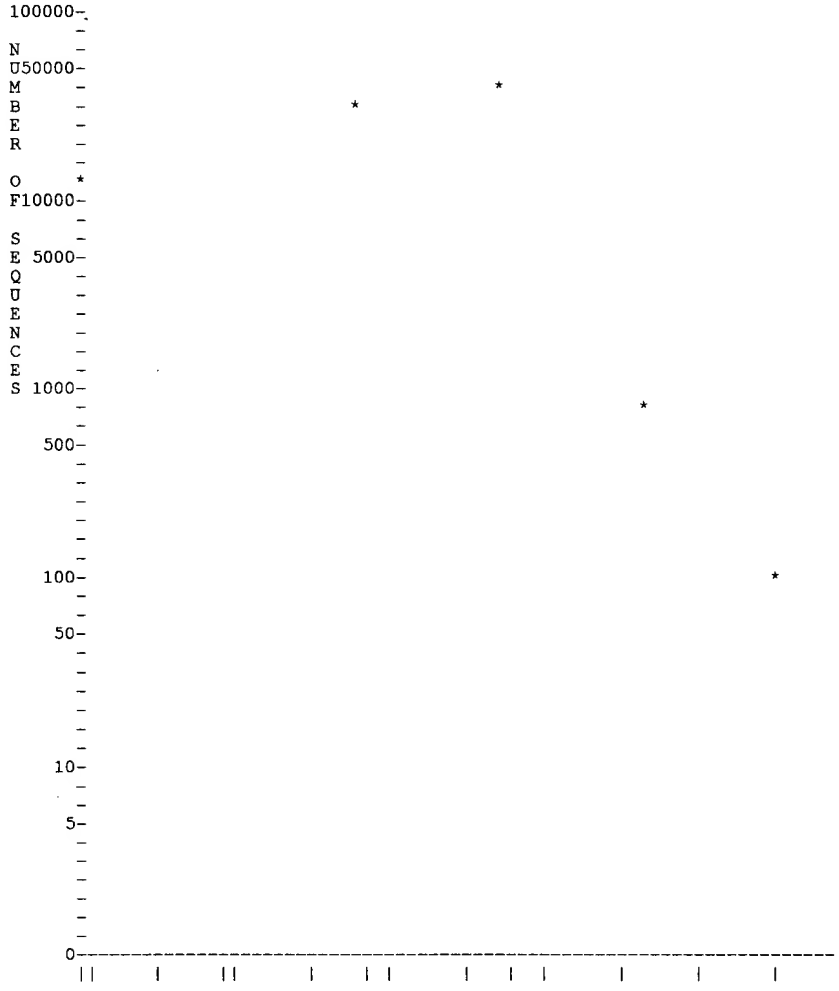
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq17pir.res made by maryh on Fri 19 May 95 10:47:00-PDT.
```



```
Query sequence being compared:US-08-121-713B-17 (1-6)
Number of sequences searched:                75511
Number of scores above cutoff:                4422

     Results of the initial comparison of US-08-121-713B-17 (1-6) with:
   Data bank : PIR 43, all entries
```



```
SCORE 0|     1     |1      2     | 2      3    |  3      4      4      5
STDEV -1           0            1             2
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	3	1.08

Times:	CPU	Total Elapsed
	00:01:10.99	00:01:11.00

Number of residues:	22468834
Number of sequences searched:	75511
Number of scores above cutoff:	4422

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 2 standard deviations above mean ****					
1. C49958	AMP-PK=AMP-activated protein	58	5	5	2.79	0
2. A41960	homoserine O-succinyltransfer	69	5	5	2.79	0
3. S31563	hypothetical protein YGL024 -	90	5	5	2.79	0
4. HRIN	hemerythrin - sipunculid (Sip	113	5	5	2.79	0
5. S13197	profilin - sea urchin (Clypea	139	5	5	2.79	0
6. S13198	profilin - sea urchin (Anthoc	139	5	5	2.79	0
7. A44777	profilin spCoel1 - sea urchin	142	5	5	2.79	0
8. S17791	aminoacyl-tRNA hydrolase (EC	194	5	5	2.79	0
9. S16753	aminoacyl-tRNA hydrolase (EC	194	5	5	2.79	0
10. S05446	tropomyosin, nonmuscle - Japa	221	5	5	2.79	0
11. B32014	traJ protein - Escherichia co	223	5	5	2.79	0
12. S44924	39K antigen - Entamoeba histo	237	5	5	2.79	0
13. S44923	39K antigen - Entamoeba histo	237	5	5	2.79	0
14. S24403	tropomyosin alpha - chicken	245	5	5	2.79	0
15. A60364	tropomyosin - migratory locus	283	5	5	2.79	0
16. C25242	tropomyosin, exon 9D - fruit	285	5	5	2.79	0
17. A25561	tropomyosin II, muscle - frui	285	5	5	2.79	0
18. B25242	tropomyosin, exon 9C - fruit	286	5	5	2.79	0
19. A25242	tropomyosin, exon 9B - fruit	286	5	5	2.79	0
20. DMHY	desmin - golden hamster (frag	298	5	5	2.79	0
21. S21688	interleukin-12 - human	306	5	5	2.79	0
22. XYECM	homoserine O-succinyltransfer	309	5	5	2.79	0

23. BWSMNG	strN protein - Streptomyces g	319	5	5	2.79	0
24. B39359	cytotoxic lymphocyte maturati	328	5	5	2.79	0
25. S46819	hypothetical protein YHL009c	330	5	5	2.79	0
26. S17823	protochlorophyllide reductase	333	5	5	2.79	0
27. B49850	chlorin reductase subunit Bch	333	5	5	2.79	0
28. S44922	39K antigen - Entamoeba histo	335	5	5	2.79	0
29. S35250	hrpN protein - Pseudomonas so	357	5	5	2.79	0
30. A36047	galactoside 2-alpha-L-fucosyl	365	5	5	2.79	0
31. DCECIS	isocitrate dehydrogenase (NAD	416	5	5	2.79	0
32. S36799	calreticulin (clone 9,4) - bo	421	5	5	2.79	0
33. A49424	patterning protein Sonic hedg	425	5	5	2.79	0
34. S15471	EAV element protein - Chicken	433	5	5	2.79	0
35. B53193	hedgehog homolog vhh-1 - rat	437	5	5	2.79	0
36. A54104	desmin - mouse	469	5	5	2.79	0
37. A24783	desmin - hamster	469	5	5	2.79	0
38. A33312	sarcoplasmic reticulum 53K gl	472	5	5	2.79	0
39. S28495	trans-cinnamate 4-monooxygena	505	5	5	2.79	0
40. A47454	trans-cinnamate 4-monooxygena	505	5	5	2.79	0
41. S19266	anthranilate synthase (EC 4.1	508	5	5	2.79	0
42. DEBSMP	IMP dehydrogenase (EC 1.1.1.2	513	5	5	2.79	0
43. S20589	Transcription factor TFIIF la	517	5	5	2.79	0
44. S20248	transcription factor TFIIF la	517	5	5	2.79	0
45. A38101	potassium channel HLK-3, volt	523	5	5	2.79	0

1. US-08-121-713B-17 (1-6)
   C49958 AMP-PK=AMP-activated protein kinase 63 kda catalyt

ENTRY	C49958 #type fragment
TITLE	AMP-PK=AMP-activated protein kinase 63 kda catalytic subunit - pig (fragment)
ORGANISM	#formal_name Sus scrofa domestica #common_name domestic pig
DATE	06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
ACCESSIONS	C49958
REFERENCE	A49958
#authors	Mitchelhill, K.I.; Stapleton, D.; Gao, G.; House, C.; Michell, B.; Katsis, F.; Witters, L.A.; Kemp, B.E.
#journal	J. Biol. Chem. (1994) 269:2361-2364
#title	Mammalian AMP-activated protein kinase shares structural and functional homology with the catalytic domain of yeast Snf1 protein kinase.
#accession	C49958
##status	preliminary
##molecule_type	protein
##residues	1-58 ##label MIT
##cross-references	NCBIP:143412
##note	sequence extracted from NCBI backbone
SUMMARY	#length 58 #checksum 6573
SEQUENCE	

Initial Score	= 5	Optimized Score	= 5	Significance	= 2.79
Residue Identity	= 66%	Matches	= 4	Mismatches	= 2
Gaps	= 0	Conservative Substitutions			= 0

```
            X   X
            FXREXA
            | | ||
   GLSNMMSDGEFLRXXAXXPNYAAPEV
         30     X  40
```

```
2. US-08-121-713B-17 (1-6)
   A41960       homoserine O-succinyltransferase (EC 2.3.1.46) - S

 ENTRY            A41960     #type fragment
 TITLE            homoserine O-succinyltransferase (EC 2.3.1.46) - Salmonella
                    typhimurium (fragment)
 ORGANISM         #formal_name Salmonella typhimurium
 DATE             31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                    31-Dec-1993
 ACCESSIONS       A41960
 REFERENCE        A41960
    #authors      Mares, R.; Urbanowski, M.L.; Stauffer, G.V.
    #journal      J. Bacteriol. (1992) 174:390-397
    #title        Regulation of the Salmonella typhimurium metA gene by the
                    metR protein and homocysteine.
    #cross-references MUID:92105004
    #accession    A41960
       ##status        preliminary
       ##molecule_type DNA
       ##residues      1-69 ##label MAR
       ##cross-references NCBIN:75596; NCBIP:75598
       ##note          sequence extracted from NCBI backbone
 KEYWORDS         acyltransferase
 SUMMARY          #length 69  #checksum 2217
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.79
Residue Identity =    50%  Matches          =      3  Mismatches   =      3
Gaps             =      0  Conservative Substitutions               =      0

             X    X
             FXREXA
             | ||
    RVLDELPAVNFLREENVFDMTTSRAS
         10   X    20


3. US-08-121-713B-17 (1-6)
   S31563       hypothetical protein YGL024 - yeast (Saccharomyces

 ENTRY            S31563     #type complete
 TITLE            hypothetical protein YGL024 - yeast (Saccharomyces
                    cerevisiae)
 ORGANISM         #formal_name Saccharomyces cerevisiae
 DATE             28-May-1993 #sequence_revision 28-May-1993 #text_change
                    18-Nov-1994
 ACCESSIONS       S31563
 REFERENCE        S15040
    #authors      Chen, W.; Balzi, E.; Capieaux, E.; Choder, M.; Goffeau, A.
    #journal      Yeast (1991) 7:287-299
    #title        The DNA sequencing of the 17 kb HindIII fragment spanning the
                    LEU1 and ATE1 loci on chromosome VII from Saccharomyces
                    cerevisiae reveals the PDR6 gene, a new member of the
                    genetic network controlling pleiotropic drug resistance.
    #cross-references MUID:91353083
    #accession    S31563
       ##molecule_type DNA
       ##residues      1-90 ##label CHE
```



```
       ##cross-references GB:S58126
       ##note          translation of nucleotide sequence not given
 GENETICS
    #map_position 7L
 SUMMARY          #length 90  #molecular-weight 10527  #checksum 7540
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.79
Residue Identity =    50%  Matches          =      3  Mismatches   =      3
Gaps             =      0  Conservative Substitutions               =      0

             X    X
             FXREXA
               || |
    MKNLLINYLLREEAEQLEMLFCSG
             10   X    20


4. US-08-121-713B-17 (1-6)
   HRIN         hemerythrin - sipunculid (Siphonosoma cumanense)

 ENTRY            HRIN       #type complete
 TITLE            hemerythrin - sipunculid (Siphonosoma cumanense)
 ORGANISM         #formal_name Siphonosoma cumanense
 DATE             30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                    30-Jun-1993
 ACCESSIONS       JT0556
 REFERENCE        JT0556
    #authors      Uchida, T.; Yano, H.; Satake, K.; Kubota, I.; Tsugita, A.
    #journal      Protein Seq. Data Anal. (1990) 3:141-147
    #title        The amino acid sequence of hemerythrin from Siphonosoma
                    cumanense.
    #cross-references MUID:90301732
    #accession    JT0556
       ##molecule_type protein
       ##residues      1-113 ##label UCH
       ##note          3-Glu, 10-Asp, 60-Gly, 66-Asn, and 83-Gln were also
                        found
 COMMENT     Hemerythrin is a respiratory protein found in several phyla of
               marine invertebrates. The functional molecule is a trimer
               composed of homologous chains, each of which contains a pair of
               nonheme iron atoms that reversibly bind molecular oxygen.
 CLASSIFICATION   #superfamily hemerythrin
 FEATURE
    25,54,58,73,77,101,
    106              #binding_site 2Fe-O cluster (His, His, Glu, His, His,
                       His, Asp) #status predicted
 SUMMARY          #length 113  #molecular-weight 12437  #checksum 1365
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.79
Residue Identity =    50%  Matches          =      3  Mismatches   =      3
Gaps             =      0  Conservative Substitutions               =      0

             X    X
             FXREXA
             |  | |
    DNAYACLVAHFLFEEAAMQVAKYGGY
        50   X   60        70
```

```
5. US-08-121-713B-17 (1-6)
   S13197       profilin - sea urchin (Clypeaster japonicus)

 ENTRY            S13197     #type complete
 TITLE            profilin - sea urchin (Clypeaster japonicus)
 ORGANISM         #formal_name Clypeaster japonicus
 DATE             02-Dec-1993; #sequence_revision 02-Dec-1993; #text_change
                    02-Dec-1993
 ACCESSIONS       S13197
 REFERENCE        S13197
    #authors      Takagi, T.; Mabuchi, I.; Hosoya, H.; Furuhashi, K.; Hatano,
                    S.
    #journal      Eur. J. Biochem. (1990) 192:777-781
    #title        Primary structure of profilins from two species of Echinoidea
                    and Physarum polycephalum.
    #cross-references MUID:91006174
    #accession    S13197
       ##status        preliminary
       ##residues      1-139 ##label TAK
 SUMMARY          #length 139  #molecular-weight 14540  #checksum 8410
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.79
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
             | ||
    GVHAEGLKYQFLREEDAKLVLAKKKG
            80     X  90


6. US-08-121-713B-17 (1-6)
   S13198       profilin - sea urchin (Anthocidaris crassispina)

 ENTRY            S13198     #type complete
 TITLE            profilin - sea urchin (Anthocidaris crassispina)
 ORGANISM         #formal_name Anthocidaris crassispina
 DATE             02-Dec-1993; #sequence_revision 02-Dec-1993; #text_change
                    02-Dec-1993
 ACCESSIONS       S13198
 REFERENCE        S13197
    #authors      Takagi, T.; Mabuchi, I.; Hosoya, H.; Furuhashi, K.; Hatano,
                    S.
    #journal      Eur. J. Biochem. (1990) 192:777-781
    #title        Primary structure of profilins from two species of Echinoidea
                    and Physarum polycephalum.
    #cross-references MUID:91006174
    #accession    S13198
       ##status        preliminary
       ##residues      1-139 ##label TAK
 SUMMARY          #length 139  #molecular-weight 14569  #checksum 895
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.79
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0
```



```
             X    X
             FXREXA
             | ||
    GIVADGTKYQFLREEDGKLVLAKKKG
            80     X  90


7. US-08-121-713B-17 (1-6)
   A44777       profilin spCoel1 - sea urchin (Strongylocentrotus

 ENTRY            A44777     #type complete
 TITLE            profilin spCoel1 - sea urchin (Strongylocentrotus purpuratus)
 ORGANISM         #formal_name Strongylocentrotus purpuratus #common_name
                    purple urchin
 DATE             03-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
                    30-Sep-1993
 ACCESSIONS       A44777
 REFERENCE        A44777
    #authors      Smith, L.C.; Britten, R.J.; Davidson, E.H.
    #journal      Mol. Biol. Cell (1992) 3:403-414
    #title        SpCoel1: a sea urchin profilin gene expressed specifically in
                    coelomocytes in response to injury.
    #accession    A44777
       ##status        preliminary
       ##molecule_type mRNA
       ##residues      1-142 ##label SMI
       ##cross-references GB:S42185
 SUMMARY          #length 142  #molecular-weight 15282  #checksum 3203
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.79
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
             | ||
    GIYVNGTKYQFLREEDSKLVLGKKKG
         80   X    90


8. US-08-121-713B-17 (1-6)
   S17791       aminoacyl-tRNA hydrolase (EC 3.1.1.29) - Escherich

 ENTRY            S17791     #type complete
 TITLE            aminoacyl-tRNA hydrolase (EC 3.1.1.29) - Escherichia coli
 ORGANISM         #formal_name Escherichia coli
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S17791
 REFERENCE        S17791
    #authors      Garcia-Villegas, M.R.; de la Vega, F.M.; Galindo, J.M.;
                    Segura, M.; Buckingham, R.H.; Guarneros, G.
    #journal      EMBO J. (1991) 10:3549-3555
    #title        Peptidyl-tRNA hydrolase is involved in lambda inhibition of
                    host protein synthesis.
    #cross-references MUID:92007806
    #accession    S17791
       ##status        preliminary
       ##residues      1-194 ##label GAR
```

```
      ##cross-references EMBL:X61941
 SUMMARY          #length 194  #molecular-weight 21082  #checksum 9661
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.79
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
               || |
    VDLLAERLRAPLREEAKFFGYTSRVT
     30        40  X     50


9. US-08-121-713B-17 (1-6)
   S16753       aminoacyl-tRNA hydrolase (EC 3.1.1.29) - Escherich

 ENTRY            S16753     #type complete
 TITLE            aminoacyl-tRNA hydrolase (EC 3.1.1.29) - Escherichia coli
 ORGANISM         #formal_name Escherichia coli
 DATE             21-Nov-1993; #sequence_revision 21-Nov-1993; #text_change
                    21-Nov-1993
 ACCESSIONS       S16753
 REFERENCE        S16753
    #authors      Garcia-Villegas, R.; de la Vega, X.Y.Z.; Galindo, J.M.;
                    Segura, E.; Buckingham, R.; Guarneros, G.
    #submission   submitted to the EMBL Data Library, August 1991
    #description  Peptidyl-tRNA Hydrolase is involved in lambda inhibition of
                    host Protein Synthesis.
    #accession    S16753
       ##status        preliminary
       ##residues      1-194 ##label GAR
       ##cross-references EMBL:X61941
 SUMMARY          #length 194  #molecular-weight 21050  #checksum 9670
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.79
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
               || |
    VDLLAERLRAPLREEAKFFGYTSRVT
     30        40  X     50


10. US-08-121-713B-17 (1-6)
    S05446       tropomyosin, nonmuscle - Japanese quail (fragment)

 ENTRY            S05446     #type fragment
 TITLE            tropomyosin, nonmuscle - Japanese quail (fragment)
 ORGANISM         #formal_name Coturnix coturnix japonica #common_name Japanese
                    quail
 DATE             07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
                    28-Oct-1994
 ACCESSIONS       S05446
 REFERENCE        S05444
    #authors      Lindquester, G.J.; Flach, J.E.; Fleenor, D.E.; Hickman, K.H.;
```



```
                  Devlin, R.B.
    #journal      Nucleic Acids Res. (1989) 17:2099-2118
    #title        Avian tropomyosin gene expression.
    #cross-references MUID:89183613
    #accession    S05446
       ##molecule_type DNA
       ##residues      1-221 ##label LIN
       ##cross-references EMBL:X16231
       ##note          the authors translated the codon TCC for residue 51 as
                        Ala and GAG for residue 187 as Asp
 GENETICS
    #introns      44/3; 89/2; 128/3; 152/2; 177/3; 198/3
 KEYWORDS         alternative splicing
 SUMMARY          #length 221  #checksum 4781
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.79
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
               || |
    RLQREVDQERALREEAESEVASLNRR
   30        40    X   50
> O <
O| |O  IntelliGenetics
> O <

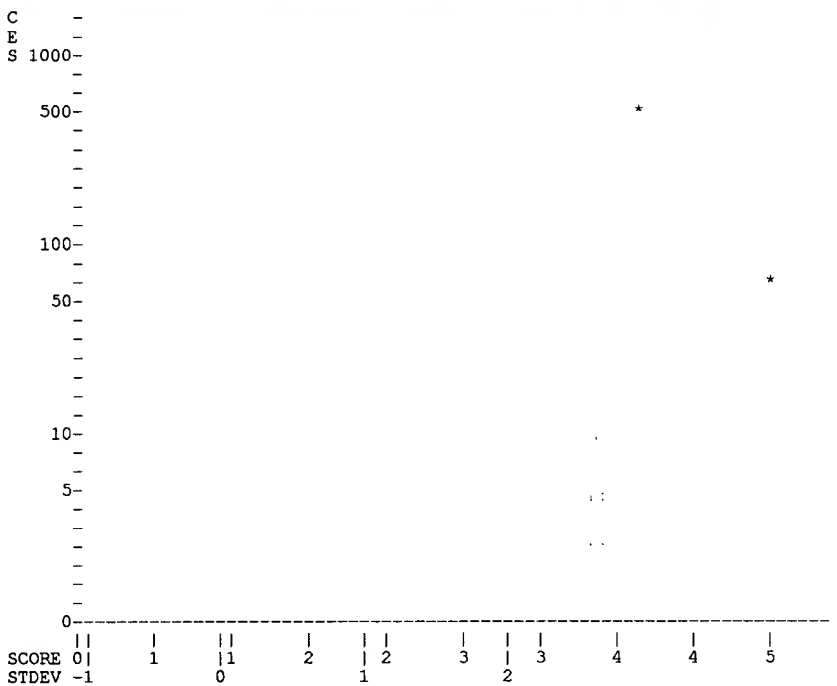
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq17spt.res made by  on Fri 19 May 95 8:57:53-PDT.


Query sequence being compared:US-08-121-713B-17 (1-6)
Number of sequences searched:                 43470
Number of scores above cutoff:                 4182

     Results of the initial comparison of US-08-121-713B-17 (1-6) with:
   Data bank : Swiss-Prot 31, all entries

100000-
      -
N     -
U50000-
M     -
B     -
E     -                                          *
R     -
      -                        *
O     -
F10000-
      -
S     -
E 5000-
Q     *
U     -
E     -
N     -
```



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	4	0.89

Times:	CPU	Total Elapsed
	00:00:44.06	00:00:46.00

Number of residues: 15335248
Number of sequences searched: 43470

Number of scores above cutoff: 4182

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 3 standard deviations above mean ****					
1. META_SALTY	HOMOSERINE O-SUCCINYLTRANSFER	69	5	5	3.38	0
2. HEMT_SIPCU	HEMERYTHRIN.	113	5	5	3.38	0
3. PROF_CLYJA	PROFILIN.	139	5	5	3.38	0
4. PROF_ANTCR	PROFILIN.	139	5	5	3.38	0
5. PRO1_STRPU	PROFILIN.	141	5	5	3.38	0
6. ATPF_THIFE	ATP SYNTHASE B CHAIN (EC 3.6.	159	5	5	3.38	0
7. PTH_ECOLI	PEPTIDYL-TRNA HYDROLASE (EC 3	194	5	5	3.38	0
8. TRJ4_ECOLI	TRAJ PROTEIN.	223	5	5	3.38	0
9. TPMM_LOCMI	TROPOMYOSIN, MUSCLE.	283	5	5	3.38	0
10. TPM2_DROME	TROPOMYOSIN II, MUSCLE ISOFOR	285	5	5	3.38	0
11. META_ECOLI	HOMOSERINE O-SUCCINYLTRANSFER	309	5	5	3.38	0
12. STRN_STRGR	STRN PROTEIN.	319	5	5	3.38	0
13. I12B_HUMAN	INTERLEUKIN-12 BETA CHAIN PRE	328	5	5	3.38	0
14. YHA9_YEAST	HYPOTHETICAL 38.0 KD PROTEIN	330	5	5	3.38	0
15. BCHX_RHOCA	CHLOROPHYLLIDE REDUCTASE 35.5	333	5	5	3.38	0
16. HRPN_BURSO	HYPERSENSITIVITY RESPONSE SEC	357	5	5	3.38	0
17. G2LF_HUMAN	GALACTOSIDE 2-L-FUCOSYLTRANSF	365	5	5	3.38	0
18. IDH_ECOLI	ISOCITRATE DEHYDROGENASE (NAD	416	5	5	3.38	0
19. DESM_MESAU	DESMIN.	468	5	5	3.38	0
20. TCMO_HELTU	TRANS-CINNAMATE 4-MONOOXYGENA	505	5	5	3.38	0
21. TRPE_BACCA	ANTHRANILATE SYNTHASE COMPONE	508	5	5	3.38	0
22. IMP_BACSU	INOSINE-5'-MONOPHOSPHATE DEHY	513	5	5	3.38	0
23. RA74_HUMAN	TRANSCRIPTION FACTOR IIF, ALP	517	5	5	3.38	0
24. CIK3_HUMAN	POTASSIUM CHANNEL PROTEIN KV1	523	5	5	3.38	0
25. CIK3_RAT	POTASSIUM CHANNEL PROTEIN KV1	525	5	5	3.38	0
26. VG01_VACCV	PROTEIN G1 (FRAGMENT).	530	5	5	3.38	0
27. CIK3_MOUSE	POTASSIUM CHANNEL PROTEIN KV1	530	5	5	3.38	0
28. PA11_YEAST	PAC11 PROTEIN.	533	5	5	3.38	0
29. MPI1_XENLA	M-PHASE INDUCER PHOSPHATASE 1	550	5	5	3.38	0
30. MPI0_XENLA	M-PHASE INDUCER PHOSPHATASE 1	550	5	5	3.38	0
31. RAD7_YEAST	DNA REPAIR PROTEIN RAD7.	565	5	5	3.38	0
32. VG01_VARV	PROTEIN G1.	591	5	5	3.38	0
33. VG01_VACCC	PROTEIN G1.	591	5	5	3.38	0
34. MPI2_XENLA	M-PHASE INDUCER PHOSPHATASE 2	599	5	5	3.38	0
35. NOF1_DROME	71 KD PROTEIN IN NOF-FB TRANS	633	5	5	3.38	0
36. EFG_THEMA	ELONGATION FACTOR G (EF-G).	682	5	5	3.38	0
37. FLBF_CAUCR	FLAGELLAR PROTEIN FLBF.	700	5	5	3.38	0
38. RRP2_INCJJ	RNA-DIRECTED RNA POLYMERASE S	709	5	5	3.38	0
39. VCA1_RAT	VASCULAR CELL ADHESION PROTEI	739	5	5	3.38	0
40. RIR1_EBV	RIBONUCLEOSIDE-DIPHOSPHATE RE	826	5	5	3.38	0
41. SRCA_RABIT	SARCALUMENIN PRECURSOR.	908	5	5	3.38	0
42. KTOR_DROME	TYROSINE-PROTEIN KINASE RECEP	923	5	5	3.38	0

```
  43. ODO1_AZOVI   2-OXOGLUTARATE DEHYDROGENASE      943      5      5   3.38   0
  44. NOF_DROME    112 KD PROTEIN IN NOF-FB TRAN     984      5      5   3.38   0
  45. ITAB_HUMAN   PLATELET MEMBRANE GLYCOPROTEI    1039      5      5   3.38   0


1. US-08-121-713B-17 (1-6)
   META_SALTY   HOMOSERINE O-SUCCINYLTRANSFERASE (EC 2.3.1.46) (HO

 ID   META_SALTY     STANDARD;      PRT;     69 AA.
 AC   P37413;
 DT   01-OCT-1994 (REL. 30, CREATED)
 DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE   HOMOSERINE O-SUCCINYLTRANSFERASE (EC 2.3.1.46) (HOMOSERINE O-
 DE   TRANSSUCCINYLASE) (FRAGMENT).
 GN   META.
 OS   SALMONELLA TYPHIMURIUM.
 OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC   ENTEROBACTERIACEAE.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RM   92105004
 RA   MARES R., URBANOWSKI M.L., STAUFFER G.V.;
 RL   J. BACTERIOL. 174:390-397(1992).
 CC   -!- CATALYTIC ACTIVITY: SUCCINYL-COA + L-HOMOSERINE = COA +
 CC       O-SUCCINYL-L-HOMOSERINE.
 CC   -!- PATHWAY: FIRST ENZYME AND ONE OF THE KEY ENZYMES OF METHIONINE
 CC       BIOSYNTHESIS PATHWAY.
 DR   EMBL; M74188; STMETA.
 DR   PIR; A41960; A41960.
 DR   STYGENE; SG10222; META.
 KW   METHIONINE BIOSYNTHESIS; TRANSFERASE; ACYLTRANSFERASE.
 FT   NON_TER       69     69
 SQ   SEQUENCE   69 AA;  7976 MW;  24970 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            FXREXA
            | ||
    RVLDELPAVNFLREENVFDMTTSRAS
        10  X    20


2. US-08-121-713B-17 (1-6)
   HEMT_SIPCU   HEMERYTHRIN.

 ID   HEMT_SIPCU     STANDARD;      PRT;   113 AA.
 AC   P22766;
 DT   01-AUG-1991 (REL. 19, CREATED)
 DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT   01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
 DE   HEMERYTHRIN.
 OS   SIPHONOSOMA CUMANENSE.
 OC   EUKARYOTA; METAZOA; SIPUNCULA; SIPUNCULIDAE.
 RN   [1]
 RP   SEQUENCE.
 RM   90301732
```



```
 RA   UCHIDA T., YANO H., SATAKE K., KUBOTA I., TSUGITA A.;
 RL   PROTEIN SEQ. DATA ANAL. 3:141-147(1990).
 CC   -!- FUNCTION: HEMERYTHRIN IS A RESPIRATORY PROTEIN IN BLOOD CELLS OF
 CC       CERTAIN MARINE WORMS. THE OXYGEN-BINDING SITE IN EACH CHAIN
 CC       CONTAINS TWO IRON ATOMS.
 CC   -!- SUBUNIT: HOMOTRIMER.
 CC   -!- SIMILARITY: TO OTHER HEMERYTHRINS AND TO MYOHEMERYTHRINS.
 DR   PIR; JT0556; HRIN.
 DR   HSSP; P02246; 2HMQ.
 DR   PROSITE; PS00550; HEMERYTHRINS.
 KW   OXYGEN TRANSPORT; METAL-BINDING; IRON.
 FT   METAL        25     25       IRON 1 (BY SIMILARITY).
 FT   METAL        54     54       IRON 1 (BY SIMILARITY).
 FT   METAL        58     58       IRON 1 AND 2 (BY SIMILARITY).
 FT   METAL        73     73       IRON 2 (BY SIMILARITY).
 FT   METAL        77     77       IRON 2 (BY SIMILARITY).
 FT   METAL       101    101       IRON 2 (BY SIMILARITY).
 FT   METAL       106    106       IRON 1 AND 2 (BY SIMILARITY).
 FT   VARIANT       3      3       P -> E.
 FT   VARIANT      10     10       W -> D.
 FT   VARIANT      60     60       A -> G.
 FT   VARIANT      66     66       K -> N.
 FT   VARIANT      83     83       K -> Q.
 SQ   SEQUENCE   113 AA;  12437 MW;  61673 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            FXREXA
            | | |
    DNAYACLVAHFLFEEAAMQVAKYGGY
        50  X   60        70


3. US-08-121-713B-17 (1-6)
   PROF_CLYJA   PROFILIN.

 ID   PROF_CLYJA     STANDARD;      PRT;   139 AA.
 AC   P18321;
 DT   01-NOV-1990 (REL. 16, CREATED)
 DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT   01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE   PROFILIN.
 OS   CLYPEASTER JAPONICUS (SAND DOLLAR).
 OC   EUKARYOTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA;
 OC   EUECHINOIDEA.
 RN   [1]
 RP   SEQUENCE.
 RM   91006174
 RA   TAKAGI T., MABUCHI I., HOSOYA H., FURUHASHI K., HATANO S.;
 RL   EUR. J. BIOCHEM. 192:777-781(1990).
 CC   -!- FUNCTION: PROFILIN PREVENTS THE POLYMERIZATION OF ACTIN.
 CC   -!- OCCURS IN MANY KINDS OF CELLS AS A COMPLEX WITH MONOMERIC ACTIN
 CC       IN A 1:1 RATIO.
 DR   PIR; S13197; S13197.
 DR   HSSP; P07763; 1ACF.
 DR   PROSITE; PS00414; PROFILIN.
 KW   ACTIN-BINDING; ACETYLATION.
```

```
 FT   MOD_RES       1       1       ACETYLATION.
 SQ   SEQUENCE   139 AA;  14540 MW;  92443 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
             | ||
    GVHAEGLKYQFLREEDAKLVLAKKKG
           80     X  90
```

4. US-08-121-713B-17 (1-6)
   PROF_ANTCR   PROFILIN.

```
 ID   PROF_ANTCR     STANDARD;      PRT;   139 AA.
 AC   P18320;
 DT   01-NOV-1990 (REL. 16, CREATED)
 DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT   01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE   PROFILIN.
 OS   ANTHOCIDARIS CRASSISPINA (SEA URCHIN).
 OC   EUKARYOTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA;
 OC   PERISCHOECHINOIDEA.
 RN   [1]
 RP   SEQUENCE.
 RM   91006174
 RA   TAKAGI T., MABUCHI I., HOSOYA H., FURUHASHI K., HATANO S.;
 RL   EUR. J. BIOCHEM. 192:777-781(1990).
 CC   -!- FUNCTION: PROFILIN PREVENTS THE POLYMERIZATION OF ACTIN.
 CC   -!- OCCURS IN MANY KINDS OF CELLS AS A COMPLEX WITH MONOMERIC ACTIN
 CC       IN A 1:1 RATIO.
 DR   PIR; S13198; S13198.
 DR   HSSP; P07763; 2ACG.
 DR   PROSITE; PS00414; PROFILIN.
 KW   ACTIN-BINDING; ACETYLATION.
 FT   MOD_RES       1       1       ACETYLATION.
 SQ   SEQUENCE   139 AA;  14569 MW;  95847 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
             | ||
    GIVADGTKYQFLREEDGKLVLAKKKG
           80     X  90
```

5. US-08-121-713B-17 (1-6)
   PRO1_STRPU   PROFILIN.

```
 ID   PRO1_STRPU     STANDARD;      PRT;   141 AA.
 AC   P32006;
 DT   01-JUL-1993 (REL. 26, CREATED)
 DT   01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
 DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
```



```
 DE   PROFILIN.
 GN   SPCOEL1.
 OS   STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).
 OC   EUKARYOTA; METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA;
 OC   EUECHINOIDEA.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RM   92360908
 RA   SMITH L.C., BRITTEN R.J., DAVIDSON E.H.;
 RL   MOL. BIOL. CELL 3:403-414(1992).
 CC   -!- FUNCTION: PROFILIN PREVENTS THE POLYMERIZATION OF ACTIN.
 CC   -!- OCCURS IN MANY KINDS OF CELLS AS A COMPLEX WITH MONOMERIC ACTIN
 CC       IN A 1:1 RATIO.
 CC   -!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN COELOMOCYTES IN
 CC       RESPONSE TO INJURY.
 DR   EMBL; S42185; S42185.
 DR   PIR; A44777; A44777.
 DR   HSSP; P07763; 2ACG.
 DR   PROSITE; PS00414; PROFILIN.
 KW   ACTIN-BINDING.
 FT   INIT_MET      0       0       BY SIMILARITY.
 SQ   SEQUENCE   141 AA;  15151 MW;  104928 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
             | ||
    GIYVNGTKYQFLREEDSKLVLGKKKG
           80  X     90
```

6. US-08-121-713B-17 (1-6)
   ATPF_THIFE   ATP SYNTHASE B CHAIN (EC 3.6.1.34).

```
 ID   ATPF_THIFE     STANDARD;      PRT;   159 AA.
 AC   P41172;
 DT   01-FEB-1995 (REL. 31, CREATED)
 DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE   ATP SYNTHASE B CHAIN (EC 3.6.1.34).
 GN   ATPF.
 OS   THIOBACILLUS FERROOXIDANS.
 OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC CHEMOLITHOTROPHIC;
 OC   SULFUR METABOLIZING.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=ATCC 33020;
 RM   95047244
 RA   BROWN L.D., DENNEHY M.E., RAWLINGS D.E.;
 RL   FEMS MICROBIOL. LETT. 122:19-26(1994).
 CC   -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC       CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC       SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC       HAS THREE MAIN SUBUNITS: A, B AND C.
 CC   -!- SIMILARITY: TO OTHER B SUBUNITS AND ALSO TO B' SUBUNITS.
 DR   EMBL; M81087; TFUNCAH.
 KW   HYDROGEN ION TRANSPORT; TRANSMEMBRANE; CF(0).
```

```
 SQ   SEQUENCE   159 AA;  17884 MW;  100442 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
               || |
    IIANAERRGVELREEAQGKAREEADR
     80        90  X    100
```

7. US-08-121-713B-17 (1-6)
   PTH_ECOLI PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29) (PTH).

```
 ID   PTH_ECOLI      STANDARD;      PRT;   194 AA.
 AC   P23932;
 DT   01-MAR-1992 (REL. 21, CREATED)
 DT   01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE   PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29) (PTH).
 GN   PTH.
 OS   ESCHERICHIA COLI.
 OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC   ENTEROBACTERIACEAE.
 RN   [1]
 RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-17.
 RC   STRAIN=K12;
 RM   92007806
 RA   GARCIA-VILLEGAS M.R., DE LA VEGA F.M., GALINDO J.M., SEGURA M.,
 RA   BUCKINGHAM R.H., GUARNEROS G.;
 RL   EMBO J. 10:3549-3555(1991).
 CC   -!- FUNCTION: THE NATURAL SUBSTRATE FOR THIS ENZYME MAY BE PEPTIDYL-
 CC       TRNAS WHICH DROP OFF THE RIBOSOME DURING PROTEIN SYNTHESIS.
 CC       INVOLVED IN LAMBDA INHIBITION OF HOST PROTEIN SYNTHESIS. PTH
 CC       ACTIVITY MAY, DIRECTLY OR INDIRECTLY, BE THE TARGET FOR LAMBDA
 CC       BAR RNA LEADING TO RAP CELL DEATH.
 CC   -!- CATALYTIC ACTIVITY: N-SUBSTITUTED AMINOACYL-TRNA + H(2)O =
 CC       N-SUBSTITUTED AMINO ACID + TRNA.
 CC   -!- SUBUNIT: MONOMER.
 DR   EMBL; X61941; ECPTHG.
 DR   PIR; S17791; S17791.
 DR   PIR; S16753; S16753.
 DR   ECOGENE; EG10785; PTH.
 KW   HYDROLASE.
 FT   MUTAGEN     101    101       G->D: PTH(TS) MUTANTS SYNTHESIZE
 FT                                THERMOSENSITIVE PTH AND DIE AT 42 DEGREES
 FT                                FROM A DEFECT IN PROTEIN SYNTHESIS.
 FT   MUTAGEN     134    134       R->H: RAP MUTANTS DO NOT SUPPORT
 FT                                VEGETATIVE GROWTH OF BACTERIOPHAGE LAMBDA
 FT                                AND DIE UPON TRANSCRIPTION OF LAMBDA DNA
 FT                                BAR SITES.
 SQ   SEQUENCE   194 AA;  21082 MW;  179056 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
```



```
             FXREXA
               || |
    VDLLAERLRAPLREEAKFFGYTSRVT
     30        40  X     50
```

8. US-08-121-713B-17 (1-6)
   TRJ4_ECOLI TRAJ PROTEIN.

```
 ID   TRJ4_ECOLI     STANDARD;      PRT;   223 AA.
 AC   P13972;
 DT   01-JAN-1990 (REL. 13, CREATED)
 DT   01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE   TRAJ PROTEIN.
 GN   TRAJ.
 OS   ESCHERICHIA COLI.
 OG   PLASMID R100.
 OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC   ENTEROBACTERIACEAE.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RM   88227859
 RA   INAMOTO S., YOSHIOKA Y., OHTSUBO E.;
 RL   J. BACTERIOL. 170:2749-2757(1988).
 CC   -!- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR POSITIVELY REGULATING THE
 CC       EXPRESSION OF TRANSFER GENES THAT ARE INVOLVED IN THE CONJUGAL
 CC       TRANSFER OF DNA BETWEEN BACTERIAL CELLS.
 CC   -!- SUBCELLULAR LOCATION: OUTER MEMBRANE.
 DR   EMBL; M20941; PRTRAJY.
 KW   OUTER MEMBRANE; CONJUGATION; TRANSCRIPTION REGULATION; ACTIVATOR;
 KW   PLASMID.
 SQ   SEQUENCE   223 AA;  25943 MW;  272537 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X    X
             FXREXA
             | ||
    YSLPVQVATSFLREELDAMSLPSSMN
          70     X  80
```

9. US-08-121-713B-17 (1-6)
   TPMM_LOCMI TROPOMYOSIN, MUSCLE.

```
 ID   TPMM_LOCMI     STANDARD;      PRT;   283 AA.
 AC   P31816;
 DT   01-JUL-1993 (REL. 26, CREATED)
 DT   01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
 DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
 DE   TROPOMYOSIN, MUSCLE.
 OS   LOCUSTA MIGRATORIA (MIGRATORY LOCUST).
 OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; ORTHOPTERA.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RA   KRIEGER J., RAMING K., KNIPPER M., GRAU M., MERTENS S., BREER H.;
 RL   INSECT BIOCHEM. 20:173-184(1990).
```

```
CC   -!- FUNCTION: TROPOMYOSIN, IN ASSOCIATION WITH THE TROPONIN COMPLEX,
CC       PLAYS A CENTRAL ROLE IN THE CALCIUM DEPENDENT REGULATION OF
CC       MUSCLE CONTRACTION.
CC   -!- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE
CC       EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
DR   PIR; A60364; A60364.
DR   PROSITE; PS00325; COFILIN_TROPOMYOSIN.
DR   PROSITE; PS00326; TROPOMYOSIN.
KW   MUSCLE PROTEIN; COILED COIL; REPEAT.
SQ   SEQUENCE   283 AA;  32439 MW;  334140 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            FXREXA
            |  | |
   ALENQLKEARFLAEEADKKYDEVARK
        150  X    160
```

10. US-08-121-713B-17 (1-6)
    TPM2_DROME TROPOMYOSIN II, MUSCLE ISOFORM.

```
ID   TPM2_DROME     STANDARD;      PRT;   285 AA.
AC   P06754;
DT   01-JAN-1988 (REL. 06, CREATED)
DT   01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   TROPOMYOSIN II, MUSCLE ISOFORM.
GN   TM2.
OS   DROSOPHILA MELANOGASTER (FRUIT FLY).
OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   87106815
RA   HANKE P.D., STORTI R.V.;
RL   GENE 45:211-214(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RM   87064486
RA   KARLIK C.C., FYRBERG E.A.;
RL   MOL. CELL. BIOL. 6:1965-1973(1986).
CC   -!- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE
CC       EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
CC   -!- ALTERNATIVE PRODUCTS: DROSOPHILA TROPOMYOSIN II GENE CAN PRODUCE
CC       FOUR DIFFERENT ISOFORMS BY ALTERNATIVE PRODUCTS: A MUSCLE FORM,
CC       A NON-MUSCLE FORM, AND TWO FUSION PROTEINS (33 AND 34) .
DR   EMBL; M15466; DMTROPII.
DR   EMBL; M12840; DMTRO01.
DR   EMBL; L00355; DMTRO02.
DR   EMBL; L00356; DMTRO03.
DR   EMBL; L00357; DMTRO04.
DR   EMBL; L00358; DMTRO05.
DR   EMBL; L00359; DMTRO06.
DR   EMBL; L00360; DMTRO07.
DR   EMBL; L00362; DMTRO09.
DR   EMBL; M13023; DMTRO13.
DR   PIR; A25561; A25561.
```



```
DR   FLYBASE; FBGN0004117; TM2.
DR   PROSITE; PS00325; COFILIN_TROPOMYOSIN.
DR   PROSITE; PS00326; TROPOMYOSIN.
KW   MUSCLE PROTEIN; COILED COIL; REPEAT; ALTERNATIVE SPLICING;
KW   MULTIGENE FAMILY.
FT   CONFLICT    106    114       LGSATAKLS -> SASAIQLAA (IN REF. 2).
FT   CONFLICT    214    214       S -> A (IN REF. 2).
SQ   SEQUENCE   285 AA;  32761 MW;  339904 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

            X    X
            FXREXA
            |  | |
   ALENQLKEARFLAEEADKKYDEVARK
        150  X    160
```

11. US-08-121-713B-17 (1-6)
    META_ECOLI HOMOSERINE O-SUCCINYLTRANSFERASE (EC 2.3.1.46) (HO

```
ID   META_ECOLI     STANDARD;      PRT;   309 AA.
AC   P07623;
DT   01-APR-1988 (REL. 07, CREATED)
DT   01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT   01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE   HOMOSERINE O-SUCCINYLTRANSFERASE (EC 2.3.1.46) (HOMOSERINE O-
DE   TRANSSUCCINYLASE).
GN   META.
OS   ESCHERICHIA COLI.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   ENTEROBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RM   89240044
RA   COZZONE A.J.;
RL   NUCLEIC ACIDS RES. 17:2856-2856(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RM   94089392
RA   BLATTNER F.R., BURLAND V.D., PLUNKETT G. III, SOFIA H.J.,
RA   DANIELS D.L.;
RL   NUCLEIC ACIDS RES. 21:5408-5417(1993).
RN   [3]
RP   SEQUENCE OF 1-69 FROM N.A.
RC   STRAIN=K12;
RM   85054633
RA   MICHAELI S., MEVARECH M., RON E.Z.;
RL   J. BACTERIOL. 160:1158-1162(1984).
CC   -!- CATALYTIC ACTIVITY: SUCCINYL-COA + L-HOMOSERINE = COA +
CC       O-SUCCINYL-L-HOMOSERINE.
CC   -!- PATHWAY: FIRST ENZYME AND ONE OF THE KEY ENZYMES OF METHIONINE
CC       BIOSYNTHESIS PATHWAY.
DR   EMBL; M10210; ECMETA.
DR   EMBL; X14501; ECMETAG.
DR   EMBL; U00006; ECUW89.
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```
 DR   PIR; A05053; XYECM.
 DR   ECOGENE; EG10581; META.
 KW   METHIONINE BIOSYNTHESIS; TRANSFERASE; ACYLTRANSFERASE.
 FT   CONFLICT     67     67       V -> I (IN REF. 2).
 SQ   SEQUENCE   309 AA;  35713 MW;  488047 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions              =     0

             X    X
             FXREXA
             | ||
    RVPDELPAVNFLREENVFVMTTSRAS
        10   X    20


12. US-08-121-713B-17 (1-6)
    STRN_STRGR   STRN PROTEIN.

 ID   STRN_STRGR     STANDARD;      PRT;   319 AA.
 AC   P29784;
 DT   01-APR-1993 (REL. 25, CREATED)
 DT   01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT   01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
 DE   STRN PROTEIN.
 GN   STRN.
 OS   STREPTOMYCES GRISEUS.
 OC   PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=N2-3-11;
 RM   92092953
 RA   PISSOWOTZKI K., MANSOURI K., PIEPERSBERG W.;
 RL   MOL. GEN. GENET. 231:113-123(1991).
 CC   -!- PATHWAY: STREPTOMYCIN BIOSYNTHESIS.
 CC   -!- SIMILARITY: CONTAINS SEQUENCE MOTIFS ALSO CONSERVED IN THE
 CC       PUTATIVE CATALYTIC AND/OR SUBSTRATE RECOGNITION DOMAINS OF
 CC       AMINOGLYCOSIDE PHOSPHOTRANSFERASES AND EUKARYOTIC PROTEIN
 CC       KINASES.
 DR   EMBL; X62567; SGSTRELMB.
 DR   PIR; S18621; BWSMNG.
 KW   STREPTOMYCIN BIOSYNTHESIS.
 SQ   SEQUENCE   319 AA;  35679 MW;  470485 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions              =     0

             X    X
             FXREXA
              || |
    RVDRCQGFLAELREEATRVAGECAAR
    190      200  X    210


13. US-08-121-713B-17 (1-6)
    I12B_HUMAN   INTERLEUKIN-12 BETA CHAIN PRECURSOR (IL-12B) (CYTO

 ID   I12B_HUMAN     STANDARD;      PRT;   328 AA.
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 AC   P29460;
 DT   01-APR-1993 (REL. 25, CREATED)
 DT   01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE   INTERLEUKIN-12 BETA CHAIN PRECURSOR (IL-12B) (CYTOTOXIC LYMPHOCYTE
 DE   MATURATION FACTOR 40 KD SUBUNIT) (CLMF P40) (NK CELL STIMULATORY
 DE   FACTOR CHAIN 2) (NKSF2).
 GN   IL12B OR NKSF2.
 OS   HOMO SAPIENS (HUMAN).
 OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC   EUTHERIA; PRIMATES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RM   91239523
 RA   GUBLER U., CHUA A.O., SCHOENHAUT D.S., DWYER C.M., MCCOMAS W.,
 RA   MOTYKA R., NABAVI N., WOLITZKY A.G., QUINN P.M., FAMILLETTI P.C.,
 RA   GATELY M.K.;
 RL   PROC. NATL. ACAD. SCI. U.S.A. 88:4143-4147(1991).
 RN   [2]
 RP   SEQUENCE FROM N.A.
 RM   91201875
 RA   WOLF S.F., TEMPLE P.A., KOBAYASHI M., YOUNG D., DICIG M., LOWE L.,
 RA   DZIALO R., FITZ L., FERENZ C., HEWICK R.M., KELLEHER K.,
 RA   HERRMANN S.H., CLARK S.C., AZZONI L., CHAN S.H., TRINCHIERI G.,
 RA   PERUSSIA B.;
 RL   J. IMMUNOL. 146:3074-3081(1991).
 RN   [3]
 RP   SEQUENCE OF 23-45.
 RM   90370873
 RA   STERN A.S., PODLASKI F.J., HULMES J.D., PAN Y.C.E., QUINN P.M.,
 RA   WOLITZKY A.G., FAMILLETTI P.C., STREMLO D.L., TRUITT T.,
 RA   CHIZZONITE R., GATELY M.K.;
 RL   PROC. NATL. ACAD. SCI. U.S.A. 87:6808-6812(1990).
 RN   [4]
 RP   SIMILARITY TO IL-6 RECEPTOR.
 RM   91300556
 RA   GEARING D.P., COSMAN D.;
 RL   CELL 66:9-10(1991).
 CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED
 CC       T AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
 CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
 CC       BY RESTING PBMC.
 CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 KD AND 35 KD SUBUNITS.
 CC       NKSF IS ESSENTIALLY A COMPLEX OF CYTOKINE AND SOLUBLE RECEPTOR.
 CC   -!- SUBCELLULAR LOCATION: SECRETED.
 CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC       ONE IG-LIKE DOMAIN.
 CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR   EMBL; M65272; HSCLMF40.
 DR   EMBL; M65290; HSNKSFP40.
 DR   PIR; B39359; B39359.
 DR   PIR; B36055; B36055.
 DR   MIM; 161561; 11TH EDITION.
 DR   PROSITE; PS00241; RECEPTOR_CYTOKINES_1.
 DR   PROSITE; PS00340; RECEPTOR_CYTOKINES_2.
 KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL.
 FT   SIGNAL       1     22
 FT   CHAIN       23    328       INTERLEUKIN-12 BETA CHAIN.
 FT   DOMAIN      23    260       EXTRACELLULAR (POTENTIAL).
 FT   TRANSMEM   261    279       POTENTIAL.
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FT   DOMAIN       280     328       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        43      97       IG-LIKE DOMAIN (BY SIMILARITY).
FT   DISULFID      50      90       POTENTIAL.
FT   CARBOHYD     135     135       POTENTIAL.
FT   CARBOHYD     222     222
FT   CARBOHYD     303     303       POTENTIAL.
FT   CONFLICT     239     239       K -> N (IN REF. 2).
SQ   SEQUENCE   328 AA;  37169 MW;  606556 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions              =     0

             X    X
             FXREXA
             | |  |
   KDQKEPKNKTFLRCEAKNYSGRFTCW
   120       130  X    140
```

14. US-08-121-713B-17 (1-6)
    YHA9_YEAST HYPOTHETICAL 38.0 KD PROTEIN IN PRPS4-STE20 INTERG

```
ID   YHA9_YEAST     STANDARD;      PRT;   330 AA.
AC   P38749;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 38.0 KD PROTEIN IN PRPS4-STE20 INTERGENIC REGION.
GN   YHL009C.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RM   94378003
RA   JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
RA   DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,
RA   KUCABA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,
RA   LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER L.,
RA   NHAN M., RIFKIN L., RILES L., ST.PETER H., TREVASKIS E., VAUGHAN K.,
RA   VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
RA   VAUDIN M.;
RL   SCIENCE 265:2077-2082(1994).
CC   -!- SIMILARITY: SOME, TO BZIP PROTEINS.
DR   EMBL; U11581; SCHL5018.
DR   PIR; S46819; S46819.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   330 AA;  37955 MW;  539642 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions              =     0

             X    X
             FXREXA
             |  | |
   GPAYPRSLIDFLVEEATLNE
          320     X 330
```


15. US-08-121-713B-17 (1-6)
    BCHX_RHOCA CHLOROPHYLLIDE REDUCTASE 35.5 KD CHAIN (EC 1.3.1.-

```
ID   BCHX_RHOCA     STANDARD;      PRT;   333 AA.
AC   P26177;
DT   01-MAY-1992 (REL. 22, CREATED)
DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   CHLOROPHYLLIDE REDUCTASE 35.5 KD CHAIN (EC 1.3.1.-) (CHLORIN
DE   REDUCTASE).
GN   BCHX.
OS   RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).
OC   PROKARYOTA; GRACILICUTES; ANOXYPHOTOBACTERIA; PURPLE BACTERIA;
OC   RHODOSPIRILLACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SB1003;
RM   93224464
RA   BURKE D.H., ALBERTI M., HEARST J.E.;
RL   J. BACTERIOL. 175:2407-2413(1993).
CC   -!- FUNCTION: CONVERTS CHLOROPHYLLS (CHL) INTO BACTERIOCHLOROPHYLLS
CC       (BCHL) BY REDUCING RING B OF THE TETRAPYRROLE.
CC   -!- PATHWAY: BACTERIOCHLOROPHYLL BIOSYNTHESIS.
CC   -!- SIMILARITY: BELONGS TO THE NIFH/FRXC FAMILY.
DR   EMBL; Z11165; RCPHSYNG.
DR   PIR; S17823; S17823.
DR   PIR; B49850; B49850.
DR   HSSP; P00459; 1NIP.
DR   PROSITE; PS00692; NIFH_FRXC_2.
DR   PROSITE; PS00746; NIFH_FRXC_1.
KW   PHOTOSYNTHESIS; CHLOROPHYLL BIOSYNTHESIS; ATP-BINDING; IRON-SULFUR;
KW   4FE-4S.
FT   NP_BIND      42     49       ATP (POTENTIAL).
FT   METAL       130    130       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       165    165       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ   SEQUENCE   333 AA;  35573 MW;  536770 CN;

Initial Score    =      5  Optimized Score  =      5  Significance =  3.38
Residue Identity =    50%  Matches          =      3  Mismatches   =     3
Gaps             =      0  Conservative Substitutions              =     0

             X    X
             FXREXA
               || |
   DAPNLKGFDARLREEAAEEPTLEIPE
        10  X     20
```

maryh@stic **stdin**

NeWSprinter20

Fri May 19 10:57:16 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

Sala 121713

SEQ 22

```
> O <
O|  |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq22asq.res made by  on Fri 19 May 95 8:41:38-PDT.


Query sequence being compared:US-08-121-713B-22 (1-7)
Number of sequences searched:                53402
Number of scores above cutoff:                4031

     Results of the initial comparison of US-08-121-713B-22 (1-7) with:
   Data bank : A-GeneSeq 18, all entries

100000-
      -
N     -
U50000-
M     *
B     -
E     -
R     -                        *
      -
O     -
F10000-
      -
S     -
E 5000-
Q     -
U     -
E     -
N     -                                                  *
C     -
E     -
S 1000-
      -
      -
   500-                              *
      -
      -
      -
      -
      -
      -
   100-
      -
      -
    50-
      -
      -
      -
      -
      -
      -
      -
    10-
      -
      -
```



```
     5-
      -
      -
      -
      -
      -
      -
     0-----------------------------------------------------------------------
      ||     |  |   |     |     |     |     |  |  |     |     |
SCORE 0|     1  |   2     2     3     4     5  |  5     6     7
STDEV  0        1                 2           3
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	1	1.78

Times:	CPU	Total Elapsed
	00:00:32.97	00:00:33.00

Number of residues: 6354270
Number of sequences searched: 53402
Number of scores above cutoff: 4031

Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

1761 100% similar sequences to the query sequence were found:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1.	R44929	T. niveum Cyclosporin synthet	15281	7	7	3.37	0
2.	R11510	Ryanodine receptor deduced fr	5072	7	7	3.37	0
3.	R25450	MH mutant porcine ryanodine r	5035	7	7	3.37	0
4.	R10834	Rianodin receptor.	4987	7	7	3.37	0
5.	R47861	Alpha 2-Macroglobulin/LDL-rec	4544	7	7	3.37	0
6.	R52971	Product of the cDNA encoding	3969	7	7	3.37	0
7.	R38470	ALL-1 protein.	3910	7	7	3.37	0
8.	R06996	Protein characteristic of hog	3898	7	7	3.37	0
9.	R10473	Hog cholera virus genome prod	3898	7	7	3.37	0
10.	R13895	ACV synthetase.	3778	7	7	3.37	0

11.	R13753	ACVS.	3768	7	7	3.37	0
12.	R10145	Cephalosporin antibiotic bios	3722	7	7	3.37	0
13.	R13896	ACV synthetase.	3712	7	7	3.37	0
14.	P90290	Human Duchenne muscular dystr	3685	7	7	3.37	0
15.	P90373	Sequence encoded by human mus	3685	7	7	3.37	0
16.	R05041	Filamentous haemagglutinin A.	3647	7	7	3.37	0
17.	R40227	ACVS.	3639	7	7	3.37	0
18.	R34712	Bacillus subtilis srfA operon	3588	7	7	3.37	0
19.	R34713	Bacillus subtilis srfA operon	3587	7	7	3.37	0
20.	R43662	DEN1-S275/90 (ECACC V92042111	3396	7	7	3.37	0
21.	P81770	Deduced sequence encoded by m	3210	7	7	3.37	0
22.	P81771	Deduced sequence encoded by b	3210	7	7	3.37	0
23.	P93285	Sequence of clone HIV-2 SBL/I	3080	7	7	3.37	0
24.	R59926	GAP protein Ira2.	3079	7	7	3.37	0
25.	R40841	Translation of TEV large ORF.	3054	7	7	3.37	0
26.	R33539	NANBH virus strain HC-J8 prot	3033	7	7	3.37	0
27.	R33214	NANBH virus strain HC-J8 prot	3033	7	7	3.37	0
28.	R33538	NANBH virus strain HC-J6 prot	3033	7	7	3.37	0
29.	P93284	Sequence of clone HIV-2 SBL/I	3025	7	7	3.37	0
30.	R35207	Hepatitis C virus protein.	3014	7	7	3.37	0
31.	R54099	NANBHV E1/E2 protein.	3014	7	7	3.37	0
32.	R21519	Compiled HCV sequence.	3011	7	7	3.37	0
33.	R22154	NANBV Hutch c59 isolate genom	3011	7	7	3.37	0
34.	R31621	Hepatitis C virus (HCV) polyp	3011	7	7	3.37	0
35.	R34468	Encoded by full-length Hepati	3011	7	7	3.37	0
36.	R40119	HCV genomic amino acid sequen	3011	7	7	3.37	0
37.	R40120	HCV genomic amino acid sequen	3011	7	7	3.37	0
38.	R20091	Non-A, non-B viral genome pro	3010	7	7	3.37	0
39.	R20111	Non-A, non-B viral genome pro	3010	7	7	3.37	0
40.	R30616	Polypeptide coded by Korean H	3010	7	7	3.37	0
41.	R34580	Human hepatitis C virus gene	3010	7	7	3.37	0
42.	R53417	Blood transmiscible NANBHV pr	3010	7	7	3.37	0
43.	R44432	eryA region polypeptide modul	2986	7	7	3.37	0
44.	R08124	Hepatitis C virus putative po	2955	7	7	3.37	0
45.	R59923	GAP protein Ira1.	2938	7	7	3.37	0

1. US-08-121-713B-22 (1-7)
R44929 T. niveum Cyclosporin synthetase.

ID R44929 standard; Protein; 15281 AA.
AC R44929;
DT 08-JUL-1994 (first entry)
DE T. niveum Cyclosporin synthetase.
KW Enzyme; cyclosporin; synthetase-like activity; Tolypocladium niveum;
KW T. inflatum GAMS; biosynthesis; vector; cyclosporin synthetase.
OS Tolypocladium niveum.
PN EP-578616-A.
PD 12-JAN-1994.
PF 05-JUL-1993; 810474.
PR 09-JUL-1992; AT-001403.
PR 08-MAR-1993; AT-000437.
PR 29-APR-1993; CH-001310.
PR 04-MAY-1993; CH-001375.
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
PI Leitner E, Schneider E, Schoergendorfer K, Weber G;
DR WPI; 94-010432/02.
DR N-PSDB; Q54386.

PT Isolated DNA sequence - which codes for enzyme having cyclosporin
PT synthetase like activity
PS Claim 1; Page 41-84; 93pp; English.
CC This sequence represents an enzyme which has cyclosporin synthetase-
CC like activity. This sequence was isolated from Tolypocladium niveum
CC (formerly known as T. inflatum GAMS). This enzyme catalyses the
CC peptide biosynthesis of cyclosporins and structurally related
CC molecules. This sequence may be used for the production of
CC cyclosporin by transforming a vector containing this sequence in
CC to a recombinant host. This allows effective production of anti-
CC biotic cyclosporin or its derivatives.
SQ Sequence 15281 AA;
SQ 1431A; 1009R; 523N; 950D; 0 B; 101C; 785Q; 972E; 0 Z; 946G; 378H;
SQ 851I; 156L; 478K; 327M; 575F; 731P; 106S; 892T; 138W; 337Y; 123V;

Initial Score = 7 Optimized Score = 7 Significance = 3.37
Residue Identity = 28% Matches = 2 Mismatches = 5
Gaps = 0 Conservative Substitutions = 0

```
            X     X
            DXVXXXX
            | |
   ASQCPSLDVHDLVQLAEDAGFRVEVSW
     2390    X 2400      2410
```

2. US-08-121-713B-22 (1-7)
R11510 Ryanodine receptor deduced from cDNA clone.

ID R11510 standard; Protein; 5072 AA.
AC R11510;
DT 17-JUN-1991 (first entry)
DE Ryanodine receptor deduced from cDNA clone.
KW Malignant hyperthermia; hypermetabolic syndrome; inhalation;
KW anaesthetics; probe; calcium release channel; sarcoplasmic;
KW reticulum.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1629..1632
FT Peptide 1742..1748
FT Peptide 3119..3130
FT Peptide 3196..3210
FT Active-site 3981..3985
FT /label= phosphorylation site
FT Active-site 4315..4318
FT /label= phosphorylation site
PN WO9104328-A.
PD 04-APR-1991.
PF 21-SEP-1990; CA0312.
PR 25-SEP-1989; US-612726.
PA (HSCR-) HSC R & D Partnership.
PA (UTOR) Univ. Toronto Innova.
PA (TORO-) Toronto Hospital.
PI Worton RG, Maclennan DH, Britt BA.
DR WPI; 91-117517/16.
DR Q-PSDB; Q11415.
PT Purified DNA specific for human ryanodine receptor - useful for
PT diagnosis of malignant melanoma.
PS Claim 11; Fig 2; 49pp; English.
CC The sequence was obtd. from several overlapping clones isolated

CC from a human skeletal muscle cDNA library in lambda gt10. The
CC protein encodes the human ryanodine receptor (HRR), a calcium
CC release channel which spans the gap between the transverse tubule
CC and the sarcoplasmic reticulum (SR) in muscle. The sustained muscle
CC contraction in malignant hyperthermia (MH) may be caused by the
CC release of calcium into the muscle cell cytoplasm from the SR. This
CC is due to a defect in the gene encoding HRR. Sequences from the
CC gene can be used for diagnosis of MH using FRPL analysis. The
CC protein sequence would give rise to several transmembrane passages
CC in the C-terminal fifth of the molecule; the bulk would be hydro-
CC phillic. This matches well with the structure of known ryanodine
CC receptors. The peptides in the feature table were determined from
CC the purified receptor protein.
SQ Sequence 5072 AA;
SQ 387A; 295R; 174N; 252D; 0 B; 100C; 207Q; 477E; 0 Z; 362G; 134H;
SQ 207I; 561L; 230K; 149M; 209F; 274P; 297S; 232T; 63 W; 142Y; 320V;

Initial Score = 7 Optimized Score = 7 Significance = 3.37
Residue Identity = 28% Matches = 2 Mismatches = 5
Gaps = 0 Conservative Substitutions = 0

```
            X     X
            DXVXXXX
            | |
   PGQQGRISHTDLVIGCLVDLATGLMTF
        1510      1520
```

3. US-08-121-713B-22 (1-7)
R25450 MH mutant porcine ryanodine receptor.

ID R25450 standard; Protein; 5035 AA.
AC R25450;
DT 08-JAN-1993 (first entry)
DE MH mutant porcine ryanodine receptor.
KW MH; RYR1; calcium release channel; sarcoplasmic reticulum;
KW transverse tubule; polymorphism; beta strand.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc_difference 615
FT /label= MH_mutation
PN WO9211387-A.
PD 09-JUL-1992.
PF 20-DEC-1991; CA0457.
PR 21-DEC-1990; GB-027869.
PR 20-MAY-1991; GB-010865.
PR 09-SEP-1991; GB-019250.
PA (UYGU-) UNIV GUELPH.
PA (UTOR) UNIV TORONTO INNOVATIONS FOUND.
PI MacLennan DH, O'Brien PJ;
DR WPI; 92-250106/30.
DR N-PSDB; Q25975.
PT Purified DNA mol. for diagnosis of porcine malignant hyperthermia
PT - comprises DNA sequence encoding normal or mutant ryanodine
PT receptor with specified endonuclease restriction map
PS Disclosure; Fig 2; 96pp; English.
CC The sequence given is encoded by the mutant pig ryanodine receptor
CC (RYR1) cDNA. A polymorphic change at position 1972 of the cDNA causes
CC the mutation from Arg to Cys and this is thought to be the molecular
CC basis of porcine malignant hyperthermia (MH). This mutation lies

CC within the region of RYR1 that is concerned with the binding of
CC regulators of Ca2+ release channel gating. Analysis of surrounding
CC sequences suggests that this mutation lies within a beta strand domain
CC comprising roughly of amino acids 520 to 830. RYR1 is the calcium
CC release channel of the sarcoplasmic reticulum and is a large protein
CC which spans the gap between the transverse tubule and the sarcoplasmic
CC reticulum. The cannel is activated by ATP, calcium, caffine, and
CC micro-molar ryanodine. It is inhibited by ruthenium red, tetracaine,
CC calmodulin, high Mg2+ and ryanodine.
SQ Sequence 5035 AA;
SQ 381A; 297R; 171N; 248D; 0 B; 100C; 198Q; 486E; 0 Z; 371G; 132H;
SQ 202I; 568L; 227K; 143M; 206F; 271P; 286S; 227T; 64 W; 143Y; 314V;

Initial Score = 7 Optimized Score = 7 Significance = 3.37
Residue Identity = 28% Matches = 2 Mismatches = 5
Gaps = 0 Conservative Substitutions = 0

```
            X     X
            DXVXXXX
            | |
   AILRSLVPLDDLVGIISLPLQIPTLGK
    2460      2470 X    2480
```

4. US-08-121-713B-22 (1-7)
R10834 Rianodin receptor.

ID R10834 standard; Protein; 4987 AA.
AC R10834;
DT 26-APR-1991 (first entry)
DE Rianodin receptor.
KW Rianodin receptor gene; calcium release modulator; tranquiliser;
KW antagonist.
OS Oryctolagus cuniculus.
PN J03011098-A.
PD 18-JAN-1991.
PF 07-JUN-1989; 144569.
PR 07-JUN-1989; JP-144569.
PA (MITU) Mitsubishi Kasei Corp.
DR WPI; 91-062003/09.
DR N-PSDB; Q10613.
PT New rianodin receptor, genes encoding it and its prepn. - useful as
PT calcium release modulator for tranquillisers and for assaying
PT calcium antagonists.
PS Disclosure; Fig 1; 18pp; Japanese.
CC RNA contg. poly(A) was prepared from rabbit skeletal muscle
CC endoplasmic reticulum. From the obtd. poly(A) mRNA, a cDNA bank
CC corresp. to it was prepared by random primer method, oligo (dT)
CC primer method, and primer extension method. A cDNA was obtained by
CC screening with a DNA probe (see Q10614-15). By introducing the obtd.
CC cDNA into an expression vector, vector pRRS7 was formed.
CC The product is said to be involved in calcium release from
CC sarcoplasmic reticulum which triggers constriction of skeletal muscle.
CC Therefore, the receptor is useful as tranquilliser and assay series for
CC screening of calcium antagonist.
SQ Sequence 4987 AA;
SQ 390A; 296R; 170N; 249D; 0 B; 101C; 198Q; 483E; 0 Z; 365G; 131H;
SQ 192I; 551L; 224K; 145M; 206F; 265P; 278S; 221T; 65 W; 142Y; 315V;

Initial Score = 7 Optimized Score = 7 Significance = 3.37

```
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    PGQQGRISHTDLVIGCLVDLATGLMTF
        1510  X   1520
```

5. US-08-121-713B-22 (1-7)
   R47861 Alpha 2-Macroglobulin/LDL-receptor related protein

```
 ID   R47861 standard; protein; 4544 AA.
 AC   R47861;
 DT   20-JUL-1994  (first entry)
 DE   Alpha 2-Macroglobulin/LDL-receptor related protein.
 KW   alpha-2 macroglobulin; Low Density Lipoprotein; LDL; receptor family;
 KW   LDL receptor related protein; LRP; small rhinovirus receptor; deriv;
 KW   minor Rhinovirus; alpha2MR/LRP.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   Misc_difference 211..260
 FT   /note= "50 residues not shown in SEQ.ID.No.4"
 FT   Misc_difference 1990
 FT   /note= "Residue not shown in SEQ.ID.No.4"
 FT   Misc_difference 3050
 FT   /note= "Residue not shown in SEQ.ID.No.4"
 PN   WO9401553-A.
 PD   20-JAN-1994.
 PF   05-JUL-1993; E01728.
 PR   08-JUL-1992; DE-222385.
 PR   22-AUG-1992; DE-227892.
 PR   19-FEB-1993; DE-305063.
 PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
 PI   Blaas D,  Gruenberger M,  Hofer F,  Huettinger M,  Kerjaschki D;
 PI   Kowalski H,  Kuechler E,  Machat H;
 DR   WPI; 94-035060/04.
 PT   New peptide derivs. of receptor for rhinovirus - of the small
 PT   receptor gp., and derived DNA, transformed cells and antibodies,
 PT   used e.g. to treat or prevent rhinovirus infection
 PS   Claim 5; Fig 2; 76pp; German.
 CC   Functional derivatives of members of the Minor Rhinovirus Receptor
 CC   group are claimed. The alpha-2 Macroglobulin/LDL-receptor related
 CC   protein of sequence R47861 (Herz et al. EMBO J. 7;4119-4127 (1988))
 CC   is a preferred parent receptor. The derivs, which are preferably
 CC   soluble, extracellular forms of the native receptors, are useful
 CC   for treating and preventing viral (esp. rhinoviral) infections.
 CC   N.B. the SEQ.ID. listing includes a sequence (no.4) which differs
 CC   from the alpha2-MR/LRP sequence as indicated in the Features Table.
 SQ   Sequence   4544 AA;
 SQ   249A; 277R; 249N; 393D; 0  B; 331C; 164Q; 235E; 0  Z; 376G; 129H;
 SQ   196I; 305L; 173K; 72 M; 133F; 231P; 308S; 259T; 88 W; 131Y; 245V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.37
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
```



```
             | |
    KIVFPHGITLDLVSRLVYWADAYLDYI
       370   X  380       390
```

6. US-08-121-713B-22 (1-7)
   R52971 Product of the cDNA encoding htrx.

```
 ID   R52971 standard; Protein; 3969 AA.
 AC   R52971;
 DT   27-SEP-1994  (first entry)
 DE   Product of the cDNA encoding htrx.
 KW   Human; trithorax gene; L01986; diagnosis; treatment;
 KW   immunodeficiency; developmental abnormalities; inherited diseases;
 KW   cancer; acute lymphocytic leukaemia; myelomonocytic leukaemia.
 OS   Homo sapiens.
 PN   WO9407502-A.
 PD   14-APR-1994.
 PF   24-SEP-1993; U09087.
 PR   30-SEP-1992; US-954112.
 PR   13-MAY-1993; US-061376.
 PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
 PI   Djabaki M,  Evans GA,  Parry P,  Selleri L;
 DR   WPI; 94-135206/16.
 PT   Nucleic acid encoding a human tri:thorax protein - used to
 PT   develop agents for diagnosis and treatment of diseases associated
 PT   with disruption of chromosome II at q23
 PS   Disclosure; Page 43-54; 68pp; English.
 CC   In the course of the construction of a physical map of human
 CC   chromosome region 11q23, a region contg. the t(4;11) translocation
 CC   breakpoint was cloned.  The cloned DNA encoded a protein homologous
 CC   to the trithorax gene prod. of Drosophila.  The gene may be used for
 CC   the diagnosis and treatment of immunodeficiency states,
 CC   developmental abnormalities, inherited diseases or cancers, e.g.
 CC   acute lymphocytic leukaemia or acute myelomonocytic leukaemia.
 CC   See also R52972-7.
 SQ   Sequence   3969 AA;
 SQ   218A; 223R; 159N; 182D; 0  B; 82 C; 184Q; 250E; 2  Z; 249G; 86 H;
 SQ   143I; 286L; 299K; 64 M; 103F; 352P; 543S; 245T; 22 W; 55 Y; 203V;
 SQ   19 Others;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.37
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    SSEMKQSSASDLVSKSSSLKGEKTKVL
       2290   X  2300       2310
```

7. US-08-121-713B-22 (1-7)
   R38470 ALL-1 protein.

```
 ID   R38470 standard; Protein; 3910 AA.
 AC   R38470;
 DT   08-NOV-1993  (first entry)
 DE   ALL-1 protein.
 KW   Acute lymphoblastic leukemia gene; ALL-1; chromosome 11; treatment;
```

```
KW   translocation breakpoint mapping; chromosomal abnormality; diagnosis;
KW   human; acute lymphocytic; myelomonocytic; monocytic; myelogenous;
KW   leukemia; Drosophila; trithorax; homology region; zinc finger domain;
KW   cysteine-rich.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Region          1021..1221
FT   /note= "Region of homology to Drosophila trithorax"
FT   Region          1462..1570
FT   /note= "Region of homology to Drosophila trithorax"
FT   Region          3348..3562
FT   /note= "Region of homology to Drosophila trithorax"
PN   WO9312136-A.
PD   24-JUN-1993.
PF   09-DEC-1992; U10930.
PR   11-DEC-1991; US-805093.
PR   27-MAY-1992; US-888839.
PR   30-OCT-1992; US-971094.
PA   (UYJE-) UNIV JEFFERSON THOMAS.
PI   Canaani E,  Croce CM;
DR   WPI; 93-214090/26.
DR   N-PSDB; Q43526.
PT   Detection and treatment of acute leukaemia(s) - using prods.
PT   derived from oligo:nucleotide sequences within the ALL-1 gene of
PT   chromosome 11
PS   Disclosure; Page 29-50; 90pp; English.
CC   This sequence is encoded by the acute lymphoblastic leukemia (ALL-1)
CC   gene of chromosome 11.  The ALL-1 gene was isolated by translocation
CC   breakpoint mapping.  Fragments of the ALL-1 cDNA may be used to
CC   identify chromosomal abnormalities within the ALL-1 gene.  These
CC   fragments may be used in the treatment and diagnosis of human
CC   leukemias such as acute lymphocytic, myelomonocytic, monocytic and
CC   myelogenous leukemia.  ALL-1 protein shows three regions of homology
CC   to the Drosophila trithorax protein.  These regions show 64%, 66% and
CC   82% similarity respectively, to the Drosophila gene.  The third region
CC   of homology constitutes the extreme C-terminus of the two proteins,
CC   both proteins end in an identical sequence.  The first homology region
CC   is cysteine-rich and contains sequence motifs analogous to four zinc
CC   finger domains (3-6) within the trithorax gene.  The second region of
CC   homology is also cysteine-rich and corresponds to zinc fingers 7 and 8
CC   of the Drosophila gene.  The multiple conserved cysteines and
CC   histidines at the 3' end of the motifs allow two or three arrangements
CC   of the putative fingers.  The structure of these cysteine-rich domains
CC   appears to be unique to the trithorax and ALL-1 genes.
SQ   Sequence   3910 AA;
SQ   214A; 222R; 159N; 181D; 0  B; 79 C; 180Q; 253E; 0  Z; 230G; 83 H;
SQ   149I; 275L; 305K; 63 M; 100F; 345P; 542S; 250T; 20 W; 53 Y; 207V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.37
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions                =     0

             X     X
             DXVXXXX
             | |
    SSEMKQSSASDLVSKSSSLKGEKTKVL
     2230      2240 X    2250
```

8. US-08-121-713B-22 (1-7)

R06996 Protein characteristic of hog cholera virus (HCV).

```
ID   R06996 standard; protein; 3898 AA.
AC   R06996;
DT   16-JAN-1991  (first entry)
DE   Protein characteristic of hog cholera virus (HCV).
KW   Vaccine; parvovirus; swine influenza virus.
OS   Hog cholera virus.
PN   EP-389034-A.
PD   26-SEP-1990.
PF   12-MAR-1990; 200573.
PR   19-MAR-1989; EP-104921.
PR   12-MAR-1990; EP-200573.
PA   (ALKU ) AKZO NV.
PI   Meyers G, Rumenapf T, Thiel HJ;
DR   WPI; 90-291979/39.
DR   N-PSDB; Q06001.
PT   New hog cholera virus vaccine and diagnostic - comprises nucleic
PT   acid sequence of poly-peptide characteristic of hog cholera virus
PS   Claim 2; Fig 2; 29pp; English.
CC   Gene product may be used to provide a vaccine and Abs for diagnosis
CC   of hog cholera viral infection in pigs.
SQ   Sequence   3898 AA;
SQ   243A; 207R; 154N; 184D; 0  B; 72 C; 120Q; 253E; 0  Z; 286G; 82 H;
SQ   211I; 384L; 296K; 79 M; 124F; 168P; 188S; 303T; 63 W; 165Y; 316V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.37
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions                =     0

             X     X
             DXVXXXX
             | |
    ISDHIKQAATDLVVYYIINRPQFPGDT
   2440      2450   X  2460
```

9. US-08-121-713B-22 (1-7)
R10473 Hog cholera virus genome product.

```
ID   R10473 standard; Protein; 3898 AA.
AC   R10473;
DT   09-APR-1991  (first entry)
DE   Hog cholera virus genome product.
KW   Swine fever virus; HCV; pestvirus; border disease virus; BDV;
KW   Bovine viral diarrhoea virus; BVDV; Togaviridae; ss.
OS   Hog Cholera Virus.
PN   WO9100352-A.
PD   10-JAN-1991.
PF   29-JUN-1990; NL0092.
PR   29-JUN-1989; NL-001651.
PA   (DIER-) CENT DIERGENEESKUND.
PI   Moorman R, Wensvoort G;
DR   WPI; 91-036746/05.
DR   P-PSDB; Q10353.
PT   Protection of animals against microbial infection - using
PT   nucleotide sequences related to the microbe and a stop transfer
PT   region
PS   Claim 15; Fig 1; 33pp; English.
CC   The genome sequence and its encoded product are sufficiently similar
```

```
CC   to other pestviruses of the family Togaviridae, that they may be
CC   used in vaccination and diagnosis of pestvirus infection.
SQ   Sequence   3898 AA;
SQ   248A; 198R; 159N; 179D; 0  B; 73 C; 122Q; 258E; 0  Z; 287G; 80 H;
SQ   210I; 381L; 290K; 94 M; 124F; 172P; 185S; 306T; 63 W; 165Y; 304V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.37
Residue Identity =     28%  Matches          =      2  Mismatches   =      5
Gaps             =      0  Conservative Substitutions               =      0

             X     X
             DXVXXXX
             | |
    IADHVKQAATDLVVYYIINRPQFPGDT
  2440      2450   X  2460
```

10. US-08-121-713B-22 (1-7)
    R13895 ACV synthetase.

```
ID   R13895 standard; Protein; 3778 AA.
AC   R13895;
DT   22-NOV-1991  (first entry)
DE   ACV synthetase.
KW   Beta lactam antibiotics; penicillin.
OS   Penicillin chrysogenum.
FH   Key             Location/Qualifiers
FT   Domain          301..1068
FT   /label= I
FT   /function= activation of amino acid substrate
FT   Region          374..423
FT   /label= subdomain
FT   Region          474..501
FT   /label= subdomain
FT   Region          655..699
FT   /label= subdomain
FT   Region          725..754
FT   /label= subdomain
FT   Domain          1392..2154
FT   /label= II
FT   /function= activation of amino acid substrate
FT   Region          1470..1518
FT   /label= subdomain
FT   Region          1564..1590
FT   /label= subdomain
FT   Region          1745..1789
FT   /label= subdomain
FT   Region          1817..1846
FT   /label= subdomain
FT   Domain          2474..3295
FT   /label= III
FT   /function= activation of amino acid substrate
FT   Region          2554..2603
FT   /label= subdomain
FT   Region          2647..2673
FT   /label= subdomain
FT   Region          2827..2871
FT   /label= subdomain
FT   Region          2899..2928
FT   /label= subdomain
```



```
FT   Domain          3560..3647
FT   /label= IV
FT   /function= thioesterase
PN   EP-445868-A.
PD   11-SEP-1991.
PF   27-FEB-1991; 200423.
PR   28-FEB-1990; EP-200475.
PR   28-FEB-1990; EP-200488.
PR   02-JUL-1990; EP-201768.
PR   03-OCT-1990; EP-202628.
PR   27-FEB-1991; EP-200423.
PA   (KONN ) GIST-BROCADES NV.
PI   Veenstra AE, Martin JF, Garcia BD, Guttierez S, Barredo JL;
PI   Montenegro PE, Von Doehren H, Palissa H, Van Liempt H;
DR   WPI; 91-268735/37.
DR   N-PSDB; Q13607.
PT   DNA encoding amino:adipyl-cysteinyl-valine synthetase - used for
PT   prodn. of the enzyme or enhanced prodn. of new or known
PT   beta-lactam antibiotic cpds.
PS   Claim 1; Page 20; 54pp; English.
CC   The isolation of DNA fragments encoding the ACV synthtase is
CC   described in EP-357119. Cosmid HM193 contains one such fragment
CC   which was sequenced using the Sequenase system 2.0.  The protein
CC   sequence was deduced from the DNA.  Three distinct regions of
CC   homology have been identified, domains I, II and III.  Within
CC   these domains several even more conserved elements can be
CC   distinguished.  Since the enzyme synthesises a tripeptide, which
CC   most probably requires the activation of three amino acids, a
CC   role for these domains in the activation reactions seems likely.
CC   A fourth domain is thought to act as a thioesterase.
CC   The gene can be used to express the synthetase enzyme which can
CC   be used for the prodn of new beta-lactam antibiotics.
CC   See also R13896.
SQ   Sequence   3778 AA;
SQ   266A; 245R; 158N; 219D; 0  B; 44 C; 170Q; 260E; 0  Z; 228G; 103H;
SQ   204I; 408L; 140K; 65 M; 146F; 169P; 289S; 209T; 36 W; 137Y; 282V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.37
Residue Identity =     28%  Matches          =      2  Mismatches   =      5
Gaps             =      0  Conservative Substitutions               =      0

             X     X
             DXVXXXX
             | |
    GRNSRLYKTGDLVRWIPGSSGEVEYLG
  1800      1810   X  1820
```

11. US-08-121-713B-22 (1-7)
    R13753 ACVS.

```
ID   R13753 standard; Protein; 3768 AA.
AC   R13753;
DT   14-NOV-1991  (first entry)
DE   ACVS.
KW   Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase;
KW   beta-lactam antibiotics.
OS   Penicillium chrysogenum.
FH   Key             Location/Qualifiers
FT   Domain          301..1068
```

```
FT   /label= domain I
FT   Domain          1392..2154
FT   /label= domain II
FT   Domain          2474..3295
FT   /label= domain III
PN   EP-444758-A.
PD   04-SEP-1991.
PF   27-FEB-1991; 200422.
PR   28-FEB-1990; EP-200475.
PR   28-FEB-1990; EP-200488.
PR   02-JUL-1990; EP-201768.
PR   03-OCT-1990; EP-202628.
PR   27-FEB-1991; EP-200422.
PA   (KONN ) GIST-BROCADES NV.
PI   Veenstra AE, Martin JF, Garcia BD, Gutierrez S, Barredo JL;
PI   Montenegro Prieto E, Von Doehren H, Palissa H, Van Liempt H.
DR   WPI; 91-261525/36.
DR   N-PDSB; Q13547.
PT   Mutant delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine
PT   synthetase - used in prodn. of beta-lactam antibiotics.
PS   Disclosure; Page 19; 56pp; English.
CC   The amino acid sequence codes for delta- (L-alpha-aminoadipyl)-L-
CC   cysteinyl-D-valine synthetase (ACVS). The prods. may be used for
CC   the enhanced expression (in vivo and in vitro) of mutant enzymes
CC   and fermentable or known and new beta- lactam antibiotics and their
CC   precursors, partic. antibiotics of the penam and cephem classes.
CC   See also R13754-R13756.
SQ   Sequence   3768 AA;
SQ   266A; 245R; 158N; 218D; 0  B; 44 C; 169Q; 260E; 0  Z; 227G; 104H;
SQ   204I; 407L; 138K; 64 M; 146F; 167P; 288S; 208T; 36 W; 137Y; 282V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.37
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            DXVXXXX
            | |
    GRNSRLYKTGDLVRWIPGSSGEVEYLG
  1790      1800   X  1810
```

12. US-08-121-713B-22 (1-7)
    R10145 Cephalosporin antibiotic biosynthetic enzyme #1.

```
ID   R10145 standard; Protein; 3722 AA.
AC   R10145;
DT   27-MAR-1991  (first entry)
DE   Cephalosporin antibiotic biosynthetic enzyme #1.
KW   cephalosporin; antibiotic;
KW   S-(L-alpha-aminoadipyl)-L-cysteinyl-D-; valine synthetase;
KW   isopenicillin N synthetase; isopenicillin N epimerase;
KW   deacetoxycephalosporin C synthetase; beta-lactamase;
KW   deacetoxycephalosporin C hydroxylase.
OS   Lysobacter lactamgenus.
PN   J02291274-A.
PD   03-DEC-1990.
PF   10-JAN-1990; 003762.
PR   01-FEB-1989; JP-024710.
PR   10-JAN-1990; JP-003762.
```



```
PA   (TAKE ) TAKEDA CHEMICAL IND KK.
DR   WPI; 91-018854/03.
DR   N-PSDB; Q10190.
PT   Prepn. of cephalosporin series antibiotics - comprises culturing
PT   transformant of microbe transformed by plasmid contg. new DNA
PT   fragment
PS   Disclosure; Fig 13; 67pp; Japanese.
CC   This protein is encoded by ORF1 of the 23666bp sequence
CC   isolated from L.lactamgenus and comprising the genes for the
CC   cephalosporin biosynthetic enzymes listed in the KEYWORDS. Plasmids
CC   containing at least one of ORF's 1-9 can be used to transform
CC   microbes, such as bacteria or yeast.
CC   See also Q10191-2.
SQ   Sequence   3722 AA;
SQ   454A; 307R; 101N; 266D; 0  B; 36 C; 138Q; 233E; 0  Z; 267G; 104H;
SQ   157I; 418L; 84 K; 51 M; 153F; 171P; 218S; 151T; 45 W; 120Y; 248V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.37
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            DXVXXXX
            | |
    GNNARLYKTGDLVRWLPNGELEYLGRN
      1750  X  1760      1770
```

13. US-08-121-713B-22 (1-7)
    R13896 ACV synthetase.

```
ID   R13896 standard; Protein; 3712 AA.
AC   R13896;
DT   22-NOV-1991  (first entry)
DE   ACV synthetase.
KW   Beta lactam antibiotics; penicillin.
OS   Acremonium chrysogenum.
FH   Key             Location/Qualifiers
FT   Domain          301..1068
FT   /label= I
FT   /function= activation of amino acid substrate
FT   Region          374..423
FT   /label= subdomain
FT   Region          474..501
FT   /label= subdomain
FT   Region          655..699
FT   /label= subdomain
FT   Region          725..754
FT   /label= subdomain
FT   Domain          1392..2154
FT   /label= II
FT   /function= activation of amino acid substrate
FT   Region          1470..1518
FT   /label= subdomain
FT   Region          1564..1590
FT   /label= subdomain
FT   Region          1745..1789
FT   /label= subdomain
FT   Region          1817..1846
FT   /label= subdomain
```

```
FT   Domain          2474..3295
FT   /label= III
FT   /function= activation of amino acid substrate
FT   Region          2554..2603
FT   /label= subdomain
FT   Region          2647..2673
FT   /label= subdomain
FT   Region          2827..2871
FT   /label= subdomain
FT   Region          2899..2928
FT   /label= subdomain
FT   Domain          3560..3647
FT   /label= IV
FT   /function= thioesterase
PN   EP-445868-A.
PD   11-SEP-1991.
PF   27-FEB-1991; 200423.
PR   28-FEB-1990; EP-200475.
PR   28-FEB-1990; EP-200488.
PR   02-JUL-1990; EP-201768.
PR   03-OCT-1990; EP-202628.
PR   27-FEB-1991; EP-200423.
PA   (KONN ) GIST-BROCADES NV.
PI   Veenstra AE, Martin JF, Garcia BD, Guttierez S, Barredo JL;
PI   Montenegro PE, Von Doehren H, Palissa H, Van Liempt H;
DR   WPI; 91-268735/37.
DR   N-PSDB; Q13608.
PT   DNA encoding amino:adipyl-cysteinyl-valine synthetase - used for
PT   prodn. of the enzyme or enhanced prodn. of new or known
PT   beta-lactam antibiotic cpds.
PS   Claim 1; Page 20; 54pp; English.
CC   The DNA sequence was obtd. from five subclones isolated from a
CC   gene library of A. chrysogenum C10 (ATCC 48). The protein
CC   sequence was deduced from the DNA. Three distinct regions of
CC   homology have been identified, domains I, II and III. Within
CC   these domains several even more conserved elements can be
CC   distinguished. Since the enzyme synthesises a tripeptide, which
CC   most probably requires the activation of three amino acids, a
CC   role for these domains in the activation reactions seems likely.
CC   A fourth domain is thought to act as a thioesterase.
CC   The gene can be used to express the synthetase enzyme which can
CC   be used for the prodn. of new beta-lactam antibiotics.
CC   See also R13896.
SQ   Sequence   3712 AA;
SQ   262A; 214R; 144N; 219D; 0  B; 42 C; 180Q; 237E; 0  Z; 237G; 127H;
SQ   190I; 413L; 135K; 58 M; 131F; 184P; 282S; 217T; 39 W; 128Y; 273V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.37
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    GRNARLYKTGDLVRWIHNANGDGEIEY
 1740      1750      1760
```

14. US-08-121-713B-22 (1-7)
    P90290 Human Duchenne muscular dystrophy gene.


```
ID   P90290 standard; protein; 3685 AA.
AC   P90290;
DT   10-JAN-1990  (first entry)
DE   Human Duchenne muscular dystrophy gene.
KW   Duchenne muscular dystrophy;protein deletion; antiserum.
OS   Homo sapiens.
PN   EP-331514-A.
PD   06-SEP-1989.
PF   03-MAR-1989; 302145.
PR   04-MAR-1988; JP-051313.
PA   (AJIN) Ajinomoto Co., Inc.
PI   Ishiguro T, Eguchi C.
DR   WPI; 89-257828/36.
PT   Detecting human Duchenne muscular dystrophy - by assaying for associated
PT   protein deletion or defect using antibody to the protein.
PS   Claim 3; page 15-16; 20pp; English.
CC   Peptides may be prepared consisting of all or part of the sequence and
CC   used to produce Abs for detecting protein deletions or defects in the
CC   gene.
SQ   Sequence   3685 AA;
SQ   213 A; 197 R; 167 N; 193 D; 0 B; 36 C; 306 Q; 388 E; 0 Z; 112 G; 88 H;
SQ   170 I; 457 L; 294 K;  78 M;80 F;132 P; 243 S; 199 T;70 W;  69 Y;191 V;
SQ   2 Others;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.37
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    ALRVLQNNNVDLVNIGSTDIVDGNHKL
  80        90      X 100
```

15. US-08-121-713B-22 (1-7)
    P90373 Sequence encoded by human muscular dystrophy (MD)

```
ID   P90373 standard; Protein; 3685 AA.
AC   P90373;
DT   29-MAR-1992  (first entry)
DE   Sequence encoded by human muscular dystrophy (MD) cDNA.
KW   Dystrophin; muscular dystrophy; probe; antibody; diagnosis;
KW   prenatal; heterozygote; gene therapy; genetic screening;
KW   foetal screening.
OS   Homo sapiens.
PN   WO8906286-A.
PD   13-JUL-1989.
PF   16-DEC-1988; U04504.
PR   22-DEC-1987; US-136618.
PA   (CHIL-) CHILDRENS MED CENT.
PI   Kunkel LM, Monaco A, Hoffman EP, Koenig M;
DR   WPI; 89-220587/30.
DR   N-PSDB; N90338.
PT   Muscular dystrophy gene - used for prepn. of probes, dystrophin
PT   polypeptide and antibodies for diagnosis and therapy of muscular
PT   dystrophy
PS   Disclosure; Fig 8; 68pp; English.
CC   The inventors claim an MD probe comprising a purified ss NA SQ which
```

```
 CC   hybridises to at least a part of the MD gene; pure dystrophin (DS)
 CC   polypeptide, purified NA encoding DS and antibodies (Ab) to DS. The
 CC   probes are equal to or greater than 10b of one of 12 cDNA sequences
 CC   deposited as ATCC 58666-57677. The MD gene is human, or a murine Dmd
 CC   gene.
 SQ   Sequence   3685 AA;
 SQ   213A; 198R; 165N; 194D; 0  B; 36 C; 308Q; 385E; 0  Z; 112G; 88 H;
 SQ   171I; 456L; 295K; 80 M; 79 F; 131P; 242S; 201T; 72 W; 62 Y; 197V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.37
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    ALRVLQNNNVDLVNIGSTDIVDGNHKL
   80        90     X 100
> O <
O| |O  IntelliGenetics
> O <

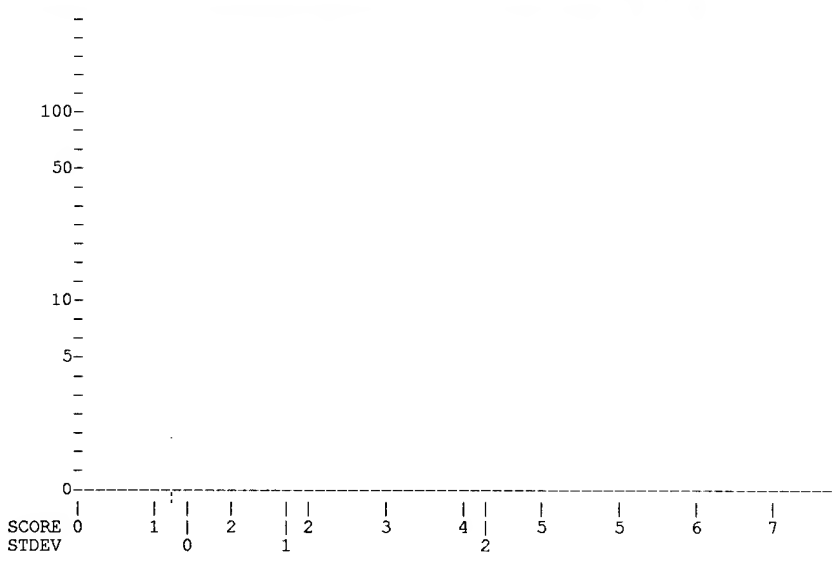
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq22pir.res made by maryh on Fri 19 May 95 10:50:24-PDT.


Query sequence being compared:US-08-121-713B-22 (1-7)
Number of sequences searched:                75511
Number of scores above cutoff:                4923

     Results of the initial comparison of US-08-121-713B-22 (1-7) with:
   Data bank : PIR 43, all entries

100000-
      -
N     -                          *
U50000-
M     -
B     -
E     -
R     -
      *
O     -
F10000-                                                          *
      -
S     -
E 5000-
Q     -
U     -
E     -
N     -
C     -
E     -                                  *
S 1000-
      -
      -
   500-
      -
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	4	1.80

Times:	CPU	Total Elapsed
	00:01:13.03	00:01:14.00

Number of residues:	22468834
Number of sequences searched:	75511
Number of scores above cutoff:	4923

The scores below are sorted by initial score.
Significance is calculated based on initial score.

4923 100% similar sequences to the query sequence were found:

Init. Opt.

Sequence Name	Description	Length	Score	Score	Sig.	Frame
1. S18135	Calcium release channel - Pig	5034	7	7	2.78	0
2. S27272	ryanodine receptor, brain - r	4872	7	7	2.78	0
3. S18252	perlecan - mouse	3707	7	7	2.78	0
4. S28916	dystrophin - mouse	3678	7	7	2.78	0
5. S43048	polyketide synthase - Strepto	3519	7	7	2.78	0
6. A46105	polyprotein(NS1, NS3, NS5, NS	3415	7	7	2.78	0
7. S44887	ZK112.7 protein - Caenorhabdi	3343	7	7	2.78	0
8. S37536	macrogolgin - human	3259	7	7	2.78	0
9. S20473	fatty-acid synthase (EC 2.3.1	3104	7	7	2.78	0
10. S28645	Fatty-acid synthase (EC 2.3.1	3104	7	7	2.78	0
11. S42373	hypothetical protein - Caenor	3051	7	7	2.78	0
12. S33642	homeotic protein zfh-2 - frui	3005	7	7	2.78	0
13. S17796	inositol-trisphosphate recept	2701	7	7	2.78	0
14. S11661	talin - mouse	2541	7	7	2.78	0
15. S30446	fatty-acid synthase (EC 2.3.1	2505	7	7	2.78	0
16. S46955	protein-tyrosine-phosphatase	2466	7	7	2.78	0
17. S42612	transmembrane protein precurs	2437	7	7	2.78	0
18. S44861	DNA topoisomerase II - Caenor	2434	7	7	2.78	0
19. S48905	Highly similar to C. elegans	2413	7	7	2.78	0
20. A46299	disabled product (alternative	2411	7	7	2.78	0
21. S46578	hypothetical protein YBR1012	2368	7	7	2.78	0
22. S41121	acetyl-CoA carboxylase (EC 6.	2339	7	7	2.78	0
23. S44625	C50C3.6 protein - Caenorhabdi	2329	7	7	2.78	0
24. S45306	notch 3 protein - mouse	2318	7	7	2.78	0
25. S16166	hexabrachion - human	2203	7	7	2.78	0
26. S14015	tenascin - human	2199	7	7	2.78	0
27. S33124	tpr protein - human	2094	7	7	2.78	0
28. S26058	probable transforming protein	2090	7	7	2.78	0
29. S39796	aggrecan - chicken	2071	7	7	2.78	0
30. S12050	protein-tyrosine-phosphatase	1997	7	7	2.78	0
31. S27356	aggrecan - chicken	1951	7	7	2.78	0
32. B43963	RNA viral polymerase - Hantav	1951	7	7	2.78	0
33. S46773	hypothetical protein - yeast	1928	7	7	2.78	0
34. S37771	ankyrin, erythrocyte - mouse	1848	7	7	2.78	0
35. S14568	microtubule-associated protei	1828	7	7	2.78	0
36. S13507	microtubule-associated protei	1825	7	7	2.78	0
37. S34131	microtubule-associated protei	1824	7	7	2.78	0
38. S44849	K12H4.8 protein - Caenorhabdi	1822	7	7	2.78	0
39. S41729	polyketide synthase - Strepto	1803	7	7	2.78	0
40. S44920	ZK688.5 protein - Caenorhabdi	1799	7	7	2.78	0
41. S13178	6-methylsalicylate decarboxyl	1774	7	7	2.78	0
42. S24600	projectin - fruit fly (Drosop	1742	7	7	2.78	0
43. A37491	orf1 putative helicase/polyme	1737	7	7	2.78	0
44. S18644	multifunctional amino acid--t	1714	7	7	2.78	0
45. S42369	Clathrin heavy chain homolog	1681	7	7	2.78	0

1. US-08-121-713B-22 (1-7)
   S18135 Calcium release channel - Pig (fragment)

```
 ENTRY            S18135     #type fragment
 TITLE            Calcium release channel - Pig (fragment)
 ORGANISM         #formal_name Sus scrofa domestica #common_name domestic pig
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S18135
 REFERENCE        S18135
    #authors      Harbitz, I.; Kristensen, T.; Bosnes, M.; Kran, S.; Davies, W.
```



```
    #submission   submitted to the EMBL Data Library, October 1991
    #accession    S18135
       ##status        preliminary
       ##residues      1-5034 ##label HAR
       ##cross-references EMBL:X62880
 SUMMARY          #length 5034  #checksum 8168
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  2.78
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    AILRSLVPLDDLVGIISLPLQIPTLGK
      2460    X 2470      2480
```

2. US-08-121-713B-22 (1-7)
   S27272 ryanodine receptor, brain - rabbit

```
 ENTRY            S27272     #type complete
 TITLE            ryanodine receptor, brain - rabbit
 ORGANISM         #formal_name Oryctolagus cuniculus #common_name domestic
                    rabbit
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S27272
 REFERENCE        S27272
    #authors      Hakamata, Y.; Nakai, J.; Takeshima, H.; Imoto, K.
    #journal      FEBS Lett. (1992) 312:229-235
    #title        Primary structure and distribution of a novel ryanodine
                    receptor/calcium release channel from rabbit brain.
    #accession    S27272
       ##status        preliminary
       ##residues      1-4872 ##label HAK
       ##cross-references EMBL:X68650
 SUMMARY          #length 4872  #molecular-weight 551925  #checksum 4706
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  2.78
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    SILRSLVPTEDLVGIISIPLKLPSLNK
          2330      2340
```

3. US-08-121-713B-22 (1-7)
   S18252 perlecan - mouse

```
 ENTRY            S18252     #type complete
 TITLE            perlecan - mouse
 ORGANISM         #formal_name Mus musculus #common_name house mouse
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
```

```
 ACCESSIONS       S18252
 REFERENCE        S18252
    #authors      Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.;
                    Sasaki, M.; Yamada, Y.; Hassell, J.R.
    #journal      J. Biol. Chem. (1991) 266:22939-22947
    #title        The complete sequence of perlecan, a basement membrane
                    heparan sulfate proteoglycan, reveals extensive similarity
                    with laminin A chain, low density lipoprotein-receptor, and
                    the neural cell adhesion molecule.
    #cross-references MUID:92078153
    #accession    S18252
       ##status        preliminary
       ##residues      1-3707 ##label NOO
       ##cross-references EMBL:M77174
 SUMMARY          #length 3707  #molecular-weight 398291  #checksum 1636
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  2.78
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    QRGSIQVDGEDLVTGRSPGPNVAVNTK
  3620      3630    X 3640
```

```
4. US-08-121-713B-22 (1-7)
   S28916       dystrophin - mouse

 ENTRY            S28916     #type complete
 TITLE            dystrophin - mouse
 ORGANISM         #formal_name Mus musculus #common_name house mouse
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S28916
 REFERENCE        S28916
    #authors      Bies, R.D.; Phelps, S.F.; Cortez, M.D.; Roberts, R.; Caskey,
                    C.T.; Chamberlain, J.S.
    #journal      Nucleic Acids Res. (1992) 20:1725-1731
    #title        Human and murine dystrophin mRNA transcripts are
                    differentially expressed during skeletal muscle, heart, and
                    brain development.
    #accession    S28916
       ##status        preliminary
       ##residues      1-3678 ##label BIE
       ##cross-references EMBL:M68859
 SUMMARY          #length 3678  #molecular-weight 425815  #checksum 2460
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  2.78
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    ALRVLQKNNVDLVNIGSTDIVDGNHKL
   80        90     X 100
```



```
5. US-08-121-713B-22 (1-7)
   S43048       polyketide synthase - Streptomyces antibioticus

 ENTRY            S43048     #type complete
 TITLE            polyketide synthase - Streptomyces antibioticus
 ORGANISM         #formal_name Streptomyces antibioticus
 DATE             20-Oct-1994; #sequence_revision 20-Oct-1994; #text_change
                    20-Oct-1994
 ACCESSIONS       S43048
 REFERENCE        S43048
    #authors      Swan, D.G.; Rodriguez, A.M.; Vilches, C.; Mendez, C.; Salas,
                    J.A.
    #submission   submitted to the EMBL Data Library, February 1993
    #accession    S43048
       ##status        preliminary
       ##residues      1-3519 ##label SWA
       ##cross-references EMBL:L09654
 SUMMARY          #length 3519  #molecular-weight 368532  #checksum 1912
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  2.78
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    RRGGSAPGAGDLVRELEGLGGARVSVR
      1240   X  1250      1260
```

```
6. US-08-121-713B-22 (1-7)
   A46105       polyprotein(NS1, NS3, NS5, NS2A, NS2B, NS4A, NS4B,

 ENTRY            A46105     #type complete
 TITLE            polyprotein(NS1, NS3, NS5, NS2A, NS2B, NS4A, NS4B, C=small
                    capsid protein, E=large envelope protein,
                    (pr)M=membrane-anchored protein precursor) - Powassan virus
 ORGANISM         #formal_name Powassan virus
 DATE             07-Apr-1994; #sequence_revision 07-Apr-1994; #text_change
                    07-Apr-1994
 ACCESSIONS       A46105
 REFERENCE        A46105
    #authors      Mandl, C.W.; Holzmann, H.; Kunz, C.; Heinz, F.X.
    #journal      Virology (1993) 194:173-184
    #title        Complete genomic sequence of Powassan virus: evaluation of
                    genetic elements in tick-borne versus mosquito-borne
                    flaviviruses.
    #cross-references MUID:93242744
    #accession    A46105
       ##status        preliminary
       ##molecule_type genomic RNA
       ##residues      1-3415 ##label MAN
       ##cross-references NCBIN:130654; NCBIP:130655
       ##note          sequence extracted from NCBI backbone
 SUMMARY          #length 3415  #molecular-weight 378568  #checksum 9967
 SEQUENCE
```

```
Initial Score    =      7  Optimized Score  =      7  Significance =  2.78
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    RDIPYLPKTQDLVCSSLVGRKERAEWA
    3350      3360  X   3370
```

7. US-08-121-713B-22 (1-7)
   S44887 ZK112.7 protein - Caenorhabditis elegans

```
 ENTRY            S44887     #type complete
 TITLE            ZK112.7 protein - Caenorhabditis elegans
 ORGANISM         #formal_name Caenorhabditis elegans
 DATE             14-Sep-1994; #sequence_revision 14-Sep-1994; #text_change
                    14-Sep-1994
 ACCESSIONS       S44887
 REFERENCE        S44613
    #authors      Du, Z.
    #submission   submitted to the EMBL Data Library, May 1993
    #accession    S44887
       ##status        preliminary
       ##residues      1-3343 ##label DUA
       ##cross-references EMBL:L14324
 SUMMARY          #length 3343  #molecular-weight 375748  #checksum 6289
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  2.78
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    PTQSELINHVDLVSTQNSDMKPFMMTL
      1070    X 1080      1090
```

8. US-08-121-713B-22 (1-7)
   S37536 macrogolgin - human

```
 ENTRY            S37536     #type complete
 TITLE            macrogolgin - human
 ORGANISM         #formal_name Homo sapiens #common_name man
 DATE             09-Dec-1993; #sequence_revision 09-Dec-1993; #text_change
                    09-Dec-1993
 ACCESSIONS       S37536
 REFERENCE        S37536
    #authors      Seelig, H.P.; Schranz, P.; Schroeter, H.; Wiemann, C.;
                    Griffiths, G.; Renz, M.
    #submission   submitted to the EMBL Data Library, September 1993
    #accession    S37536
       ##status        preliminary
       ##residues      1-3259 ##label SEE
       ##cross-references EMBL:X75304
 SUMMARY          #length 3259  #molecular-weight 376075  #checksum 4495
 SEQUENCE
```



```
Initial Score    =      7  Optimized Score  =      7  Significance =  2.78
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    AEERVAELARDLVEMEQKLLMVTKENK
          2710      2720
```

9. US-08-121-713B-22 (1-7)
   S20473 fatty-acid synthase (EC 2.3.1.85) - Brevibacterium

```
 ENTRY            S20473     #type complete
 TITLE            fatty-acid synthase (EC 2.3.1.85) - Brevibacterium
                    ammoniagenes
 ORGANISM         #formal_name Brevibacterium ammoniagenes
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S20473
 REFERENCE        S20473
    #authors      Meurer, G.; Biermann, G.; Schuetz, A.; Harth, S.; Schweizer,
                    E.
    #journal      Mol. Gen. Genet. (1992) 232:106-116
    #title        Molecular structure of the multifunctional fatty acid
                    synthetase gene of Brevibacterium ammoniagenes: its
                    sequence of catalytic domains is formally consistent with a
                    head-to-tail fusion of the two yeast genes FAS1 and FAS2.
    #cross-references MUID:92204122
    #accession    S20473
       ##status        preliminary
       ##residues      1-3104 ##label MEU
       ##cross-references EMBL:X64795
 SUMMARY          #length 3104  #molecular-weight 327466  #checksum 3966
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  2.78
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    SEADDNAAVVDLVTSELGADWPRLVSP
         1970 X    1980
```

10. US-08-121-713B-22 (1-7)
    S28645 Fatty-acid synthase (EC 2.3.1.85) - Brevibacterium

```
 ENTRY            S28645     #type complete
 TITLE            Fatty-acid synthase (EC 2.3.1.85) - Brevibacterium
                    ammoniagenes
 ORGANISM         #formal_name Brevibacterium ammoniagenes
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S28645
 REFERENCE        S28645
```

```
    #authors      Schweizer, E.
    #submission   submitted to the EMBL Data Library, December 1992
    #accession    S28645
       ##status        preliminary
       ##residues      1-3104 ##label SCH
       ##cross-references EMBL:X64795
 SUMMARY          #length 3104  #molecular-weight 327452  #checksum 4026
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  2.78
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    SEADDNAAVVDLVTSELGADWPRLVSP
         1970 X    1980
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq22spt.res made by  on Fri 19 May 95 8:58:53-PDT.


Query sequence being compared:US-08-121-713B-22 (1-7)
Number of sequences searched:                43470
Number of scores above cutoff:                4077

      Results of the initial comparison of US-08-121-713B-22 (1-7) with:
   Data bank : Swiss-Prot 31, all entries

100000-
      -
N     -
U50000-
M     -                          *
B     -
E     -
R     -
      -
O     -
F10000-
      -
S     *
E 5000-                                                          *
Q     -
U     -
E     -
N     -
C     -
E     -
S 1000-                                  *
      -
      -
   500-
      -
```



```
      -
      -
      -
      -
    100-
      -
      -
     50-
      -
      -
      -
      -
      -
      -
      -
     10-
      -
      -
      5-
      -
      -
      -
      -
      -
      -
      -
      0----------------------------------------------------------------------
       ||     |      |     | |      |      |      |   |  |      |      |
SCORE 0|     1      2     | 2      3      4      5   |  5      6      7
STDEV -1                  0        1                 2
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	3	4	1.71

Times:	CPU	Total Elapsed
	00:00:44.05	00:00:46.00

```
Number of residues:              15335248
Number of sequences searched:       43470
Number of scores above cutoff:       4077

Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.
Cut-off raised to 6.
Cut-off raised to 7.
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

4077 100% similar sequences to the query sequence were found:

	Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1.	YHP9_YEAST	HYPOTHETICAL 433.2 KD PROTEIN	3744	7	7	2.35	0
2.	YOG7_CAEEL	HYPOTHETICAL 375.7 KD PROTEIN	3343	7	7	2.35	0
3.	YNX3_CAEEL	HYPOTHETICAL 337.6 KD PROTEIN	3051	7	7	2.35	0
4.	ZFH2_DROME	ZINC-FINGER PROTEIN 2 (ZINC-F	3005	7	7	2.35	0
5.	YLJ6_CAEEL	HYPOTHETICAL 272.0 KD PROTEIN	2329	7	7	2.35	0
6.	YCF2_EPIVI	HYPOTHETICAL 260 KD PROTEIN (	2216	7	7	2.35	0
7.	YE02_YEAST	HYPOTHETICAL 264.2 KD PROTEIN	2163	7	7	2.35	0
8.	YCF2_SPIOL	HYPOTHETICAL 250 KD PROTEIN (	2131	7	7	2.35	0
9.	YHD0_YEAST	HYPOTHETICAL 210.4 KD PROTEIN	1868	7	7	2.35	0
10.	YM68_CAEEL	HYPOTHETICAL 208.3 KD PROTEIN	1822	7	7	2.35	0
11.	YO25_CAEEL	HYPOTHETICAL 202.6 KD PROTEIN	1799	7	7	2.35	0
12.	YKB4_YEAST	HYPOTHETICAL 203.3 KD PROTEIN	1764	7	7	2.35	0
13.	YIR7_YEAST	HYPOTHETICAL 197.5 KD PROTEIN	1758	7	7	2.35	0
14.	YCFX_TOBAC	HYPOTHETICAL 199 KD PROTEIN (	1708	7	7	2.35	0
15.	YK11_YEAST	HYPOTHETICAL 195.2 KD PROTEIN	1683	7	7	2.35	0
16.	YHD5_YEAST	PROBABLE ATP-DEPENDENT PERMEA	1592	7	7	2.35	0
17.	YCFI_YEAST	METAL RESISTANCE PROTEIN YCF1	1515	7	7	2.35	0
18.	YKB0_YEAST	HYPOTHETICAL 167.8 KD PROTEIN	1483	7	7	2.35	0
19.	YES3_YEAST	HYPOTHETICAL 164.4 KD PROTEIN	1430	7	7	2.35	0
20.	YIP9_YEAST	HYPOTHETICAL 156.9 KD PROTEIN	1375	7	7	2.35	0
21.	YOL4_CAEEL	HYPOTHETICAL 152.4 KD PROTEIN	1351	7	7	2.35	0
22.	YKF5_CAEEL	HYPOTHETICAL 153.4 KD PROTEIN	1330	7	7	2.35	0
23.	YTX2_XENLA	TRANSPOSON TX1 HYPOTHETICAL 1	1308	7	7	2.35	0
24.	YKZ8_CAEEL	HYPOTHETICAL 143.2 KD PROTEIN	1257	7	7	2.35	0
25.	YNCA_CAEEL	HYPOTHETICAL 142.5 KD PROTEIN	1254	7	7	2.35	0
26.	YED1_YEAST	PROBABLE E1-E2 ATPASE YEL031W	1215	7	7	2.35	0
27.	YK76_YEAST	HYPOTHETICAL 137.5 KD PROTEIN	1195	7	7	2.35	0
28.	YKD8_YEAST	PUTATIVE 128.2 KD TRANSCRIPTI	1170	7	7	2.35	0
29.	YK62_YEAST	HYPOTHETICAL 133.3 KD PROTEIN	1157	7	7	2.35	0
30.	YIE8_YEAST	PROBABLE E1-E2 ATPASE YIL048W	1151	7	7	2.35	0
31.	YHJL_ECOLI	HYPOTHETICAL 125.7 KD PROTEIN	1139	7	7	2.35	0
32.	YEU0_YEAST	HYPOTHETICAL 122.6 KD PROTEIN	1113	7	7	2.35	0
33.	YLD5_CAEEL	HYPOTHETICAL 127.9 KD PROTEIN	1112	7	7	2.35	0
34.	YJEP_ECOLI	HYPOTHETICAL 123.8 KD PROTEIN	1107	7	7	2.35	0
35.	YKD5_CAEEL	PUTATIVE SERINE/THREONINE-PRO	1087	7	7	2.35	0
36.	YJ84_YEAST	HYPOTHETICAL 121.4 KD PROTEIN	1058	7	7	2.35	0
37.	YMG2_MYCGE	HYPOTHETICAL 114.4 KD PROTEIN	1052	7	7	2.35	0
38.	YKT3_CAEEL	PUTATIVE SERINE/THREONINE-PRO	1044	7	7	2.35	0
39.	YO43_CAEEL	HYPOTHETICAL 115.4 KD PROTEIN	1040	7	7	2.35	0
40.	YHIV_ECOLI	HYPOTHETICAL 111.5 KD PROTEIN	1037	7	7	2.35	0
41.	YKF7_YEAST	HYPOTHETICAL 120.4 KD PROTEIN	1037	7	7	2.35	0
42.	YIM8_YEAST	HYPOTHETICAL 117.9 KD PROTEIN	1032	7	7	2.35	0
43.	YKZ6_CAEEL	HYPOTHETICAL 113.7 KD PROTEIN	1018	7	7	2.35	0
44.	PCK2_SCHPO	PROTEIN KINASE C-LIKE 2 (EC 2	1016	7	7	2.35	0
45.	DPOL_EBV	DNA POLYMERASE (EC 2.7.7.7).	1015	7	7	2.35	0

1. US-08-121-713B-22 (1-7)
   YHP9_YEAST HYPOTHETICAL 433.2 KD PROTEIN IN HXT5-CDC12 INTERG


```
ID   YHP9_YEAST     STANDARD;      PRT;  3744 AA.
AC   P38811;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 433.2 KD PROTEIN IN HXT5-CDC12 INTERGENIC REGION.
GN   YHR099W.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RM   94378003
RA   JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
RA   DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,
RA   KUCABA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,
RA   LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER L.,
RA   NHAN M., RIFKIN L., RILES L., ST.PETER H., TREVASKIS E., VAUGHAN K.,
RA   VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
RA   VAUDIN M.;
RL   SCIENCE 265:2077-2082(1994).
DR   EMBL; U00060; SCH9332.
DR   PIR; S46715; S46715.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   3744 AA;  433171 MW;  20943107 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             DXVXXXX
             | |
    PLVFALQQYPDLVSQGLRTLELCIDNL
          890 X     900
```

2. US-08-121-713B-22 (1-7)
   YOG7_CAEEL HYPOTHETICAL 375.7 KD PROTEIN ZK112.7 PRECURSOR IN

```
ID   YOG7_CAEEL     STANDARD;      PRT;  3343 AA.
AC   P34616;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 375.7 KD PROTEIN ZK112.7 PRECURSOR IN CHROMOSOME III.
GN   ZK112.7.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RM   94150718
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA   FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA   JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
RA   LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
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RA   SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA   SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA   WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA   WOHLDMAN P.;
RL   NATURE 368:32-38(1994).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC   -!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY OF CELL ADHESION
CC       MOLECULES. STRONG, TO D.MELANOGASTER FAT TUMOR SUPPRESSOR.
DR   EMBL; L14324; CEZK112.
DR   PIR; S44887; S44887.
DR   WORMPEP; ZK112.7; CE00378.
DR   PROSITE; PS00232; CADHERIN.
KW   HYPOTHETICAL PROTEIN; CELL ADHESION; SIGNAL; TRANSMEMBRANE;
KW   CYTOSKELETON; GLYCOPROTEIN; CALCIUM-BINDING; REPEAT.
FT   SIGNAL        1      ?       POTENTIAL.
FT   CHAIN         ?   3343       HYPOTHETICAL PROTEIN ZK112.7.
FT   DOMAIN        ?   3228       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   3229   3250       POTENTIAL.
FT   DOMAIN     3251   3343       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     22     22       POTENTIAL.
FT   CARBOHYD    149    149       POTENTIAL.
FT   CARBOHYD    250    250       POTENTIAL.
FT   CARBOHYD    288    288       POTENTIAL.
FT   CARBOHYD    369    369       POTENTIAL.
FT   CARBOHYD    467    467       POTENTIAL.
FT   CARBOHYD    612    612       POTENTIAL.
FT   CARBOHYD    752    752       POTENTIAL.
FT   CARBOHYD    806    806       POTENTIAL.
FT   CARBOHYD    941    941       POTENTIAL.
FT   CARBOHYD    966    966       POTENTIAL.
FT   CARBOHYD    970    970       POTENTIAL.
FT   CARBOHYD    985    985       POTENTIAL.
FT   CARBOHYD   1042   1042       POTENTIAL.
FT   CARBOHYD   1335   1335       POTENTIAL.
FT   CARBOHYD   1425   1425       POTENTIAL.
FT   CARBOHYD   1429   1429       POTENTIAL.
FT   CARBOHYD   1557   1557       POTENTIAL.
FT   CARBOHYD   1563   1563       POTENTIAL.
FT   CARBOHYD   1597   1597       POTENTIAL.
FT   CARBOHYD   1624   1624       POTENTIAL.
FT   CARBOHYD   1695   1695       POTENTIAL.
FT   CARBOHYD   1702   1702       POTENTIAL.
FT   CARBOHYD   1895   1895       POTENTIAL.
FT   CARBOHYD   1900   1900       POTENTIAL.
FT   CARBOHYD   2053   2053       POTENTIAL.
FT   CARBOHYD   2129   2129       POTENTIAL.
FT   CARBOHYD   2203   2203       POTENTIAL.
FT   CARBOHYD   2382   2382       POTENTIAL.
FT   CARBOHYD   2391   2391       POTENTIAL.
FT   CARBOHYD   2410   2410       POTENTIAL.
FT   CARBOHYD   2414   2414       POTENTIAL.
FT   CARBOHYD   2431   2431       POTENTIAL.
FT   CARBOHYD   2527   2527       POTENTIAL.
FT   CARBOHYD   2530   2530       POTENTIAL.
FT   CARBOHYD   2564   2564       POTENTIAL.
FT   CARBOHYD   2621   2621       POTENTIAL.
FT   CARBOHYD   2665   2665       POTENTIAL.
FT   CARBOHYD   2712   2712       POTENTIAL.
FT   CARBOHYD   2798   2798       POTENTIAL.
FT   CARBOHYD   2809   2809       POTENTIAL.
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FT   CARBOHYD   2927   2927       POTENTIAL.
FT   CARBOHYD   2976   2976       POTENTIAL.
FT   CARBOHYD   3045   3045       POTENTIAL.
FT   CARBOHYD   3222   3222       POTENTIAL.
FT   CARBOHYD   3225   3225       POTENTIAL.
SQ   SEQUENCE   3343 AA;  375745 MW;  22105723 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    PTQSELINHVDLVSTQNSDMKPFMMTL
      1070    X 1080      1090


3. US-08-121-713B-22 (1-7)
   YNX3_CAEEL   HYPOTHETICAL 337.6 KD PROTEIN T20G5.3 IN CHROMOSOM

ID   YNX3_CAEEL     STANDARD;      PRT;  3051 AA.
AC   P34576;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 337.6 KD PROTEIN T20G5.3 IN CHROMOSOME III.
GN   T20G5.3.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   BERKS M., SMITH A.;
RL   SUBMITTED (DEC-1993) TO THE SWISS-PROT DATA BANK.
CC   -!- SIMILARITY: TO EGF AND CMP REPEATS.
DR   EMBL; Z30423; CET20G5.
DR   PIR; S42373; S42373.
DR   WORMPEP; T20G5.3; CE00478.
DR   PROSITE; PS00022; EGF.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   3051 AA;  337581 MW;  20021622 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    VQTTCPKQKTDLVFLIDGSGSIGSYVF
        510   X   520       530


4. US-08-121-713B-22 (1-7)
   ZFH2_DROME   ZINC-FINGER PROTEIN 2 (ZINC-FINGER HOMEODOMAIN PRO

ID   ZFH2_DROME     STANDARD;      PRT;  3005 AA.
AC   P28167;
DT   01-OCT-1994 (REL. 30, CREATED)
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DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   ZINC-FINGER PROTEIN 2 (ZINC-FINGER HOMEODOMAIN PROTEIN 2).
GN   ZFH-2.
OS   DROSOPHILA MELANOGASTER (FRUIT FLY).
OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92001539
RA   FORTINI M.E., LAI Z., RUBIN G.M.;
RL   MECH. DEV. 34:113-122(1991).
CC   -!- FUNCTION: INVOLVED IN THE DEVELOPMENT OF THE EMBRYONIC CENTRAL
CC       NERVOUS SYSTEM.
CC   -!- TISSUE SPECIFICITY: LARGELY RESTRICTED TO THE CNS OF LATE EMBRYO.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC   -!- SIMILARITY: CONTAINS THREE HOMEOBOX DOMAINS.
DR   EMBL; M63450; DMZFH2.
DR   PIR; S27817; S27817.
DR   PIR; S33642; S33642.
DR   HSSP; P02836; 1HDD.
DR   FLYBASE; FBGN0004607; ZFH2.
KW   ZINC-FINGER; METAL-BINDING; DNA-BINDING; HOMEOBOX; NUCLEAR PROTEIN;
KW   REPEAT.
FT   ZN_FING     133    156       C2H2-TYPE.
FT   ZN_FING     559    582       C2H2-TYPE.
FT   ZN_FING     614    638       C2H2-TYPE.
FT   ZN_FING     732    756       C2H2-TYPE.
FT   ZN_FING     897    916       C2H2-TYPE (DEGENERATE).
FT   ZN_FING     940    964       C2H2-TYPE.
FT   ZN_FING     999   1023       C2H2-TYPE.
FT   ZN_FING    1074   1098       C2H2-TYPE.
FT   ZN_FING    1210   1233       C2H2-TYPE.
FT   ZN_FING    1341   1365       C2H2-TYPE.
FT   ZN_FING    1438   1462       C2H2-TYPE.
FT   ZN_FING    1477   1500       C2H2-TYPE (DEGENERATE).
FT   ZN_FING    1513   1535       C2H2-TYPE.
FT   ZN_FING    1541   1564       C2H2-TYPE.
FT   DNA_BIND   1797   1856       HOMEOBOX 1.
FT   DNA_BIND   2154   2213       HOMEOBOX 2.
FT   ZN_FING    2234   2256       C2H2-TYPE.
FT   ZN_FING    2371   2393       C2H2-TYPE.
FT   DNA_BIND   2760   2819       HOMEOBOX 3.
SQ   SEQUENCE   3005 AA;  332056 MW;  22430417 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             DXVXXXX
             | |
    SSFSFLKQQQDLVDPPEQCLTNQNADT
2010       2020       2030
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5. US-08-121-713B-22 (1-7)
   YLJ6_CAEEL HYPOTHETICAL 272.0 KD PROTEIN C50C3.6 IN CHROMOSOM

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ID   YLJ6_CAEEL     STANDARD;      PRT;  2329 AA.
AC   P34369;
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DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 272.0 KD PROTEIN C50C3.6 IN CHROMOSOME III.
GN   C50C3.6.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RM   94150718
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA   FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA   JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
RA   LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA   SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA   WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA   WOHLDMAN P.;
RL   NATURE 368:32-38(1994).
DR   EMBL; L14433; CEC50C3.
DR   PIR; S44625; S44625.
DR   WORMPEP; C50C3.6; CE00122.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   2329 AA;  272025 MW;  19536537 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             DXVXXXX
             | |
   LYRLANQLLTDLVDDNYFYLFDMKSFF
    230       240  X    250
```

6. US-08-121-713B-22 (1-7)
   YCF2_EPIVI HYPOTHETICAL 260 KD PROTEIN (ORF 2216).

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ID   YCF2_EPIVI     STANDARD;      PRT;  2216 AA.
AC   P30072;
DT   01-APR-1993 (REL. 25, CREATED)
DT   01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 260 KD PROTEIN (ORF 2216).
GN   YCF2.
OS   EPIFAGUS VIRGINIANA (BEECHDROPS).
OG   CHLOROPLAST.
OC   EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC   SCROPHULARIALES; OROBANCHACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   93066301
RA   WOLFE K.H., MORDEN C.W., PALMER J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 89:10648-10652(1992).
CC   -!- SIMILARITY: TO A SIMILAR ORF IN OTHER PLANTS CHLOROPLAST.
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 DR   EMBL; M81884; CHEVCG.
 KW   CHLOROPLAST; HYPOTHETICAL PROTEIN.
 SQ   SEQUENCE   2216 AA;  259511 MW;  21025832 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    DLFTLSITEPDLVYHKGFSFSIYMDQK
           630       640
```

7. US-08-121-713B-22 (1-7)
   YE02_YEAST   HYPOTHETICAL 264.2 KD PROTEIN IN RAD3-BMH1 INTERGE

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 ID   YE02_YEAST     STANDARD;      PRT;  2163 AA.
 AC   P32639;
 DT   01-OCT-1993 (REL. 27, CREATED)
 DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE   HYPOTHETICAL 264.2 KD PROTEIN IN RAD3-BMH1 INTERGENIC REGION.
 GN   YER172C OR SYGP-ORF66.
 OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=S288C / AB972;
 RA   DIETRICH F.S., MULLIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R.,
 RA   AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M.,
 RA   CHUNG E., DUNCAN M., GUZMAN E., HARTZELL G., HUNICKE-SMITH S.,
 RA   HYMAN R., KAYSER A., KOMP C., LASHKARI D., LEW H., LIN D.,
 RA   MOSEDALE D., NAKAHARA K., NAMATH A., NORGREN R., OEFNER P., OH C.,
 RA   PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN T., SMITH V.,
 RA   TAYLOR P., WEI Y., YELTON M., BOTSTEIN D., DAVIS R.W.;
 RL   SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RN   [2]
 RP   SEQUENCE OF 1-169 FROM N.A.
 RA   MULLIGAN J.T., DIETRICH F.S., HENNESSEY K.M., SEHL P., KOMP C.,
 RA   WEI Y., TAYLOR P., NAKAHARA K., ROBERTS D., DAVIS R.W.;
 RL   SUBMITTED (FEB-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
 CC   -!- SIMILARITY: TO HUMAN HYPOTHETICAL MYELOBLAST PROTEIN (D29641).
 DR   EMBL; U18922; U18922.
 DR   EMBL; L11229; SCSYGP5.
 DR   PIR; S30856; S30856.
 KW   HYPOTHETICAL PROTEIN; ATP-BINDING.
 FT   NP_BIND      79     86       ATP (POTENTIAL).
 FT   NP_BIND     521    528       ATP (POTENTIAL).
 SQ   SEQUENCE   2163 AA;  246183 MW;  18812673 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    IEKMVAKGLNDLVEQYKFRETTHSKRE
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        380   X   390       400
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8. US-08-121-713B-22 (1-7)
   YCF2_SPIOL   HYPOTHETICAL 250 KD PROTEIN (ORF 2131).

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 ID   YCF2_SPIOL     STANDARD;      PRT;  2131 AA.
 AC   P08973;
 DT   01-NOV-1988 (REL. 09, CREATED)
 DT   01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
 DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
 DE   HYPOTHETICAL 250 KD PROTEIN (ORF 2131).
 GN   YCF2.
 OS   SPINACIA OLERACEA (SPINACH).
 OG   CHLOROPLAST.
 OC   EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
 OC   CARYOPHYLLALES; CHENOPODIACEAE.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RM   88295221
 RA   ZHOU D.X., MASSENET O., QUIGLEY F., MARION M.J., MONEGER F.,
 RA   HUBER P., MACHE R.;
 RL   CURR. GENET. 13:433-439(1988).
 CC   -!- SIMILARITY: TO A SIMILAR ORF IN OTHER PLANTS CHLOROPLAST.
 DR   EMBL; X07908; CHSO2131.
 DR   PIR; S01446; S01446.
 KW   CHLOROPLAST; HYPOTHETICAL PROTEIN.
 SQ   SEQUENCE   2131 AA;  249964 MW;  19992229 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             DXVXXXX
             | |
    GSITMGSNVRDLVAFINEALSISITQK
        1680  X   1690
```

9. US-08-121-713B-22 (1-7)
   YHD0_YEAST   HYPOTHETICAL 210.4 KD PROTEIN IN GUT1-RIM1 INTERGE

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 ID   YHD0_YEAST     STANDARD;      PRT;  1868 AA.
 AC   P38737;
 DT   01-FEB-1995 (REL. 31, CREATED)
 DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE   HYPOTHETICAL 210.4 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION.
 GN   YHL030W.
 OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=S288C / AB972;
 RM   94378003
 RA   JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
 RA   DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,
 RA   KUCABA T., HILLIER L., JIER M., JOHNSTON L., LANGSTON Y.,
 RA   LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER L.,
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RA   NHAN M., RIFKIN L., RILES L., ST.PETER H., TREVASKIS E., VAUGHAN K.,
RA   VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
RA   VAUDIN M.;
RL   SCIENCE 265:2077-2082(1994).
DR   EMBL; U11583; SCH9196.
DR   PIR; S48938; S48938.
KW   HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
FT   TRANSMEM    695    715       POTENTIAL.
FT   TRANSMEM    747    767       POTENTIAL.
SQ   SEQUENCE   1868 AA;  210430 MW;  17651645 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =     28%  Matches         =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             DXVXXXX
             | |
    VRNFALTTLIDLVKHSPGAIKPFTPKL
       1300   X  1310      1320
```

10. US-08-121-713B-22 (1-7)
    YM68_CAEEL HYPOTHETICAL 208.3 KD PROTEIN K12H4.8 IN CHROMOSOM

```
ID   YM68_CAEEL     STANDARD;      PRT;  1822 AA.
AC   P34529;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 208.3 KD PROTEIN K12H4.8 IN CHROMOSOME III.
GN   K12H4.8.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RM   94150718
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA   FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA   JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
RA   LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA   SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA   WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA   WOHLDMAN P.;
RL   NATURE 368:32-38(1994).
CC   -!- SIMILARITY: TO EUKARYOTIC INITIATION FACTOR-4A AND RIBONUCLEASE
CC       III.
DR   EMBL; L14331; CEK12H4.
DR   PIR; S44849; S44849.
DR   WORMPEP; K12H4.8; CE00273.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   1822 AA;  208291 MW;  15724531 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =     28%  Matches         =      2  Mismatches   =     5
```



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Gaps             =      0  Conservative Substitutions              =     0

             X     X
             DXVXXXX
             | |
    AMDSVIETASDLVSLSKYGAKPYEVVI
         210  X    220
```

11. US-08-121-713B-22 (1-7)
    YO25_CAEEL HYPOTHETICAL 202.6 KD PROTEIN ZK688.5 IN CHROMOSOM

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ID   YO25_CAEEL     STANDARD;      PRT;  1799 AA.
AC   P34675;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 202.6 KD PROTEIN ZK688.5 IN CHROMOSOME III.
GN   ZK688.5.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RM   94150718
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA   FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA   JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
RA   LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA   SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA   WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA   WOHLDMAN P.;
RL   NATURE 368:32-38(1994).
DR   EMBL; L16621; CEZK688.
DR   PIR; S44920; S44920.
DR   WORMPEP; ZK688.5; CE00463.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   1799 AA;  202641 MW;  15440747 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =     28%  Matches         =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             DXVXXXX
             | |
    DKKTRDVIESDLVKMRGYKRNIGSRNQ
         1610 X    1620
```

12. US-08-121-713B-22 (1-7)
    YKB4_YEAST HYPOTHETICAL 203.3 KD PROTEIN IN PUT3-CCE1 INTERGE

```
ID   YKB4_YEAST     STANDARD;      PRT;  1764 AA.
AC   P34241; P34242;
DT   01-FEB-1994 (REL. 28, CREATED)
```

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DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 203.3 KD PROTEIN IN PUT3-CCE1 INTERGENIC REGION.
GN   YKL014C.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   94205264
RA   WIEMANN S., VOSS H., SCHWAGER C., RUPP T., STEGEMANN J.,
RA   ZIMMERMANN J., GROTHUES D., SENSEN C., ERFLE H., HEWITT N.,
RA   BANREVI A., ANSORGE W.;
RL   YEAST 9:1343-1348(1993).
RN   [2]
RP   REVISIONS.
RA   WIEMANN S., VOSS H., SCHWAGER C., RUPP T., STEGEMANN J.,
RA   ZIMMERMANN J., GROTHUES D., SENSEN C., ERFLE H., HEWITT N.,
RA   BANREVI A., ANSORGE W.;
RL   SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; X74152; SCPUKGA.
DR   EMBL; Z28014; SCYKL014C.
DR   PIR; S37827; S37827.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   1764 AA;  203286 MW;  16178809 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            DXVXXXX
            | |
    TNNYDATTRCDLVKKYYDDTERSGVDM
        1400 X    1410
```

13. US-08-121-713B-22 (1-7)
    YIR7_YEAST HYPOTHETICAL 197.5 KD PROTEIN IN SUC2 5'REGION.

```
ID   YIR7_YEAST     STANDARD;      PRT;  1758 AA.
AC   P40434;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 197.5 KD PROTEIN IN SUC2 5'REGION.
GN   YIL177C.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RA   BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,
RA   CHURCHER C.M., CONNOR R., COPSEY T., DEAR S., DEVLIN K., FRASER A.,
RA   GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES M.,
RA   LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D.,
RA   RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
RA   WALSH S.V., WHITEHEAD S.;
RL   SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SIMILARITY: TO HYPOTHETICAL PROTEIN IN SUBTELOMERIC Y'REPEAT
CC       (Z46921).
```



```
DR   EMBL; Z47047; SCCHRIX.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   1758 AA;  197511 MW;  15509879 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            DXVXXXX
            | |
    EFESALNNKNDLVHCPSITLFESIPTE
       20     X  30 X      40
```

14. US-08-121-713B-22 (1-7)
    YCFX_TOBAC HYPOTHETICAL 199 KD PROTEIN (ORF 1708).

```
ID   YCFX_TOBAC     STANDARD;      PRT;  1708 AA.
AC   P09977;
DT   01-MAR-1989 (REL. 10, CREATED)
DT   01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 199 KD PROTEIN (ORF 1708).
GN   YCF2.
OS   NICOTIANA TABACUM (COMMON TOBACCO).
OG   CHLOROPLAST.
OC   EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC   SOLANALES; SOLANACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. BRIGHT YELLOW 4;
RA   SUGIURA M.;
RL   SUBMITTED (AUG-1986) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   COMPLETE GENOME.
RA   SHINOZAKI K., OHME M., TANAKA M., WAKASUGI T., HAYASHIDA N.,
RA   MATSUBAYASHI T., ZAITA N., CHUNWONGSE J., OBOKATA J.,
RA   YAMAGUCHI-SHINOZAKI K., OHTO C., TORAZAWA K., MENG B.Y., SUGITA M.,
RA   DENO H., KAMOGASHIRA T., YAMADA K., KUSUDA J., TAKAIWA F., KATO A.,
RA   TOHDOH N., SHIMADA H., SUGIURA M.;
RL   EMBO J. 5:2043-2049(1986).
CC   -!- FUNCTION: NOT YET KNOWN.
CC   -!- SIMILARITY: TO A SIMILAR ORF IN OTHER PLANTS CHLOROPLAST.
CC   -!- CAUTION: IN TOBACCO THIS ORF IS IN TWO PARTS: ORF 581 (N-TERMINAL)
CC       AND ORF 1708 (C-TERMINAL). IT COULD BE DUE TO A FRAMESHIFT ERROR.
DR   EMBL; Z00044; CHNTXX.
DR   PIR; A05205; A05205.
KW   CHLOROPLAST; HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   1708 AA;  199282 MW;  15156803 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.35
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            DXVXXXX
            | |
    DLFTLSITEPDLVYHKGFAFSIDSCGL
      50      X 60  X     70
```

15. US-08-121-713B-22 (1-7)
YK11_YEAST HYPOTHETICAL 195.2 KD PROTEIN IN GCN3-DAL80 INTERG

ID YK11_YEAST STANDARD; PRT; 1683 AA.
AC P36126;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 195.2 KD PROTEIN IN GCN3-DAL80 INTERGENIC REGION.
GN YKR031C.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RA URRESTARAZU L.A., JAUNIAUX J.-C.;
RL SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; Z28256; SCYKR031C.
DR PIR; S38103; S38103.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 1683 AA; 195203 MW; 14046134 CN;

Initial Score = 7 Optimized Score = 7 Significance = 2.35
Residue Identity = 28% Matches = 2 Mismatches = 5
Gaps = 0 Conservative Substitutions = 0

```
            X     X
            DXVXXXX
            | |
   LMREHLGCDVDLVEFVEKKFERFEKFA
 1160      1170    X 1180
```

maryh@stic **stdin**

NeWSprinter20

Fri May 19 11:10:08 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

Salata 121713

SEQ 24

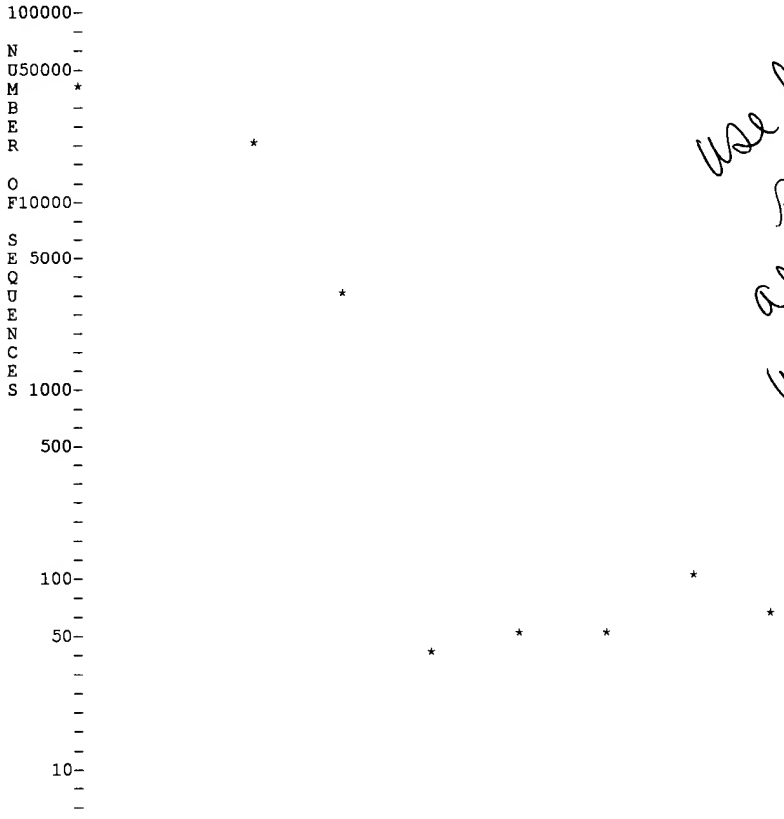
```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

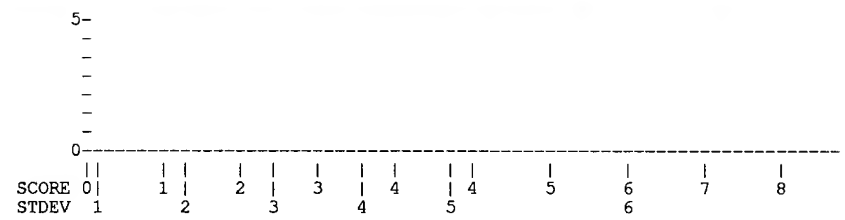
Results file sq24asq.res made by  on Fri 19 May 95 8:41:37-PDT.


Query sequence being compared:US-08-121-713B-24 (1-8)
Number of sequences searched:               53402
Number of scores above cutoff:               3843

     Results of the initial comparison of US-08-121-713B-24 (1-8) with:
   Data bank : A-GeneSeq 18, all entries
```



use less search all amino acids were "X"



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	0	1	1.09

Times:	CPU	Total Elapsed
	00:00:30.06	00:00:31.00

Number of residues: 6354270
Number of sequences searched: 53402
Number of scores above cutoff: 3843

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

63 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. R11749	Human alpha-2 macroglobulin b	1484	8	8	7.32	0
2. R11334	Recombinant human alpha-2 mac	1474	8	8	7.32	0
3. R32356	Excitory amino acid receptor	956	8	8	7.32	0
4. R41232	GAT-3 transporter.	632	8	8	7.32	0
5. R41229	GAT-3 GABA transporter.	627	8	8	7.32	0
6. R49590	GAT-B transporter.	627	8	8	7.32	0
7. R51267	Sequence of human prostagland	604	8	8	7.32	0
8. R51268	Sequence of murine prostaglan	604	8	8	7.32	0
9. R36533	Gp85-97 clone 18 prod.	585	8	8	7.32	0
10. R40213	Sequence of a 90K tumour-asso	585	8	8	7.32	0

11.	R40172	Sequence of an immunoregulin	585	8	8	7.32	0
12.	R41359	Tumour associated 90K antigen	585	8	8	7.32	0
13.	R40784	Sequence of cyclophilin assoc	574	8	8	7.32	0
14.	R26843	GDP dissociation stimulatory	558	8	8	7.32	0
15.	R07466	Polypeptide with enzymatic ac	492	8	8	7.32	0
16.	R13984	Phytoene dehydrogenase-4H.	489	8	8	7.32	0
17.	R13985	Phytoene_dehydrogenase-4H fro	489	8	8	7.32	0
18.	P93630	Sequence of rat transin.	463	8	8	7.32	0
19.	R11704	Cytolysis Inhibitor.	448	8	8	7.32	0
20.	P60326	Interleukin-1 gene product.	295	8	8	7.32	0
21.	P60680	Prepro- and mature interleuki	295	8	8	7.32	0
22.	R14855	Mature Interleukin-1.	295	8	8	7.32	0
23.	P81197	Sequence encoded by human per	269	8	8	7.32	0
24.	R15747	Interleukin-1 beta with 116 a	269	8	8	7.32	0
25.	R15748	Interleukin-1 beta with 116 a	269	8	8	7.32	0
26.	P50043	Sequence of interleukin-1 (IL	269	8	8	7.32	0
27.	R42213	Human Interleukin-1.	269	8	8	7.32	0
28.	R06358	Monkey IL-2 beta deduced from	268	8	8	7.32	0
29.	P70306	Sequence of interleukin 1-bet	238	8	8	7.32	0
30.	P60307	Sequence of new antitumour su	238	8	8	7.32	0
31.	R42447	Human interleukin-1 beta prec	238	8	8	7.32	0
32.	P61521	Sequence of new antitumour su	199	8	8	7.32	0
33.	P61520	Sequence of new antitumour su	193	8	8	7.32	0
34.	P81873	Partial sequence of rabbit st	170	8	8	7.32	0
35.	R10613	Hybrid IL-1 beta/alpha-1 anti	159	8	8	7.32	0
36.	P94906	Sequence of amino-terminal ex	157	8	8	7.32	0
37.	R03065	Human interleukin-1-beta expr	154	8	8	7.32	0
38.	P70525	Interleukin-2 encoded by plas	154	8	8	7.32	0
39.	R23668	Interleukin-1 beta Ser 63, Se	154	8	8	7.32	0
40.	R23669	Interleukin-1 beta Ala 126 Al	154	8	8	7.32	0
41.	P90473	Human interleukin-1-beta modi	153	8	8	7.32	0
42.	R04209	Interleukin - 1 beta sequence	153	8	8	7.32	0
43.	R05386	polypeptide with pysiological	153	8	8	7.32	0
44.	R06269	Radioactive iodine labeled in	153	8	8	7.32	0
45.	R07286	Interleukin-1-beta deriv.	153	8	8	7.32	0

1. US-08-121-713B-24 (1-8)
R11749 Human alpha-2 macroglobulin bait region mutant.

ID R11749 standard; Protein; 1484 AA.
AC R11749;
DT 04-JUN-1991 (first entry)
DE Human alpha-2 macroglobulin bait region mutant.
KW Human alpha-2 macroglobulin; growth media; proteinase inhibitor.
OS Homo sapiens.
FH Region 701..759
FH /label= PZP bait region
FT Key Location/Qualifiers
PN WO9103557-A.
PD 21-MAR-1991.
PF 29-AUG-1990; DK0225.
PR 29-AUG-1989; DK-004237.
PR 29-AUG-1989; DK-004235.
PR 29-AUG-1989; DK-004236.
PA (NOVO) NOVO NORDISK A/S.
PI Esper B, Lars S-J;
DR WPI; 91-102075/14.
DR N-PSDB; Q11581.
PT DNA encoding alpha macro-globulin - used to produce recombinant

PT protein for use in growth media, proteinase inhibitors and as
PT carriers
PS Disclosure; page 47; 78pp; English.
CC This alpha-2 macroglobulin bait mutant comprises a bait region from
CC the human pregnancy zone protein (PZP). It has a proteinase inhib-
CC itor profile similar to that of the human PZP. It is useful as an
CC additive to growth-media and as a carrier in gene- and enzyme rep-
CC lacement-therapy as well as being a proteinase inhibitor..
CC See also Q11176.
SQ Sequence 1484 AA;
SQ 95 A; 44 R; 66 N; 51 D; 0 B; 25 C; 75 Q; 101E; 0 Z; 94 G; 37 H;
SQ 58 I; 144L; 89 K; 24 M; 61 F; 82 P; 125S; 101T; 12 W; 58 Y; 142V;

Initial Score = 8 Optimized Score = 8 Significance = 7.32
Residue Identity = 0% Matches = 0 Mismatches = 8
Gaps = 0 Conservative Substitutions = 0

X X
XXXXXXXX

PKGNRIAQWQSFQLEGGLKQFSFPLSSE
170 180 190

2. US-08-121-713B-24 (1-8)
R11334 Recombinant human alpha-2 macroglobulin.

ID R11334 standard; Protein; 1474 AA.
AC R11334;
DT 04-JUN-1991 (first entry)
DE Recombinant human alpha-2 macroglobulin.
KW Human alpha-2 macroglobulin; growth media; proteinase inhibitor.
OS Homo sapiens.
PN WO9103557-A.
PD 21-MAR-1991.
PF 29-AUG-1990; DK0225.
PR 29-AUG-1989; DK-004237.
PR 29-AUG-1989; DK-004235.
PR 29-AUG-1989; DK-004236.
PA (NOVO) NOVO NORDISK A/S.
PI Esper B, Lars S-J;
DR WPI; 91-102075/14.
DR N-PSDB; Q11581.
PT DNA encoding alpha macro-globulin - used to produce recombinant
PT protein for use in growth media, proteinase inhibitors and as
PT carriers
PS Disclosure; page 34; 78pp; English.
CC This recombinant human alpha-2 macroglobulin is useful as an add-
CC itive to growth-media, as a proteinase inhibitor and as a carrier
CC in gene- and enzyme replacement-therapy. See also Q11581.
SQ Sequence 1474 AA;
SQ 94 A; 46 R; 63 N; 53 D; 0 B; 25 C; 73 Q; 104E; 0 Z; 91 G; 41 H;
SQ 57 I; 143L; 89 K; 26 M; 62 F; 76 P; 123S; 101T; 11 W; 56 Y; 140V;

Initial Score = 8 Optimized Score = 8 Significance = 7.32
Residue Identity = 0% Matches = 0 Mismatches = 8
Gaps = 0 Conservative Substitutions = 0

X X
XXXXXXXX

```
    PKGNRIAQWQSFQLEGGLKQFSFPLSSE
  170       180       190
```

3. US-08-121-713B-24 (1-8)
   R32356 Excitory amino acid receptor 1.

```
ID   R32356 standard; Protein; 956 AA.
AC   R32356;
DT   21-JUN-1993  (first entry)
DE   Excitory amino acid receptor 1.
KW   EAAR-1; brain; kainate; glutamate; assay; CNS.
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT   /note= "signal peptide"
FT   Protein         21..956
FT   /note= "mature protein"
PN   EP-529994-A.
PD   03-MAR-1993.
PF   25-AUG-1992; 307723.
PR   26-AUG-1991; US-750090.
PA   (ALLE-) ALLELIX BIOPHARMACEUTICALS INC.
PI   Kamboj R,  Nutt SL,  Shekter L,  Wosnick MA;
DR   WPI; 93-069001/09.
DR   N-PSDB; Q36915.
PT   Polynucleotide sequence encoding human excitatory amino acid-1
PT   receptor - for assaying cpds. which bind to the receptor in
PT   screening for new CNS drugs
PS   Disclosure; Fig 1; 28pp; English.
CC   Human hippocampal cNDA was subjected to PCR amplification using
CC   primers corresp. to regions of the rat GluR1 gene.  The amplified
CC   prod. was labelled and used to probe a cDNA library from the same
CC   source and 50 positive clones isolated; one contained a 1058 bp
CC   sequence.  This was labelled and used to screen a different
CC   hippocampal cDNA library to identify two overlapping clones from
CC   which the 67 kb phagemid pBS/HumEPP1a (ATCC 75063) contg. the entire
CC   open reading frame for EAA1a receptor was constructed.  This
CC   complete insert could be removed as a 3.7 kb NotI fragment.  The
CC   sequence encodes the excitatory amino acid -1 receptor (R) or a
CC   kainate binding fragment of it.  (R) binds glutamate and has ligand
CC   binding properties characteristic of Kainate-type EAA receptors.  Cells
CC   contg. the gene may be used to assay cpds. for possible use in treatment
CC   of CNS disorders.
SQ   Sequence   956 AA;
SQ   71 A; 59 R; 42 N; 34 D; 0  B; 24 C; 39 Q; 65 E; 0  Z; 61 G; 19 H;
SQ   58 I; 105L; 33 K; 28 M; 45 F; 45 P; 71 S; 54 T; 15 W; 28 Y; 60 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.32
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    ACLICAKAECLLNLEKLLRQFLISKDTL
         170 X     180
```

4. US-08-121-713B-24 (1-8)

R41232 GAT-3 transporter.

```
ID   R41232 standard; Protein; 632 AA.
AC   R41232;
DT   22-MAR-1994  (first entry)
DE   GAT-3 transporter.
KW   GABA transporter; gamma-aminobutyric acid; taurine transporter;
KW   translation inhibition; monoclonal antibodies; transgenic animals;
KW   cell membranes; epilepsy; anxiety; migraine; ischaemia.
OS   Homo sapiens.
PN   WO9318143-A.
PD   16-SEP-1993.
PF   04-MAR-1993; U01959.
PR   04-MAR-1992; US-847742.
PR   13-OCT-1992; US-959936.
PA   (SYNA-) SYNAPTIC PHARM CORP.
PI   Borden LA,  Hartig PR,  Smith KE,  Weinshank RL;
DR   WPI; 93-303457/38.
DR   N-PSDB; Q48764.
PT   New mammalian transporters for GABA or taurine - are used in
PT   drugs for treating epilepsy, anxiety ischaemia and form
PT   antibodies for detecting presence of the transporters on cell
PT   surface
PS   Claim 1; Fig 10B; 218pp; English.
CC   The sequences (Q48760-61) encode novel mammalian GABA transporters,
CC   sequences (Q48763-64) encode human GABA transporters. The sequences
CC   can be used as probes to detect specific mRNA (i.e expression of
CC   the transporter) and also for diagnosing a predisposition to disease
CC   associated with expression of a specific allele. Sequence (Q48762)
CC   shows a related taurine transporter gene.
SQ   Sequence   632 AA;
SQ   48 A; 20 R; 24 N; 15 D; 0  B; 27 C; 10 Q; 33 E; 0  Z; 55 G; 9  H;
SQ   49 I; 67 L; 26 K; 20 M; 38 F; 29 P; 35 S; 35 T; 19 W; 32 Y; 41 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.32
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    VVFFICCGIPVFFLETALGQFTSEGGIT
         100  X    110       120
```

5. US-08-121-713B-24 (1-8)
   R41229 GAT-3 GABA transporter.

```
ID   R41229 standard; Protein; 627 AA.
AC   R41229;
DT   22-MAR-1994  (first entry)
DE   GAT-3 GABA transporter.
KW   GABA transporter; gamma-aminobutyric acid; taurine transporter;
KW   translation inhibition; monoclonal antibodies; transgenic animals;
KW   cell membranes; epilepsy; anxiety; migraine; ischaemia.
OS   Rattus rattus.
PN   WO9318143-A.
PD   16-SEP-1993.
PF   04-MAR-1993; U01959.
PR   04-MAR-1992; US-847742.
```

```
PR   13-OCT-1992; US-959936.
PA   (SYNA-) SYNAPTIC PHARM CORP.
PI   Borden LA,  Hartig PR,  Smith KE,  Weinshank RL;
DR   WPI; 93-303457/38.
DR   N-PSDB; Q48761.
PT   New mammalian transporters for GABA or taurine - are used in
PT   drugs for treating epilepsy, anxiety ischaemia and form
PT   antibodies for detecting presence of the transporters on cell
PT   surface
PS   Claim 1; Fig 1B; 218pp; English.
CC   The sequences (Q48760-61) encode novel mammalian GABA transporters,
CC   sequences (Q48763-64) encode human GABA transporters. The sequences
CC   can be used as probes to detect specific mRNA (i.e expression of
CC   the transporter) and also for diagnosing a predisposition to disease
CC   associated with expression of a specific allele. Sequence (Q48762)
CC   shows a related taurine transporter gene.
SQ   Sequence   627 AA;
SQ   47 A; 22 R; 23 N; 14 D; 0  B; 25 C; 11 Q; 34 E; 0  Z; 58 G; 7  H;
SQ   45 I; 71 L; 26 K; 18 M; 40 F; 27 P; 33 S; 33 T; 19 W; 32 Y; 42 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.32
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    VVFFICCGIPVFFLETALGQFTSEGGIT
     90       100    X  110


6. US-08-121-713B-24 (1-8)
   R49590       GAT-B transporter.

 ID   R49590 standard; Protein; 627 AA.
 AC   R49590;
 DT   15-AUG-1994  (first entry)
 DE   GAT-B transporter.
 KW   GAT-B transporter; GABA transporter; neuron.
 OS   Rattus sp.
 FH   Key             Location/Qualifiers
 FT   Region          54..74
 FT   /note= "putative transmembrane region"
 FT   Region          81..101
 FT   /note= "putative transmembrane region"
 FT   Region          126..146
 FT   /note= "putative transmembrane region"
 FT   Misc_difference 148
 FT   /note= "potential N-glycosylation site"
 FT   Misc_difference 151
 FT   /note= "potential N-glycosylation site"
 FT   Misc-difference 159
 FT   /note= "potential N-glycosylation site"
 FT   Region          223..239
 FT   /note= "putative transmembrane region"
 FT   Region          248..270
 FT   /note= "putative transmembrane region"
 FT   Region          297..317
 FT   /note= "putative transmembrane region"
 FT   Region          330..351
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 FT   /note= "putative transmembrane region"
 FT   Region          383..403
 FT   /note= "putative transmembrane region"
 FT   Region          433..450
 FT   /note= "putative transmembrane region"
 FT   Region          468..488
 FT   /note= "putative transmembrane region"
 FT   Misc_difference 505
 FT   /note= "potential phosphorylation site for Ca2+
 FT   calmodulin-dependent protein-kinase II"
 FT   Region          509..528
 FT   /note= "putative transmembrane region"
 FT   Region          548..566
 FT   /note= "putative transmembrane region"
 FT   Misc_difference 598
 FT   /note= "potential phosphorylation site for
 FT   protein-kinase C"
 FT   Misc_difference 603
 FT   /note= "potential phosphorylation site for Ca2+
 FT   calmodulin-dependent protein-kinase II"
 PN   WO9404573-A.
 PD   03-MAR-1994.
 PF   12-AUG-1993; U07576.
 PR   14-AUG-1992; US-930078.
 PA   (UYOR-) UNIV OREGON HEALTH SCI.
 PI   Amara SG,  Clark JA;
 DR   WPI; 94-083116/10.
 DR   P-PSDB; Q44335.
 PT   DNA encoding a GAT-B transporter expressed in neurons but not in
 PT   glia - used to confer GAT-B expression on non-GAT-B producing
 PT   cells and render cells capable of GABA uptake
 PS   Disclosure; Fig 1; 44pp; English.
 CC   A sense primer (given in Q44336) and antisense primer (Q44337) were
 CC   used for PCR amplification of GAT-B cDNA isolated from a rat mid-
 CC   brain genomic library.  A cDNA clone was sequenced (Q44335) and
 CC   encoded GAT-B transporter (R49590).  Expression of GAT-B mRNA in rat
 CC   CNS was demonstrated by in situ hybridization using antisense
 CC   (Q44338) and sense (Q44339) probes.
 SQ   Sequence   627 AA;
 SQ   49 A; 21 R; 23 N; 14 D; 0  B; 25 C; 11 Q; 34 E; 0  Z; 59 G; 7  H;
 SQ   45 I; 68 L; 26 K; 18 M; 40 F; 25 P; 33 S; 33 T; 19 W; 32 Y; 45 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.32
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    VVFFICCGIPVFFLETALGQFTSEGGIT
     90       100    X  110


7. US-08-121-713B-24 (1-8)
   R51267       Sequence of human prostaglandin G/H synthase-2 (PG

 ID   R51267 standard; Protein; 604 AA.
 AC   R51267;
 DT   12-OCT-1994  (first entry)
 DE   Sequence of human prostaglandin G/H synthase-2 (PGHS-2).
```

```
KW   Prostaglandin; hormone; eicosanoid; fatty acid metabolism.
OS   Homo sapiens.
PN   WO9406919-A.
PD   31-MAR-1994.
PF   22-SEP-1993; U09167.
PR   22-SEP-1992; US-949780.
PR   01-DEC-1992; US-983835.
PR   22-MAR-1993; US-034143.
PR   28-APR-1993; US-054364.
PA   (UYRP ) UNIV ROCHESTER.
PI   Obanion MK,  Winn VD,  Young DA;
DR   WPI; 94-118468/14.
DR   N-PSDB; Q61790.
PT   New prostaglandin G/H synthase-2 gene - used for producing
PT   transgenic cell lines for testing ability of cpds. to inhibit
PT   synthesis of prostaglandin(s)
PS   Claim 40; Page 45-47; 76pp; English.
CC   RNA was isolated from a human fibroblast cell line (W138). PCR
CC   primers specific for the human PGHS-1 and PGHS-2 sequences were
CC   engineered to amplify the coding regions of either one transcript or
CC   the other (see Q61792-95). PCR products of about 2 kb were generated.
CC   Three PGHS-2 clones were sequenced in both directions. The clone
CC   comprising the PGHS-2 sequence disclosed in Q61790 was selected for
CC   transfection. This sequence differs from the human PGHS-2 sequence
CC   dislcosed by Hla and Heilson, PNAS, 89, 7384 (19920 due to a Glu
CC   rather than a Gly at AA posn. 165. Mouse PGHS-2 also has a Glu at
CC   this posn.
SQ   Sequence   604 AA;
SQ   32 A; 28 R; 29 N; 26 D; 0  B; 14 C; 33 Q; 34 E; 0  Z; 34 G; 19 H;
SQ   35 I; 60 L; 35 K; 14 M; 38 F; 40 P; 34 S; 34 T; 6  W; 26 Y; 33 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.32
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    YNYQQFIYNNSILLEHGITQFVESFTRQ
    390       400    X  410


8. US-08-121-713B-24 (1-8)
   R51268       Sequence of murine prostaglandin G/H synthase-2 (P

ID   R51268 standard; Protein; 604 AA.
AC   R51268;
DT   12-OCT-1994  (first entry)
DE   Sequence of murine prostaglandin G/H synthase-2 (PGHS-2).
KW   Prostaglandin; hormone; eicosanoid; fatty acid metabolism;
KW   griPGHS.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   Cleavage_site   17..18
FT   /label= signal peptide cleavage site
FT   Modified_site   54..56
FT   /label= potential N-glycosylation site
FT   /note= "see also 130-132,396-398,580-582"
FT   Modified_site   516
FT   /label= putative aspirin modified Ser
```



```
PN   WO9406919-A.
PD   31-MAR-1994.
PF   22-SEP-1993; U09167.
PR   22-SEP-1992; US-949780.
PR   01-DEC-1992; US-983835.
PR   22-MAR-1993; US-034143.
PR   28-APR-1993; US-054364.
PA   (UYRP ) UNIV ROCHESTER.
PI   Obanion MK,  Winn VD,  Young DA;
DR   WPI; 94-118468/14.
DR   N-PSDB; Q61791.
PT   New prostaglandin G/H synthase-2 gene - used for producing
PT   transgenic cell lines for testing ability of cpds. to inhibit
PT   synthesis of prostaglandin(s)
PS   Example; Figure 1; 76pp; English.
CC   cDNA was prepd. from poly-A enriched RNA from C127 cells of mouse
CC   fibroblasts. A directionally cloned cDNA library was constructed in
CC   lambda ZAP II. Several positive plaques were isolated and analysed.
CC   One about 4.1 kb in length was fully sequenced. This clone encodes
CC   a 70 kDa protein. The full sequence has been deposited in GenBank,
CC   accession number M88242. Comparison of the 4.1 kb sequence with
CC   that previously cloned 2.8 kb PGHS cDNA from mice revealed a
CC   single ORF with 64% AA identity to the protein encoded by the 2.8
CC   kb PGHS cDNA. The deduced portein sequences are colinear except
CC   that the 4.1 kb cDNA has a shorter amino-terminus and longer
CC   carboxy-terminus. 'X' in R51268 denotes the translation of codon
CC   TAN in Q61790, following the sequence as published.
SQ   Sequence   604 AA;
SQ   29 A; 27 R; 30 N; 25 D; 0  B; 13 C; 30 Q; 38 E; 0  Z; 38 G; 18 H;
SQ   34 I; 60 L; 35 K; 14 M; 37 F; 39 P; 34 S; 37 T; 6  W; 26 Y; 33 V;
SQ   1 Others;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.32
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    YSFKQFLYNNSILLEHGLTQFVESFTRQ
    390       400    X  410


9. US-08-121-713B-24 (1-8)
   R36533       Gp85-97 clone 18 prod.

ID   R36533 standard; Protein; 585 AA.
AC   R36533;
DT   19-AUG-1993  (first entry)
DE   Gp85-97 clone 18 prod.
KW   Glycoprotein; lectin; Mac-2; PHA; lymphocytes; leucoagglutinating;
KW   phytoheamagglutinin; cancer; amplification; PCR.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         1..18
FT   /note= "leader sequence"
FT   Protein         19..585
FT   /note= "mature gp85-97"
PN   WO9308215-A.
PD   29-APR-1993.
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PF   15-OCT-1992; U08878.
PR   16-OCT-1991; US-777121.
PR   15-OCT-1992; US-961404.
PA   (CETU ) CETUS ONCOLOGY CORP.
PI   Casipit CL,  Halenbeck R,  Koths KE,  Taylor EW,  Wang AM;
DR   WPI; 93-152424/18.
PT   New glyco:protein complex binding to human lectin Mac-2 - also
PT   interferes with PHA activation of lymphocytes for treating and
PT   preventing cancer, infectious diseases, etc.
PS   Claim 1; Page 41; 57pp; English.
CC   SK-BR-3 gp97 recovered in partially proteolysed form was denatured
CC   and reduced and the 97 and 70 kD mols. were purified using size
CC   exclusion HPLC in 0.1 percent SDS.  The 97 and 70 kD mols. were
CC   digested with Lys-C protease and the resulting peptides purified and
CC   sequenced.  The N-terminal sequence of gp97 was used to design
CC   degenerate primers for use in a PCR reaction on SK-BR-3 mRNA.  PCR
CC   reactions using primer 2 in combination with primers 1 and 3 gave prods.
CC   of 97 and 121 bp.  Further PCR using primers 2, 3 and 4 yielded DNA
CC   sequences of 740 and 765 respectively.  A DNA sequence was obtd. from
CC   the PCR prods. Two additional oligonucleotide sequences were
CC   synthesised based on this sequence and used to probe a THP-1 cDNA
CC   library to obtain the full-length cDNA sequence that encodes SK-BR-3
CC   gp97.  Both strands of clone 218 were sequenced.  It encodes a novel
CC   glycoprotein binds the Mac-2 lectin and interferes with PHA activation
CC   of lymphocytes.  It can be used for treating or preventing diseases that
CC   result from binding of a disease-causing agent to the cell surface of a
CC   target cell.  The gp. can be used in treatment of cancers, partic.
CC   breast  cancer.    See also R36532.
SQ   Sequence   585 AA;
SQ   48 A; 29 R; 17 N; 33 D; 0  B; 16 C; 29 Q; 31 E; 0  Z; 38 G; 9  H;
SQ   14 I; 72 L; 19 K; 9  M; 30 F; 28 P; 54 S; 36 T; 16 W; 22 Y; 35 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.32
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    DLYAYAVATGDALLEKLCLQFLAWNFEA
          270 X     280


10. US-08-121-713B-24 (1-8)
    R40213       Sequence of a 90K tumour-associated antigen, IR-95

ID   R40213 standard; Protein; 585 AA.
AC   R40213;
DT   03-FEB-1994  (first entry)
DE   Sequence of a 90K tumour-associated antigen, IR-95, capable
DE   of binding to SP-2 (Accession No. I-1083).
KW   Tumour-associated antigen; breast cancer cell line CG-5;
KW   90 K antigen.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         1..18
FT   /label= signal
FT   Region          24..125
FT   /label= SCRC homology region
FT   Binding_site    69
```



```
FT   /label= potential glycosylation site
FT   /note= "see also AAs 125,192,363,398,551,580"
PN   WO9316181-A.
PD   19-AUG-1993.
PF   17-FEB-1993; E00385.
PR   17-FEB-1992; IT-RM0099.
PA   (UYCH-) UNIV CHIETI ANNUNZIO G D.
PA   (UYNY ) UNIV NEW YORK STATE.
PI   Iacobelli S,  Natoli C,  Schlessinger J;
DR   WPI; 93-272885/34.
DR   N-PSDB; Q48170.
PT   New 90K tumour-associated antigen, IR-95 - is for use in
PT   diagnosis and therapy of cancer, HIV and auto-immune diseases
PS   Claim 2; pages 45-48; 68pp; English.
CC   90K antigen has an apparent molecular weight of approx. 95 kd. It is
CC   a tumour associated antigen and is elevated in the serum of patients
CC   with cancer and also in patients with HIV. It reacts with MAb SP-2
CC   which was prod. by immunising mice with proteins that had been
CC   released into tissue culture fluid by human MCF-7 breast cancer
CC   cells. MAb SP-2 cell line is deposited at the Institut Pasteur,
CC   Paris, Accession number 1-1083. 90K is also present in normal
CC   subjects. It is purified from the culture fluid of the human breast
CC   cancer cell line, CG-5. N-terminal sequencing of the 90K antigen
CC   was used to design a 'guessmer' nucleotide sequence (Q48171) as a
CC   probe to screen a lambda-gt10 library prepd. from MCF7 polyA+ RNA.
CC   The complete nucleotide sequence of isolated clones is given in
CC   Q48170.
SQ   Sequence   585 AA;
SQ   49 A; 29 R; 17 N; 32 D; 0  B; 16 C; 30 Q; 29 E; 0  Z; 41 G; 10 H;
SQ   14 I; 71 L; 19 K; 9  M; 30 F; 31 P; 51 S; 34 T; 16 W; 22 Y; 35 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.32
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    DLYAYAVATGDALLEKLCLQFLAWNFEA
          270 X     280


11. US-08-121-713B-24 (1-8)
    R40172       Sequence of an immunoregulin (IR)-95 polypeptide.

ID   R40172 standard; Protein; 585 AA.
AC   R40172;
DT   08-FEB-1994  (first entry)
DE   Sequence of an immunoregulin (IR)-95 polypeptide.
KW   Tumour associated antigen; breast cancer; cell line CG-5;
KW   ovarian cancer; immunoregulin-95; IR-95.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         1..17
FT   /label= signal
FT   Region          24..125
FT   /label= SRCR homology region
FT   Modified_site   71
FT   /label= glycosylation site
FT   /note= "see also AAs 125,192,362,398,551,580"
```

PN WO9316180-A.
PD 19-AUG-1993.
PF 17-FEB-1993; E00382.
PR 17-FEB-1992; IT-RM0100.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (UYCH-) UNIV CHIETI ANNUNIO G D.
PI Azam M, Iacobelli S, Natoli C, Sures I, Ullrich A;
DR WPI; 93-272884/34.
DR N-PSDB; Q46888.
PT Recombinant DNA - encoding tumour associated antigen,
PT immuno-regulin-95
PS Disclosure; Fig 1; 69pp; English.
CC Immunoregulin-95 is a 90K tumour-associated antigen purified from
CC the culture fluid of the human breast cancer cell line, CG-5, the
CC serum of a breast cancer patient, or the ascitic fluid from an
CC ovarian cancer patient. The native antigen, which has a mol. wt. of
CC 95 kD, is present as a high mol. wt. complex. Homology in the region
CC of AAs 35-80 of the 90K antigen is found with type I macrophage
CC scavenger receptor; sea urchin speract receptor; and human
CC lymphocyte glycoprotein T1/Leu-1.
SQ Sequence 585 AA;
SQ 49 A; 29 R; 17 N; 32 D; 0 B; 16 C; 30 Q; 29 E; 0 Z; 41 G; 10 H;
SQ 14 I; 71 L; 19 K; 9 M; 30 F; 31 P; 51 S; 34 T; 16 W; 22 Y; 35 V;

Initial Score = 8 Optimized Score = 8 Significance = 7.32
Residue Identity = 0% Matches = 0 Mismatches = 8
Gaps = 0 Conservative Substitutions = 0

X X
XXXXXXXX

DLYAYAVATGDALLEKLCLQFLAWNFEA
270 X 280

12. US-08-121-713B-24 (1-8)
R41359 Tumour associated 90K antigen.

ID R41359 standard; Protein; 585 AA.
AC R41359;
DT 03-MAR-1994 (first entry)
DE Tumour associated 90K antigen.
KW Antigen; cancer; inflammation; autoimmune disease; viral infection;
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..18
FT /label= Signal peptide.
FT Region 24..125
FT /note= "Region homologous with sea urchin speract
FT receptor"
FT Modified_site 69
FT /note= "Potential asparagine linked N-glycosylation
FT site"
FT Modified_site 125
FT /note= "Potential asparagine linked N-glycosylation
FT site"
FT Modified_site 192
FT /note= "Potential asparagine linked N-glycosylation
FT site"
FT Modified_site 362

FT /note= "Potential asparagine linked N-glycosylation
FT site"
FT Modified_site 398
FT /note= "Potential asparagine linked N-glycosylation
FT site"
FT Modified_site 551
FT /note= "Potential asparagine linked N-glycosylation
FT site"
FT Modified_site 580
FT /note= "Potential asparagine linked N-glycosylation
FT site"
PN WO9317119-A.
PD 02-SEP-1993.
PF 16-FEB-1993; E00379.
PR 17-FEB-1992; IT-RM0099.
PA (UYCH-) UNIV CHIETI ANNUNZIO G D.
PA (UYNY) UNIV NEW YORK STATE.
PI Iacobelli S, Natoli C, Schlessinger J;
DR WPI; 93-288423/36.
DR N-PSDB; Q46161.
PT 90K Tumour-associated antigen - purified from serum of breast
PT cancer patient or ascitic fluid from ovarian cancer patient
PS Claim 1; Figure 1; 73pp; English.
CC The purified 90K antigen or its antigenic determinant containing
CC fragment can be assayed to diagnose a disorder, such as cancer (
CC especially breast or ovarian cancer) or a viral infection,
CC inflammation, autoimmune disease and/or arthritis in a patient.
CC It may also be used in the preperation of an agent for the
CC treatment of these disorders.
SQ Sequence 585 AA;
SQ 49 A; 29 R; 17 N; 32 D; 0 B; 16 C; 30 Q; 29 E; 0 Z; 41 G; 10 H;
SQ 14 I; 71 L; 19 K; 9 M; 30 F; 31 P; 51 S; 34 T; 16 W; 22 Y; 35 V;

Initial Score = 8 Optimized Score = 8 Significance = 7.32
Residue Identity = 0% Matches = 0 Mismatches = 8
Gaps = 0 Conservative Substitutions = 0

X X
XXXXXXXX

DLYAYAVATGDALLEKLCLQFLAWNFEA
270 X 280

13. US-08-121-713B-24 (1-8)
R40784 Sequence of cyclophilin associated membrane protei

ID R40784 standard; Protein; 574 AA.
AC R40784;
DT 04-FEB-1994 (first entry)
DE Sequence of cyclophilin associated membrane protein (CAMP-c).
KW Cyclophilin associated membrane protein; CAMP-c.
OS Acomys cahirinus.
PN WO9316183-A.
PD 19-AUG-1993.
PF 08-FEB-1993; U01123.
PR 07-FEB-1992; US-832862.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Friedman JS, Weissman IL;
DR WPI; 93-272887/34.

```
DR   N-PSDB; Q47694.
PT   Cyclophilin C-associated membrane proteins and DNA - used for
PT   screening for immunomodulatory agents and for diagnosis and
PT   therapy
PS   Claim 7; Figure 2; 105pp; English.
CC   Q47694 is a murine cDNA sequence which encodes the CAMP-c 77kD
CC   polypeptide. The full sequence, including untranslated sequences,
CC   is shown in Q47695. The cDNA sequence encodes a polypeptide of 64kD
CC   which is glycosylated to give a 77 kD protein. The human homologue
CC   of the murine CAMP-c gene is identified and isolated by screening a
CC   human genomic clone library with a probe comprising a sequence of
CC   about at least 20 contiguous nucleotides (or their complement) of
CC   the cDNA sequence of Q47694 or Q48695.
SQ   Sequence   574 AA;
SQ   40 A; 26 R; 20 N; 27 D; 0  B; 17 C; 28 Q; 33 E; 0  Z; 37 G; 10 H;
SQ   16 I; 70 L; 13 K; 13 M; 25 F; 26 P; 54 S; 41 T; 12 W; 27 Y; 39 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.32
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    DLYAYARATGDSMLEDLCVQFLAWNFEP
          270 X     280
```

14. US-08-121-713B-24 (1-8)
    R26843 GDP dissociation stimulatory protein.

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ID   R26843 standard; Protein; 558 AA.
AC   R26843;
DT   11-FEB-1993  (first entry)
DE   GDP dissociation stimulatory protein.
KW   Guanosine 5'-diphosphate; mass production.
OS   Not known.
PN   J04211700-A.
PD   03-AUG-1992.
PF   08-FEB-1991; 018105.
PR   24-MAY-1990; JP-134480.
PA   (MITU ) MITSUBISHI KASEI CORP.
DR   WPI; 92-305013/37.
DR   N-PSDB; Q28232.
PT   High mol. wt. mass producible protein - accelerates dissociation
PT   of guanosine 5'-di:phosphate from complex of GDP and GDP protein
PT   binding type low mol guanosine 5'-tri:phosphate
PS   Claim 1; Fig 1; 17pp; Japanese.
CC   The sequence is that of a protein which accelerates dissociation of
CC   guanosine 5'-di:phosphate (GDP) from a complex of GDP and GDP protein
CC   binding type low molecular guanosine 5'-triphosphate (GTP) binding
CC   protein. It may be mass produced using genetic engineering techniques.
SQ   Sequence   558 AA;
SQ   54 A; 16 R; 26 N; 28 D; 0  B; 12 C; 32 Q; 46 E; 0  Z; 27 G; 14 H;
SQ   32 I; 85 L; 38 K; 18 M; 12 F; 10 P; 39 S; 19 T; 2  W; 2  Y; 46 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.32
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0
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             X      X
             XXXXXXXX

    TEMCLVAFGNLAELESSKEQFASTNIAE
  150       160       170
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15. US-08-121-713B-24 (1-8)
    R07466 Polypeptide with enzymatic activity for the conver

```
ID   R07466 standard; protein; 492 AA.
AC   R07466;
DT   28-JAN-1991  (first entry)
DE   Polypeptide with enzymatic activity for the conversion of phytoene
DE   into lycopene.
KW   Carotenoid biosynthesis; vitamin A; cancer; food coloring.
OS   Erwinia uredovora.
PN   EP-393690-A.
PD   24-OCT-1990.
PF   20-APR-1990; 107493.
PR   21-APR-1989; JP-103078.
PR   05-MAR-1990; JP-053255.
PA   (KIRI ) KIRIN BEER KK.
PI   Misawa N, Kobayashi K, Nakamura K;
DR   WPI; 90-322212/43.
DR   N-PSDB; Q06296.
PT   DNA sequences encoding enzymes for carotenoid biosynthesis - for
PT   prodn. of carotenoid cpds. e.g. beta-carotene, lycopene,
PT   phytoene, etc.
PS   Claim 4; Fig 4; 40pp; English.
CC   Gene products are useful for the synthesis of carotenoids, useful as
CC   food coloring, vitamin A precursor, and possibly in prevention of
CC   cancer.
CC   See also Q06293-9.
SQ   Sequence   492 AA;
SQ   43 A; 28 R; 15 N; 25 D; 0  B; 4  C; 23 Q; 26 E; 0  Z; 41 G; 20 H;
SQ   18 I; 57 L; 17 K; 8  M; 28 F; 25 P; 26 S; 27 T; 6  W; 21 Y; 34 V;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.32
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

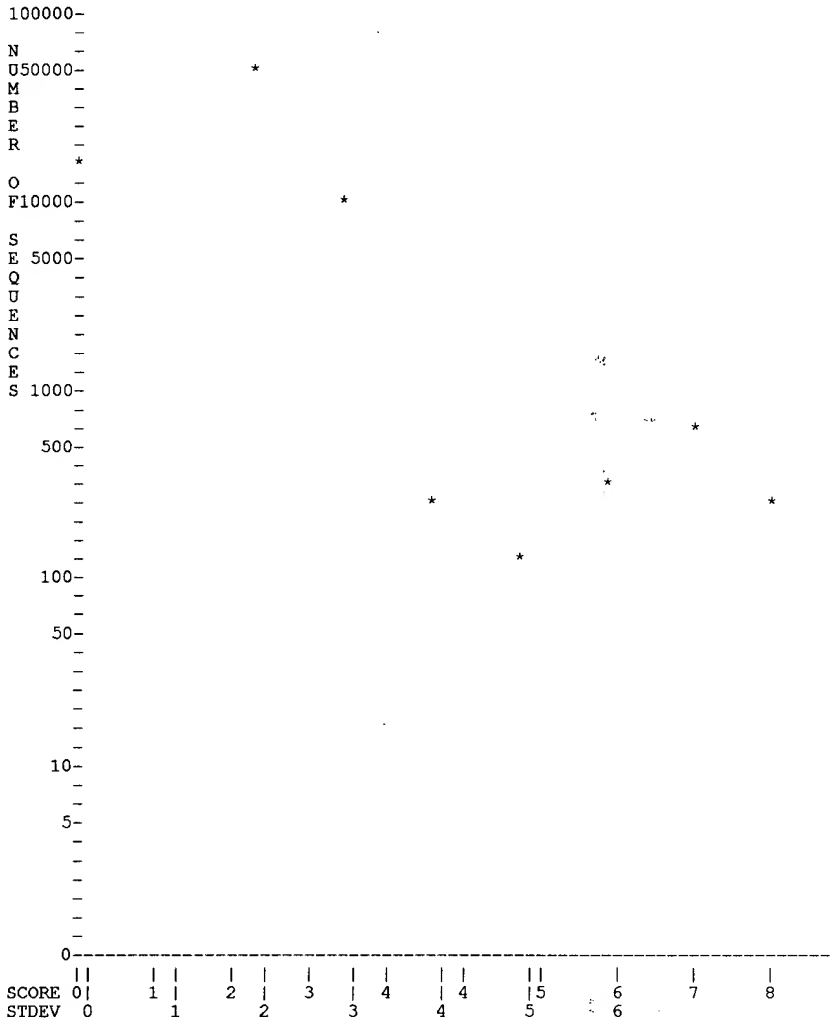
    SGKVFNYDNDQTRLEAQIQQFNPRDVEG
        100  X    110       120
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq24pir.res made by maryh on Fri 19 May 95 10:48:42-PDT.


Query sequence being compared:US-08-121-713B-24 (1-8)
Number of sequences searched:                75511
Number of scores above cutoff:                4749
```

Results of the initial comparison of US-08-121-713B-24 (1-8) with:
Data bank : PIR 43, all entries



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	1.00

Times:	CPU	Total Elapsed
	00:01:10.03	00:01:10.00

Number of residues: 22468834
Number of sequences searched: 75511
Number of scores above cutoff: 4749

The scores below are sorted by initial score.
Significance is calculated based on initial score.

220 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. A45086	HC-toxin synthetase - fungus	5232	8	8	7.00	0
2. A38905	dynein heavy chain, cytosolic	4644	8	8	7.00	0
3. S38128	dynein heavy chain - yeast (S	4092	8	8	7.00	0
4. A48126	GCN4 translational activator	2672	8	8	7.00	0
5. S43940	TOR1 protein - yeast (Sacchar	2470	8	8	7.00	0
6. GNNYED	genome polyprotein - encephal	2292	8	8	7.00	0
7. GNNYEB	genome polyprotein - encephal	2292	8	8	7.00	0
8. S35961	capsid polyprotein precursor	2292	8	8	7.00	0
9. GNNYE	genome polyprotein - encephal	2290	8	8	7.00	0
10. GNVVGV	genome polyprotein - grapevin	2284	8	8	7.00	0
11. S19444	hypothetical protein YCR032W	2167	8	8	7.00	0
12. S17478	hypothetical protein YCR032W	2167	8	8	7.00	0
13. A61231	myosin heavy chain NMMHC-A, n	1961	8	8	7.00	0
14. A33977	myosin heavy chain, cellular	1959	8	8	7.00	0
15. A45973	trichohyalin - human	1898	8	8	7.00	0
16. S13178	6-methylsalicylate decarboxyl	1774	8	8	7.00	0
17. SAZQGM	major merozoite surface antig	1726	8	8	7.00	0
18. A45948	major merozoite surface antig	1726	8	8	7.00	0
19. A54498	major merozoite surface antig	1701	8	8	7.00	0
20. A26868	major merozoite surface antig	1701	8	8	7.00	0
21. A40691	trichohyalin (EF hand calcium	1549	8	8	7.00	0
22. S32633	trichohyalin - sheep	1549	8	8	7.00	0
23. DVLNS	multidrug resistance protein	1548	8	8	7.00	0
24. S12457	P-glycoprotein - Sauroleishma	1548	8	8	7.00	0
25. RGBYS3	regulatory protein SIN3 - yea	1538	8	8	7.00	0
26. MAHU	alpha-2-macroglobulin precurs	1474	8	8	7.00	0
27. S28589	trichohyalin - rabbit	1407	8	8	7.00	0
28. JN0791	Tf2 protein, Retrotransposon	1333	8	8	7.00	0
29. RMXRR3	mRNA guanylyltransferase (EC	1289	8	8	7.00	0

30. A43488	genome polyprotein - feline c	1287	8	8	7.00	0
31. S18738	pol protein - simian foamy vi	1161	8	8	7.00	0
32. GNLJLK	pol polyprotein - simian foam	1157	8	8	7.00	0
33. A35098	MHC class III histocompatibil	1132	8	8	7.00	0
34. A47058	Fe-regulated RTX cytotoxin ho	1115	8	8	7.00	0
35. A45761	Ca2+-transporting ATPase (EC	1115	8	8	7.00	0
36. A39299	DNA-directed DNA polymerase (	1106	8	8	7.00	0
37. P1XRPC	inner layer protein VP1 - por	1082	8	8	7.00	0
38. GNWEC	genome polyprotein M - cowpea	1046	8	8	7.00	0
39. A31982	Ca2+-transporting ATPase (EC	1043	8	8	7.00	0
40. PWRBMC	Ca2+-transporting ATPase (EC	1042	8	8	7.00	0
41. B40812	Ca2+-transporting ATPase (EC	1042	8	8	7.00	0
42. A31981	Ca2+-transporting ATPase (EC	1042	8	8	7.00	0
43. S04652	Ca2+-transporting ATPase (EC	1042	8	8	7.00	0
44. A33881	Ca2+-transporting ATPase (EC	1042	8	8	7.00	0
45. S27540	hyaluronidase - Clostridium p	1042	8	8	7.00	0

1. US-08-121-713B-24 (1-8)
A45086 HC-toxin synthetase - fungus (Cochliobolus carbonu

```
ENTRY            A45086     #type complete
TITLE            HC-toxin synthetase - fungus (Cochliobolus carbonum)
ORGANISM         #formal_name Cochliobolus carbonum
DATE             10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
                   04-Dec-1994
ACCESSIONS       A45086
REFERENCE        A45086
   #authors      Scott-Craig, J.S.; Panaccione, D.G.; Pocard, J.A.; Walton,
                   J.D.
   #journal      J. Biol. Chem. (1992) 267:26044-26049
   #title        The cyclic peptide synthetase catalyzing HC-toxin production
                   in the filamentous fungus Cochliobolus carbonum is encoded
                   by a 15.7-kilobase open reading frame.
   #cross-references MUID:93100328
   #contents     SB111
   #accession    A45086
      ##status          preliminary
      ##molecule_type nucleic acid
      ##residues       1-5232 ##label SCO
      ##cross-references NCBIP:120884
      ##note           sequence extracted from NCBI backbone
      ##note           sequence not compared to nucleotide translation
SUMMARY          #length 5232  #molecular-weight 576294  #checksum 2412
SEQUENCE
```

```
Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

   RVHSDPDCIEVQLLERLMEQFGHNLQTL
  2920      2930    X 2940
```

2. US-08-121-713B-24 (1-8)
A38905 dynein heavy chain, cytosolic - rat


```
ENTRY            A38905     #type complete
TITLE            dynein heavy chain, cytosolic - rat
CONTAINS         dynein ATPase (EC 3.6.1.33)
ORGANISM         #formal_name Rattus norvegicus #common_name Norway rat
DATE             15-Apr-1994 #sequence_revision 02-May-1994 #text_change
                   08-Dec-1994
ACCESSIONS       A38905
REFERENCE        A38905
   #authors      Zhang, Z.; Tanaka, Y.; Nonaka, S.; Aizawa, H.; Kawasaki, H.;
                   Nakata, T.; Hirokawa, N.
   #journal      Proc. Natl. Acad. Sci. U.S.A. (1993) 90:7928-7932
   #title        The primary structure of rat brain (cytoplasmic) dynein heavy
                   chain, a cytoplasmic motor enzyme.
   #accession    A38905
      ##molecule_type mRNA
      ##residues       1-4644 ##label ZHA
      ##cross-references GB:D13896
      ##note           the nucleotide sequence is not given in this paper
CLASSIFICATION   #superfamily dynein heavy chain, cytosolic
KEYWORDS         ATP; blocked amino end; heterotetramer; hydrolase;
                   microtubule binding
FEATURE
   1904-1911          #region nucleotide-binding motif A (P-loop)\
   2222-2229          #region nucleotide-binding motif A (P-loop)\
   2593-2600          #region nucleotide-binding motif A (P-loop)\
   2935-2942          #region nucleotide-binding motif A (P-loop)\
   1910               #binding_site ATP (Lys) #status predicted\
   2228               #binding_site ATP (Lys) #status predicted\
   2599               #binding_site ATP (Lys) #status predicted\
   2941               #binding_site ATP (Lys) #status predicted
SUMMARY          #length 4644  #molecular-weight 532247  #checksum 1141
SEQUENCE
```

```
Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

   EKQVELYRNGQRLLEKQRFQFPPSWLYI
       1190 X    1200
```

3. US-08-121-713B-24 (1-8)
S38128 dynein heavy chain - yeast (Saccharomyces cerevisi

```
ENTRY            S38128     #type complete
TITLE            dynein heavy chain - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES  protein YKR054c
ORGANISM         #formal_name Saccharomyces cerevisiae
DATE             03-May-1994 #sequence_revision 03-May-1994 #text_change
                   08-Dec-1994
ACCESSIONS       S38128; S43077; S38130; S37701
REFERENCE        S38118
   #authors      Vissers, S.; Urrestarazu, L.A.; Jauniaux, J.C.
   #submission   submitted to the Protein Sequence Database, March 1994
   #accession    S38128
      ##molecule_type DNA
      ##residues       1-4092 ##label VIS
```

```
      ##cross-references EMBL:Z28279
REFERENCE        S43077
   #authors      Eshel, D.
   #submission   submitted to the EMBL Data Library, March 1993
   #accession    S43077
      ##molecule_type DNA
      ##residues      1-2117,'IV',2120-4092 ##label ESH
      ##cross-references EMBL:Z21877
REFERENCE        S38130
   #authors      van Vliet-Reedijk, J.C.; Planta, R.J.
   #submission   submitted to the Protein Sequence Database, March 1994
   #accession    S38130
      ##molecule_type DNA
      ##residues      1-787 ##label VAN
      ##cross-references EMBL:Z28279
REFERENCE        S37701
   #authors      Li, Y.Y.; Yeh, E.Y.; Hays, T.; Bloom, K.S.
   #submission   submitted to the EMBL Data Library, May 1993
   #description  Disruption of mitotic spindle orientation in a yeast dynein
                   mutant.
   #accession    S37701
      ##molecule_type DNA
      ##residues      1-588,'C',590-600,'A',602-1363,'A',1365-2631,'P',
                       2633-2657,2659,'IGW',2660-2661 ##label LIY
      ##cross-references EMBL:L15626
GENETICS
   #gene         DYN1; DHC1
   #map_position 11R
KEYWORDS         P-loop; purine nucleotide binding
FEATURE
   1796-1803          #region purine nucleotide-binding motif A (P-loop)\
   2074-2081          #region purine nucleotide-binding motif A (P-loop)\
   2418-2425          #region purine nucleotide-binding motif A (P-loop)\
   2760-2767          #region purine nucleotide-binding motif A (P-loop)\
   1802               #binding_site ATP/GTP (Lys) #status predicted\
   2080               #binding_site ATP/GTP (Lys) #status predicted\
   2424               #binding_site ATP/GTP (Lys) #status predicted\
   2766               #binding_site ATP/GTP (Lys) #status predicted
SUMMARY          #length 4092  #molecular-weight 471343  #checksum 4662
SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions              =     0

             X      X
             XXXXXXXX

   DSLKMIKSSLSTFLERQRRQFPRFYFLG
      1520   X  1530      1540


4. US-08-121-713B-24 (1-8)
   A48126       GCN4 translational activator GCN1 - yeast (Sacchar

ENTRY            A48126     #type complete
TITLE            GCN4 translational activator GCN1 - yeast (Saccharomyces
                   cerevisiae)
ORGANISM         #formal_name Saccharomyces cerevisiae
DATE             21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change
```



```
                 18-Nov-1994
ACCESSIONS       A48126
REFERENCE        A48126
   #authors      Marton, M.J.; Crouch, D.; Hinnebusch, A.G.
   #journal      Mol. Cell. Biol. (1993) 13:3541-3556
   #title        GCN1, a translational activator of GCN4 in Saccharomyces
                   cerevisiae, is required for phosphorylation of eukaryotic
                   translation initiation factor 2 by protein kinase GCN2.
   #cross-references MUID:93268304
   #accession    A48126
      ##status        preliminary
      ##molecule_type nucleic acid
      ##residues      1-2672 ##label MAR
      ##cross-references NCBIN:132672; NCBIP:132673
      ##note          sequence extracted from NCBI backbone
SUMMARY          #length 2672  #molecular-weight 296695  #checksum 2104
SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions              =     0

             X      X
             XXXXXXXX

   NDLLNFYKEKAKPLEPILDQFGLVLVSA
   1150      1160   X  1170


5. US-08-121-713B-24 (1-8)
   S43940       TOR1 protein - yeast (Saccharomyces cerevisiae)

ENTRY            S43940     #type complete
TITLE            TOR1 protein - yeast (Saccharomyces cerevisiae)
ORGANISM         #formal_name Saccharomyces cerevisiae
DATE             28-Oct-1994; #sequence_revision 28-Oct-1994; #text_change
                   28-Oct-1994
ACCESSIONS       S43940
REFERENCE        S43940
   #authors      Helliwell, S.B.; Wagner, P.; Kunz, J.; Deuter-Reinhard, M.;
                   Henriquez, R.; Hall, M.N.
   #journal      Mol. Biol. Cell (1994) 5:105-118
   #title        TOR1 and TOR2 are structurally and functionally similar but
                   not identical phosphatidylinositol kinase homologues in
                   yeast.
   #accession    S43940
      ##status        preliminary
      ##residues      1-2470 ##label HEL
      ##cross-references EMBL:X74857
SUMMARY          #length 2470  #molecular-weight 281354  #checksum 1019
SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions              =     0

             X      X
             XXXXXXXX

   RVAVLWHELWYEGLEDASRQFFVEHNIE
```

```
      1960    X 1970 X    1980


6. US-08-121-713B-24 (1-8)
   GNNYED       genome polyprotein - encephalomyocarditis virus (s

 ENTRY            GNNYED     #type complete
 TITLE            genome polyprotein - encephalomyocarditis virus (strain
                    EMC-D, diabetogenic)
 CONTAINS         coat protein VP1; coat protein VP2; coat protein VP3; coat
                    protein VP4; core protein P2-A; core protein P2-B; core
                    protein P2-C; core protein P3-A; genome-linked protein VPg;
                    protease; RNA-directed RNA polymerase (EC 2.7.7.48)
 ORGANISM         #formal_name encephalomyocarditis virus, EMCV
    #note         host Homo sapiens (man)
 DATE             31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
                    04-Dec-1994
 ACCESSIONS       A31473; A60498
 REFERENCE        A94395
    #authors      Bae, Y.S.; Eun, H.M.; Yoon, J.W.
    #journal      Virology (1989) 170:282-287
    #title        Genomic differences between the diabetogenic and
                    nondiabetogenic variants of encephalomyocarditis virus.
    #cross-references MUID:89243189
    #accession    A31473
       ##molecule_type genomic RNA
       ##residues      1-2292 ##label BAE
       ##note          the authors translated the codon ATG for residue 1079 as
                        Asn and GAC for residue 1564 as Val
 REFERENCE        A60498
    #authors      Bae, Y.S.; Eun, H.M.; Yoon, J.W.
    #journal      Diabetes (1989) 38:316-320
    #title        Molecular identification of diabetogenic viral gene.
    #accession    A60498
       ##molecule_type genomic RNA
       ##residues      1-1522,'D',1524-2292 ##label BA2
 CLASSIFICATION   #superfamily foot-and-mouth disease virus genome polyprotein
 KEYWORDS         coat protein; core protein; genome-linked protein;
                    nucleotidyltransferase; polyprotein; proteinase

 FEATURE
    1-67              #domain leader peptide #status predicted #label LDP\
    68-137            #product coat protein VP4 #status predicted #label VP4\
    138-393           #product coat protein VP2 #status predicted #label VP2\
    394-624           #product coat protein VP3 #status predicted #label VP3\
    625-901           #product coat protein VP1 #status predicted #label VP1\
    902-1058          #product core protein P2-A #status predicted #label P2A\
    1059-1194         #product core protein P2-B #status predicted #label P2B\
    1195-1519         #product core protein P2-C #status predicted #label P2C\
    1520-1607         #product core protein P3-A #status predicted #label P3A\
    1608-1627         #product genome-linked protein VPg #status predicted
                        #label VPG\
    1628-1832         #product proteinase #status predicted #label PTS\
    1833-2292         #product RNA-directed RNA polymerase #status predicted
                        #label RDP
 SUMMARY          #length 2292  #molecular-weight 255382  #checksum 3920
 SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0
```



```
                X      X
                XXXXXXXX

    DAPLPCFQNNCLFLEKAGLQFRDNRTKE
          1470      1480


7. US-08-121-713B-24 (1-8)
   GNNYEB       genome polyprotein - encephalomyocarditis virus (s

 ENTRY            GNNYEB     #type complete
 TITLE            genome polyprotein - encephalomyocarditis virus (strain
                    EMC-B, nondiabetogenic)
 CONTAINS         coat protein VP1; coat protein VP2; coat protein VP3; coat
                    protein VP4; core protein P2-A; core protein P2-B; core
                    protein P2-C; core protein P3-A; genome-linked protein VPg;
                    protease; RNA-directed RNA polymerase (EC 2.7.7.48)
 ORGANISM         #formal_name encephalomyocarditis virus, EMCV
    #note         host Homo sapiens (man)
 DATE             31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
                    04-Dec-1994
 ACCESSIONS       B31473; B60498
 REFERENCE        A94395
    #authors      Bae, Y.S.; Eun, H.M.; Yoon, J.W.
    #journal      Virology (1989) 170:282-287
    #title        Genomic differences between the diabetogenic and
                    nondiabetogenic variants of encephalomyocarditis virus.
    #cross-references MUID:89243189
    #accession    B31473
       ##molecule_type genomic RNA
       ##residues      1-2292 ##label BAE
       ##note          the authors translated the codon ATG for residue 1079 as
                        Asn and GAC for residue 1564 as Val
 REFERENCE        A60498
    #authors      Bae, Y.S.; Eun, H.M.; Yoon, J.W.
    #journal      Diabetes (1989) 38:316-320
    #title        Molecular identification of diabetogenic viral gene.
    #accession    B60498
       ##molecule_type genomic RNA
       ##residues      1-15;17-2292 ##label BA2
 CLASSIFICATION   #superfamily foot-and-mouth disease virus genome polyprotein
 KEYWORDS         coat protein; core protein; genome-linked protein;
                    nucleotidyltransferase; polyprotein; proteinase

 FEATURE
    1-67              #domain leader peptide #status predicted #label LDP\
    68-137            #product coat protein VP4 #status predicted #label VP4\
    138-393           #product coat protein VP2 #status predicted #label VP2\
    394-624           #product coat protein VP3 #status predicted #label VP3\
    625-901           #product coat protein VP1 #status predicted #label VP1\
    902-1058          #product core protein P2-A #status predicted #label P2A\
    1059-1194         #product core protein P2-B #status predicted #label P2B\
    1195-1519         #product core protein P2-C #status predicted #label P2C\
    1520-1607         #product core protein P3-A #status predicted #label P3A\
    1608-1627         #product genome-linked protein VPg #status predicted
                        #label VPG\
    1628-1832         #product proteinase #status predicted #label PTS\
    1833-2292         #product RNA-directed RNA polymerase #status predicted
                        #label RDP
 SUMMARY          #length 2292  #molecular-weight 255495  #checksum 6728
```

```
  SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    DAPLPCFQNNCLFLEKAGLQFRDNRTKE
         1470      1480


8. US-08-121-713B-24 (1-8)
   S35961       capsid polyprotein precursor - encephalomyocarditi

 ENTRY            S35961     #type complete
 TITLE            capsid polyprotein precursor - encephalomyocarditis virus
 ORGANISM         #formal_name encephalomyocarditis virus, EMCV
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S35961
 REFERENCE        S35961
    #authors      Zimmermann, A.; Nelsen-Slaz, B.; Kruppenbacher, J.P.; Eggers,
                    H.J.
    #submission   submitted to the EMBL Data Library, July 1993
    #accession    S35961
       ##status        preliminary
       ##residues      1-2292 ##label ZIM
       ##cross-references EMBL:X74312
 SUMMARY          #length 2292  #molecular-weight 255727  #checksum 8853
 SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    EAPLPCFQNNCLFLEKAGLQFRDNRTKE
         1470      1480


9. US-08-121-713B-24 (1-8)
   GNNYE        genome polyprotein - encephalomyocarditis virus

 ENTRY            GNNYE      #type complete
 TITLE            genome polyprotein - encephalomyocarditis virus
 CONTAINS         coat protein VP1; coat protein VP2; coat protein VP3; coat
                    protein VP4; core protein P2-A; core protein P2-B; core
                    protein P2-C; core protein P3-A; genome-linked protein VPg;
                    proteinase (EC 3.4.-.-); RNA-directed RNA polymerase (EC
                    2.7.7.48)
 ORGANISM         #formal_name encephalomyocarditis virus, EMCV
    #note         host Homo sapiens (man)
 DATE             28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change
                    08-Dec-1994
 ACCESSIONS       A03906; JN0383
 REFERENCE        A03906
```



```
    #authors      Palmenberg, A.C.; Kirby, E.M.; Janda, M.R.; Drake, N.L.;
                    Duke, G.M.; Potratz, K.F.; Collett, M.S.
    #journal      Nucleic Acids Res. (1984) 12:2969-2985
    #title        The nucleotide and deduced amino acid sequences of the
                    encephalomyocarditis viral polyprotein coding region.
    #cross-references MUID:84169586
    #accession    A03906
       ##molecule_type genomic RNA
       ##residues      1-2290 ##label PAL
       ##cross-references GB:X00463
 REFERENCE        JN0383
    #authors      Petrov, N.A.; Chizhikov, V.E.; Blinov, V.M.; Karginov, V.A.;
                    Mikryukov, N.N.; Gutorov, V.V.; Grishaev, M.P.;
                    Beklemishev, A.B.; Vassilenko, S.K.
    #journal      Bioorg. Khim. (1984) 10:274-279
    #title        Nucleotide sequence of the 3'-terminus of
                    encephalomyocarditis virus RNA.
    #cross-references MUID:85022788
    #accession    JN0383
       ##molecule_type genomic RNA
       ##residues      1337-1396,'L',1398-1517,'A',1519-1536,'E',1538-1556,'S',
                        1558-1611,'T',1613-1915,'N',1917-1986,'IH',1989-2007,
                        'I',2009-2048,'H',2050-2193,'K',2195-2290 ##label PET
       ##cross-references GB:M54935
       ##note          the authors translated the codon CAU for residue 713 as
                        Thr and AAC for residue 857 as Asp
 CLASSIFICATION   #superfamily foot-and-mouth disease virus genome polyprotein
 KEYWORDS         coat protein; core protein; genome-linked protein;
                    nucleotidyltransferase; polyprotein; proteinase

 FEATURE
    1-67              #domain leader peptide #status predicted #label LDP\
    68-136            #product coat protein VP4 #status predicted #label VP4\
    137-391           #product coat protein VP2 #status predicted #label VP2\
    392-622           #product coat protein VP3 #status predicted #label VP3\
    623-910           #product coat protein VP1 #status predicted #label VP1\
    911-1056          #product core protein P2-A #status predicted #label P2A\
    1057-1192         #product core protein P2-B #status predicted #label P2B\
    1193-1517         #product core protein P2-C #status predicted #label P2C\
    1518-1605         #product core protein P3-A #status predicted #label P3A\
    1606-1625         #product genome-linked protein VPg #status predicted
                        #label VPG\
    1626-1830         #product proteinase #status predicted #label PTS\
    1831-2290         #product RNA-directed RNA polymerase #status predicted
                        #label RDP
 SUMMARY          #length 2290  #molecular-weight 255756  #checksum 8698
 SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    EAPLPCFQNNCLFLEKAGLQFRDNRTKE
  1460      1470      1480


10. US-08-121-713B-24 (1-8)
    GNVVGV       genome polyprotein - grapevine fanleaf virus
```

```
ENTRY            GNVVGV     #type complete
TITLE            genome polyprotein - grapevine fanleaf virus
CONTAINS         63K protein; 72K protein; genome-linked protein; proteinase
                   (EC 3.4.-.-); RNA-directed RNA polymerase (EC 2.7.7.48)
ORGANISM         #formal_name grapevine fanleaf virus
DATE             30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
                   02-Aug-1994
ACCESSIONS       JQ1373; S15873
REFERENCE        JQ1373
   #authors      Ritzenthaler, C.; Viry, M.; Pinck, M.; Margis, R.; Fuchs, M.;
                   Pinck, L.
   #journal      J. Gen. Virol. (1991) 72:2357-2365
   #title        Complete nucleotide sequence and genetic organization of
                   grapevine fanleaf nepovirus RNA1.
   #cross-references MUID:92013951
   #accession    JQ1373
      ##molecule_type genomic RNA
      ##residues      1-2284 ##label RIT
      ##cross-references DDBJ:D00915
REFERENCE        S15873
   #authors      Pinck, M.; Reinbolt, J.; Loudes, A.M.; le Ret, M.; Pinck, L.
   #journal      FEBS Lett. (1991) 284:117-119
   #title        Primary structure and location of the genome-linked protein
                   (VPg) of grapevine fanleaf nepovirus.
   #cross-references MUID:91285092
   #accession    S15873
      ##molecule_type protein
      ##residues      1218-1241 ##label PIN
GENETICS
   #map_position segment 1
CLASSIFICATION   #superfamily cowpea aphid-borne mosaic virus genome
                   polyprotein B
KEYWORDS         genome-linked protein; hydrolase; membrane protein;
                   nucleotidyltransferase; polyprotein; proteinase

FEATURE
   1-568             #product 63K protein #status predicted #label STK\
   569-1217          #product 72K protein #status predicted #label SKP\
   1218-1241         #product genome-linked protein #status experimental
                       #label GLP\
   1242-1460         #product proteinase #status predicted #label TKP\
   1461-2284         #product RNA-directed RNA polymerase #status predicted
                       #label RRP
SUMMARY          #length 2284  #molecular-weight 252930  #checksum 8511
SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

   ISPNVAVKCCVARLEDGIPQFHFWSKYA
    1360      1370  X   1380


11. US-08-121-713B-24 (1-8)
    S19444       hypothetical protein YCR032W (version 1) - yeast
```



```
ENTRY            S19444     #type complete
TITLE            hypothetical protein YCR032W (version 1) - yeast
                   (Saccharomyces cerevisiae)
ALTERNATE_NAMES  hypothetical protein YCR591; hypothetical protein YCR601
ORGANISM         #formal_name Saccharomyces cerevisiae
DATE             31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
                   07-May-1993
ACCESSIONS       S19444; S15052; S19751
REFERENCE        S19437
   #authors      Pohl, F.; Richterich, P.; Wurst, H.
   #submission   submitted to the Protein Sequence Database, March 1992
   #accession    S19444
      ##molecule_type DNA
      ##residues      1-334 ##label POH
      ##cross-references EMBL:X59720
REFERENCE        S15052
   #authors      Jia, Y.; Slonimski, P.P.; Herbert, C.J.
   #journal      Yeast (1991) 7:413-424
   #title        The complete sequence of the unit YCR59, situated between
                   CRY1 and MAT, reveals two long open reading frames, which
                   cover 91% of the 10.1 kb segment.
   #cross-references MUID:91335897
   #accession    S15052
      ##molecule_type DNA
      ##residues      335-2167 ##label JIA
      ##cross-references EMBL:X59075
REFERENCE        S19445
   #authors      Herbert, C.J.; Jia, Y.; Slonimski, P.P.
   #submission   submitted to the Protein Sequence Database, March 1992
   #accession    S19751
      ##molecule_type DNA
      ##residues      335-2167 ##label HER
      ##cross-references EMBL:X59720
GENETICS
   #map_position 3R
SUMMARY          #length 2167  #molecular-weight 250972  #checksum 6407
SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

   TSNRIMTIEKHIYLEIKEGQFCISNDNY
        260 X      270


12. US-08-121-713B-24 (1-8)
    S17478       hypothetical protein YCR032W (version 2) - yeast

ENTRY            S17478     #type complete
TITLE            hypothetical protein YCR032W (version 2) - yeast
                   (Saccharomyces cerevisiae)
ALTERNATE_NAMES  hypothetical protein YCR591; hypothetical protein YCR601
ORGANISM         #formal_name Saccharomyces cerevisiae
DATE             07-May-1993 #sequence_revision 07-May-1993 #text_change
                   02-Aug-1994
ACCESSIONS       S17478; S40917
```

```
 REFERENCE        S17478
    #authors      Rodriguez, F.; Martegani, E.; Mauri, I.; Alberghina, L.
    #journal      Yeast (1991) 7:631-641
    #title        The sequence of 8.8 kb of yeast chromosome III cloned in
                    lambda PM3270 contains an unusual long ORF (YCR601).
    #accession    S17478
       ##molecule_type DNA
       ##residues      1-2167 ##label ROD
       ##cross-references EMBL:X62452
 REFERENCE        S40917
    #authors      Wicksteed, B.L.; Roberts, A.B.; Sagliocco, F.A.; Brown,
                    A.J.P.
    #journal      Yeast (1991) 7:761-772
    #title        The complete sequence of a 7.5 kb region of chromosome III
                    from Saccharomyces cerevisiae that lies between CRY1 and
                    MAT.
    #accession    S40917
       ##molecule_type DNA
       ##residues      1760-1892,'N',1894-2167 ##label WIC
       ##cross-references EMBL:S78624
 GENETICS
    #map_position 3R
 SUMMARY          #length 2167  #molecular-weight 250870  #checksum 7348
 SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    TSNRIMTIERHIYLEIKEGQFCISNDNY
          260 X     270
```

13. US-08-121-713B-24 (1-8)
    A61231 myosin heavy chain NMMHC-A, nonmuscle - human

```
 ENTRY            A61231     #type complete
 TITLE            myosin heavy chain NMMHC-A, nonmuscle - human
 CONTAINS         myosin ATPase (EC 3.6.1.32)
 ORGANISM         #formal_name Homo sapiens #common_name man
 DATE             12-May-1994 #sequence_revision 14-Jul-1994 #text_change
                    08-Dec-1994
 ACCESSIONS       A61231; A34876
 REFERENCE        A61231
    #authors      Simons, M.; Wang, M.; McBride, O.W.; Kawamoto, S.; Yamakawa,
                    K.; Gdula, D.; Adelstein, R.S.; Weir, L.
    #journal      Circ. Res. (1991) 69:530-539
    #title        Human nonmuscle myosin heavy chains are encoded by two genes
                    located on different chromosomes.
    #accession    A61231
       ##molecule_type mRNA
       ##residues      1-715 ##label SIM
       ##cross-references GB:M69180
 REFERENCE        A34876
    #authors      Saez, C.G.; Myers, J.C.; Shows, T.B.; Leinwand, L.A.
    #journal      Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1164-1168
    #title        Human nonmuscle myosin heavy chain mRNA: generation of
```



```
                   diversity through alternative polyadenylylation.
    #cross-references MUID:90138958
    #accession    A34876
       ##molecule_type mRNA
       ##residues      715-1961 ##label SAE
       ##cross-references GB:M31013
 GENETICS
    #gene         GDB:MYH9
    #map_position 22q12.3-q13.1
 CLASSIFICATION   #superfamily myosin heavy chain; myosin head homology
 KEYWORDS         actin binding; ATP; coiled coil; hydrolase; methylation;
                    tandem repeat
 FEATURE
    84-900            #domain myosin head homology #label HEA\
    174-181           #region nucleotide-binding motif A (P-loop)\
    552-565           #region actin-binding #status predicted\
    626-640           #region actin-binding #status predicted\
    837-1938          #domain coiled coil #status predicted #label COI\
    837-1277          #region S2\
    1278-1961         #region light meromyosin\
    1939-1961         #domain carboxyl-terminal #label CBT\
    125               #modified_site N6,N6,N6-trimethyllysine (Lys) #status
                        predicted\
    180               #binding_site ATP (Lys) #status predicted\
    694,704           #active_site Cys #status predicted
 SUMMARY          #length 1961  #molecular-weight 226741  #checksum 9108
 SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    ARALEEAMEQKAELERLNKQFRTEMEDL
        1490  X   1500      1510
```

14. US-08-121-713B-24 (1-8)
    A33977 myosin heavy chain, cellular - chicken

```
 ENTRY            A33977     #type complete
 TITLE            myosin heavy chain, cellular - chicken
 CONTAINS         myosin ATPase (EC 3.6.1.32)
 ORGANISM         #formal_name Gallus gallus #common_name chicken
 DATE             31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                    08-Dec-1994
 ACCESSIONS       A33977
 REFERENCE        A33977
    #authors      Shohet, R.V.; Conti, M.A.; Kawamoto, S.; Preston, Y.A.;
                    Brill, D.A.; Adelstein, R.S.
    #journal      Proc. Natl. Acad. Sci. U.S.A. (1989) 86:7726-7730
    #title        Cloning of the cDNA encoding the myosin heavy chain of a
                    vertebrate cellular myosin.
    #cross-references MUID:90046668
    #accession    A33977
       ##molecule_type mRNA
       ##residues      1-1959 ##label SHO
       ##cross-references GB:M26510
```

```
,

  CLASSIFICATION   #superfamily myosin heavy chain; myosin head homology
  KEYWORDS         actin binding; ATP; coiled coil; hydrolase; methylation;
                     tandem repeat
  FEATURE
     84-836            #domain myosin head homology #label HEA\
     174-181           #region nucleotide-binding motif A (P-loop)\
     552-565           #region actin-binding #status predicted\
     626-640           #region actin-binding #status predicted\
     837-1936          #domain coiled coil #status predicted #label COI\
     837-1277          #region S2\
     1278-1959         #region light meromyosin\
     1937-1959         #domain carboxyl-terminal #label CBT\
     125               #modified_site N6,N6,N6-trimethyllysine (Lys) #status
                         predicted\
     180               #binding_site ATP (Lys) #status predicted\
     694,704           #active_site Cys #status predicted
  SUMMARY          #length 1959  #molecular-weight 226502  #checksum 3641
  SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =      8
Gaps             =      0  Conservative Substitutions               =      0

              X      X
              XXXXXXXX

     ARALEEAIEQKAELERVNKQFRTEMEDL
          1490 X    1500


15. US-08-121-713B-24 (1-8)
     A45973       trichohyalin - human

  ENTRY            A45973     #type complete
  TITLE            trichohyalin - human
  ORGANISM         #formal_name Homo sapiens #common_name man
  DATE             03-May-1994 #sequence_revision 03-May-1994 #text_change
                     03-May-1994
  ACCESSIONS       A45973
  REFERENCE        A45973
     #authors      Lee, S.C.; Kim, I.G.; Marekov, L.N.; O'Keefe, E.J.; Parry,
                     D.A.D.; Steinert, P.M.
     #journal      J. Biol. Chem. (1993) 268:12164-12176
     #title        The structure of human trichohyalin. Potential multiple roles
                     as a functional EF-hand-like calcium-binding protein, a
                     cornified cell envelope precursor, and an intermediate
                     filament-associated (cross-linking) protein.
     #accession    A45973
        ##status        preliminary
        ##molecule_type DNA
        ##residues      1-1898 ##label LEE
        ##cross-references GB:L09190
        ##note          authors translated the codon AGG for residue 1714 as Pro
  SUMMARY          #length 1898  #molecular-weight 247219  #checksum 4094
  SEQUENCE

Initial Score    =      8  Optimized Score  =      8  Significance =  7.00
Residue Identity =     0%  Matches          =      0  Mismatches   =      8
Gaps             =      0  Conservative Substitutions               =      0
```



```
              X      X
              XXXXXXXX

     EIQSQEGKGHGRLLEPGTHQFASVPVRS
       1860     X 1870 X    1880
> O <
O| |O  IntelliGenetics
> O <

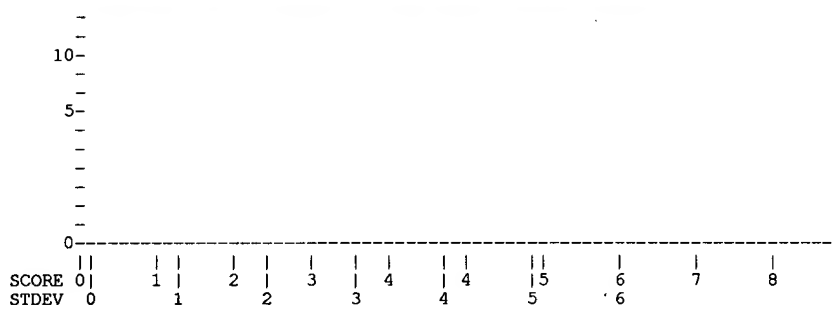
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq24spt.res made by  on Fri 19 May 95 8:59:52-PDT.


Query sequence being compared:US-08-121-713B-24 (1-8)
Number of sequences searched:                43470
Number of scores above cutoff:                4385

      Results of the initial comparison of US-08-121-713B-24 (1-8) with:
   Data bank : Swiss-Prot 31, all entries

100000-
      -
N     -
U50000-
M     -
B     -              *
E     -
R     -
      -
O     -
F10000-
      -                        *
S     *
E 5000-
Q     -
U     -
E     -
N     -
C     -
E     -
S 1000-
      -
      -
   500-
      -                                                      *
      -
      -                                          *
      -
      -                        *                                    *
      -
   100-
      -                                  *
      -
     50-
      -
      -
      -
      -
```



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	3	0.94

Times:	CPU	Total Elapsed
	00:00:43.06	00:00:44.00

Number of residues: 15335248
Number of sequences searched: 43470
Number of scores above cutoff: 4385

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

152 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. HTS1_COCCA	HC-TOXIN SYNTHETASE (EC 6.3.2	5217	8	8	7.42	0
2. DYHC_RAT	DYNEIN HEAVY CHAIN, CYTOSOLIC	4644	8	8	7.42	0
3. DYHC_DROME	DYNEIN HEAVY CHAIN, CYTOSOLIC	4639	8	8	7.42	0
4. DYHC_YEAST	DYNEIN HEAVY CHAIN, CYTOSOLIC	4092	8	8	7.42	0
5. GCN1_YEAST	TRANSLATIONAL ACTIVATOR GCN1.	2672	8	8	7.42	0

6. TOR1_YEAST	PHOSPHATIDYLINOSITOL 3-KINASE	2470	8	8	7.42	0
7. POLG_EMCVB	GENOME POLYPROTEIN (COAT PROT	2292	8	8	7.42	0
8. POLG_EMCVD	GENOME POLYPROTEIN (COAT PROT	2292	8	8	7.42	0
9. POLG_EMCV	GENOME POLYPROTEIN (COAT PROT	2290	8	8	7.42	0
10. POL1_GFLV	RNA1 POLYPROTEIN (253 KD PROT	2284	8	8	7.42	0
11. YCS2_YEAST	HYPOTHETICAL 251.0 KD PROTEIN	2167	8	8	7.42	0
12. MYSN_HUMAN	MYOSIN HEAVY CHAIN, NONMUSCLE	1961	8	8	7.42	0
13. MYSN_CHICK	MYOSIN HEAVY CHAIN, NONMUSCLE	1959	8	8	7.42	0
14. TRHY_HUMAN	TRICHOHYALIN.	1898	8	8	7.42	0
15. MSAS_PENPA	6-METHYLSALICYLIC ACID SYNTHA	1774	8	8	7.42	0
16. MSAP_PLAFC	MEROZOITE SURFACE ANTIGENS PR	1726	8	8	7.42	0
17. MSAP_PLAFF	MEROZOITE SURFACE ANTIGENS PR	1701	8	8	7.42	0
18. MSAP_PLAFM	MEROZOITE SURFACE ANTIGENS PR	1701	8	8	7.42	0
19. TRHY_SHEEP	TRICHOHYALIN.	1549	8	8	7.42	0
20. MDR_LEITA	MULTIDRUG RESISTANCE PROTEIN	1548	8	8	7.42	0
21. SIN3_YEAST	PAIRED AMPHIPATHIC HELIX PROT	1538	8	8	7.42	0
22. A2MG_HUMAN	ALPHA-2-MACROGLOBULIN PRECURS	1474	8	8	7.42	0
23. TRHY_RABIT	TRICHOHYALIN.	1407	8	8	7.42	0
24. MCE_REOVD	MRNA CAPPING ENZYME (MRNA GUA	1289	8	8	7.42	0
25. POLN_FCVC6	NON-STRUCTURAL POLYPROTEIN (C	1287	8	8	7.42	0
26. POL_SFV1	POL POLYPROTEIN (CONTAINS: PR	1161	8	8	7.42	0
27. POL_SFV3L	POL POLYPROTEIN (CONTAINS: PR	1157	8	8	7.42	0
28. YEU0_YEAST	HYPOTHETICAL 122.6 KD PROTEIN	1113	8	8	7.42	0
29. DPOD_BOVIN	DNA POLYMERASE DELTA CATALYTI	1106	8	8	7.42	0
30. RRPO_ROTPC	RNA-DIRECTED RNA POLYMERASE S	1082	8	8	7.42	0
31. VGNM_CPMV	GENOME POLYPROTEIN M (CONTAIN	1046	8	8	7.42	0
32. ATCE_RAT	CALCIUM-TRANSPORTING ATPASE E	1043	8	8	7.42	0
33. ATCE_HUMAN	CALCIUM-TRANSPORTING ATPASE E	1042	8	8	7.42	0
34. ATCE_PIG	CALCIUM-TRANSPORTING ATPASE E	1042	8	8	7.42	0
35. ATCE_RABIT	CALCIUM-TRANSPORTING ATPASE E	1042	8	8	7.42	0
36. NAGH_CLOPE	HYALURONOGLUCOSAMINIDASE (EC	1042	8	8	7.42	0
37. ODO1_HUMAN	2-OXOGLUTARATE DEHYDROGENASE	1003	8	8	7.42	0
38. ATCD_FELCA	CALCIUM-TRANSPORTING ATPASE S	997	8	8	7.42	0
39. ATCD_HUMAN	CALCIUM-TRANSPORTING ATPASE S	997	8	8	7.42	0
40. ATCD_PIG	CALCIUM-TRANSPORTING ATPASE S	997	8	8	7.42	0
41. ATCD_RABIT	CALCIUM-TRANSPORTING ATPASE S	997	8	8	7.42	0
42. ATCD_RAT	CALCIUM-TRANSPORTING ATPASE S	997	8	8	7.42	0
43. YB53_YEAST	HYPOTHETICAL 104.5 KD PROTEIN	924	8	8	7.42	0
44. YKF0_YEAST	HYPOTHETICAL 103.1 KD PROTEIN	922	8	8	7.42	0
45. POL_FOAMV	POL POLYPROTEIN (REVERSE TRAN	886	8	8	7.42	0

1. US-08-121-713B-24 (1-8)
   HTS1_COCCA HC-TOXIN SYNTHETASE (EC 6.3.2.-) (HTS).

ID HTS1_COCCA STANDARD; PRT; 5217 AA.
AC Q01886;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE HC-TOXIN SYNTHETASE (EC 6.3.2.-) (HTS).
GN HTS1.
OS COCHLIOBOLUS CARBONUM (BIPOLARIS ZEICOLA).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; LOCULOASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=SB111;
RM 93100328
RA SCOTT-CRAIG J.S., PANACCIONE D.G., POCARD J.-A., WALTON J.D.;
RL J. BIOL. CHEM. 267:26044-26049(1992).

```
CC   -!- FUNCTION: THIS PROTEIN IS A MULTIFUNCTIONAL ENZYME, ABLE TO
CC       ACTIVATE THE AMINO ACIDS PRO, L-ALA, D-ALA AND AEO (2-AMINO-9,10-
CC       EPOXI-8-OXODECANIOC ACID), AND EPIMERIZE PRO AND L-ALA. IT
CC       CATALYZES THE PRODUCTION OF HC-TOXIN; A CYCLIC TETRAPEPTIDE.
CC       HTS CONSISTS OF HTS-1 AND HTS-2 WHICH ARE PART OF THE SAME
CC       POLYPEPTIDE. HTS-1 ACTIVATES L-PROLINE, THIOESTERIFIES L-PRO, AND
CC       EPIMERIZES IT TO D-PRO; HTS-2 ACTIVATES AND THIOESTERIFIES L-ALA
CC       AND D-ALA AND EPIMERIZES L-ALA TO D-ALA.
CC   -!- PATHWAY: NON-RIBOSOMAL BIOSYNTHESIS OF HC-TOXIN.
CC   -!- COFACTOR: CONTAINS FOUR COVALENTLY BOUND PHOSPHOPANTETHEINES.
CC   -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
CC       COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
DR   EMBL; M98024; CCHTS1X.
DR   PROSITE; PS00455; AMP_BINDING.
KW   LIGASE; MULTIFUNCTIONAL ENZYME; PHOSPHOPANTETHEINE; REPEAT.
FT   REPEAT      249    842       DOMAIN 1.
FT   REPEAT     1854   2452       DOMAIN 2.
FT   REPEAT     3006   3606       DOMAIN 3.
FT   REPEAT     4158   4738       DOMAIN 4.
FT   BINDING     803    803       PHOSPHOPANTETHEINE (BY SIMILARITY).
FT   BINDING    2414   2414       PHOSPHOPANTETHEINE (BY SIMILARITY).
FT   BINDING    3568   3568       PHOSPHOPANTETHEINE (BY SIMILARITY).
FT   BINDING    4700   4700       PHOSPHOPANTETHEINE (BY SIMILARITY).
SQ   SEQUENCE   5217 AA;  574637 MW;  21594385 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    RVHSDPDCIEVQLLERLMEQFGHNLQTL
        2910  X   2920      2930


2. US-08-121-713B-24 (1-8)
   DYHC_RAT     DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).

ID   DYHC_RAT       STANDARD;      PRT;  4644 AA.
AC   P38650;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=BRAIN;
RM   93376715
RA   ZHANG Z., TANAKA Y., NONAKA S., AIZAWA H., KAWASAKI H., NAKATA T.,
RA   HIROKAWA N.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 90:7928-7932(1993).
CC   -!- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN IS
CC       THOUGHT TO ACT AS A MOTOR FOR VESICLE TRANSPORT, AND IS THOUGHT
CC       TO CONTRIBUTE TO CHROMOSOME MOVEMENTS.
CC   -!- SUBUNIT: CONSIST OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
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CC       INTERMEDIATE AND LOW MASS POLYPEPTIDES.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- SIMILARITY: TO OTHER DYNEIN HEAVY CHAINS.
DR   EMBL; D13896; RNCDHC.
DR   PIR; A38905; A38905.
KW   MOTOR PROTEIN; MICROTUBULES; DYNEIN; ATP-BINDING;
KW   HEPTAD REPEAT PATTERN.
FT   NP_BIND    1904   1911       ATP (POTENTIAL).
FT   NP_BIND    2222   2229       ATP (POTENTIAL).
FT   NP_BIND    2593   2600       ATP (POTENTIAL).
FT   NP_BIND    2935   2942       ATP (POTENTIAL).
SQ   SEQUENCE   4644 AA;  532240 MW;  23196763 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    EKQVELYRNGQRLLEKQRFQFPPSWLYI
        1190 X    1200


3. US-08-121-713B-24 (1-8)
   DYHC_DROME   DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).

ID   DYHC_DROME     STANDARD;      PRT;  4639 AA.
AC   P37276;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).
GN   CDHC.
OS   DROSOPHILA MELANOGASTER (FRUIT FLY).
OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   LI M.G., MCGRAIL M., SERR M., GEPNER J., HAYS T.;
RL   SUBMITTED (AUG-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN IS
CC       THOUGHT TO ACT AS A MOTOR FOR VESICLE TRANSPORT, AND IS THOUGHT
CC       TO CONTRIBUTE TO CHROMOSOME MOVEMENTS.
CC   -!- SUBUNIT: CONSIST OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
CC       INTERMEDIATE AND LOW MASS POLYPEPTIDES.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- SIMILARITY: TO OTHER DYNEIN HEAVY CHAINS.
DR   EMBL; L23195; DMCYTHA.
DR   FLYBASE; FBGN0010349; CDHC.
KW   MOTOR PROTEIN; MICROTUBULES; DYNEIN; ATP-BINDING;
KW   HEPTAD REPEAT PATTERN.
FT   NP_BIND    1895   1902       ATP (POTENTIAL).
FT   NP_BIND    2210   2217       ATP (POTENTIAL).
FT   NP_BIND    2580   2587       ATP (POTENTIAL).
FT   NP_BIND    2922   2929       ATP (POTENTIAL).
SQ   SEQUENCE   4639 AA;  530152 MW;  22186784 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0
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              X      X
              XXXXXXXX

     DKQVEVFREAQRILERQRFQFPNTWLHV
        1180   X  1190      1200
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4. US-08-121-713B-24 (1-8)
   DYHC_YEAST DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).

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ID   DYHC_YEAST     STANDARD;      PRT;  4092 AA.
AC   P36022;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).
GN   DYN1 OR DHC1 OR YKR054C.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   94068566
RA   ESHEL D., URRESTARAZU L.A., VISSERS S., JAUNIAUX J.-C.,
RA   VAN VLIET-REEDIJK J.C., PLANTA R.J., GIBBONS I.R.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 90:11172-11176(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   VISSERS S., URRESTARAZU L.A., JAUNIAUX J.-C.;
RL   SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [3]
RP   SEQUENCE OF 1-2657 FROM N.A.
RM   94052110
RA   LI Y.-Y., YEH E.Y., HAYS T., BLOOM K.S.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 90:10096-10100(1993).
CC   -!- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN IS
CC       THOUGHT TO ACT IN CYTOPLASMIC MICROTUBULE-BASED MOTILE PROCESSES
CC       INCLUDING VESICLE TRANSPORT, AND CHROMOSOME MOVEMENTS. MAY PLAY AN
CC       IMPORTANT ROLE IN THE PROPER ORIENTATION OF THE MITOTIC SPINDLE
CC       INTO THE BUDDING DAUGHTER CELL YEAST. PROBABLY REQUIRED FOR NORMAL
CC       PROGRESSION OF THE CELL CYCLE.
CC   -!- SUBUNIT: CONSIST OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
CC       INTERMEDIATE AND LOW MASS POLYPEPTIDES.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC. PROBABLY BINDS INDIRECTLY TO
CC       THE INNER PLASMA MEMBRANE.
CC   -!- SIMILARITY: TO OTHER DYNEIN HEAVY CHAINS.
DR   EMBL; Z21877; SCDYN1A.
DR   EMBL; L15626; SCDHC1A.
DR   EMBL; Z28279; SCYKR054C.
DR   PIR; S38128; S38128.
DR   LISTA; SC00299; DYN1.
KW   MOTOR PROTEIN; MICROTUBULES; DYNEIN; ATP-BINDING;
KW   HEPTAD REPEAT PATTERN.
FT   NP_BIND     1796   1803       ATP (POTENTIAL).
FT   NP_BIND     2074   2081       ATP (POTENTIAL).
FT   NP_BIND     2418   2425       ATP (POTENTIAL).
FT   NP_BIND     2760   2767       ATP (POTENTIAL).
FT   CONFLICT     589    589       Y -> C (IN REF. 3).
FT   CONFLICT     601    601       V -> A (IN REF. 3).
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FT   CONFLICT    1364   1364       E -> A (IN REF. 3).
FT   CONFLICT    2118   2119       ML -> IV (IN REF. 1).
FT   CONFLICT    2632   2632       A -> P (IN REF. 3).
SQ   SEQUENCE   4092 AA;  471337 MW;  21476769 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions              =     0

             X      X
             XXXXXXXX

    DSLKMIKSSLSTFLERQRRQFPRFYFLG
       1520   X  1530      1540
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5. US-08-121-713B-24 (1-8)
   GCN1_YEAST TRANSLATIONAL ACTIVATOR GCN1.

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ID   GCN1_YEAST     STANDARD;      PRT;  2672 AA.
AC   P33892;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   TRANSLATIONAL ACTIVATOR GCN1.
GN   GCN1.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   93268304
RA   MARTON M.J., CROUCH D., HINNEBUSCH A.G.;
RL   MOL. CELL. BIOL. 13:3541-3556(1993).
CC   -!- FUNCTION: TRANSLATIONAL ACTIVATOR OF GCN4. MAY BE INVOLVED IN
CC       SENSING CHARGED TRNA AND STIMULATING THE KINASE ACTIVITY OF GCN2
CC       IN AMINO ACID-STARVED CELLS. REQUIRED IN VIVO FOR THE
CC       PHOSPHORYLATION OF EIF-2-ALPHA ON SERINE-52 BY THE PROTEIN KINASE
CC       GCN2.
CC   -!- SIMILARITY: TO ELONGATION FACTOR 3 (EF-3) OF FUNGI.
DR   EMBL; L12467; SCGCN1A.
DR   PIR; A48126; A48126.
DR   LISTA; SC00382; GCN1.
KW   TRANSLATION REGULATION; ACTIVATOR; REPEAT.
FT   DOMAIN      1344   2327       4 X 16 AA APPROXIMATE REPEATS OF R-X-X-
FT                                 A-A-X-X-L-X-X-L-V-X-X-X-G.
FT   REPEAT      1344   1359       1-1.
FT   REPEAT      1624   1639       1-2.
FT   REPEAT      1663   1678       1-3.
FT   REPEAT      2312   2326       1-4.
FT   DOMAIN      1385   1790       2 X 90 AA APPROXIMATE REPEATS.
FT   REPEAT      1385   1474       2-1.
FT   REPEAT      1701   1790       2-2.
FT   DOMAIN      1385   1937       2 APPROXIMATE REPEATS.
FT   REPEAT      1385   1674       3-1.
FT   REPEAT      1701   1937       3-2.
FT   DOMAIN      1624   1937       2 X 51 AA APPROXIMATE REPEATS.
FT   REPEAT      1624   1674       4-1.
FT   REPEAT      1887   1937       4-2.
SQ   SEQUENCE   2672 AA;  296693 MW;  22333332 CN;
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Initial Score     =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity  =     0%  Matches          =      0  Mismatches   =     8
Gaps              =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    NDLLNFYKEKAKPLEPILDQFGLVLVSA
    1150      1160   X  1170
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6. US-08-121-713B-24 (1-8)
TOR1_YEAST PHOSPHATIDYLINOSITOL 3-KINASE TOR1 (EC 2.7.1.137)

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ID   TOR1_YEAST     STANDARD;      PRT;  2470 AA.
AC   P35169;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   PHOSPHATIDYLINOSITOL 3-KINASE TOR1 (EC 2.7.1.137) (PI3-KINASE)
DE   (PTDINS-3-KINASE) (PI3K).
GN   TOR1 OR DRR1.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   94019276
RA   CAFFERKEY R., YOUNG P.R., MCLAUGHLIN M.M., BERGSMA D.J., KOLTIN Y.,
RA   SATHE G.M., FAUCETTE L., ENG W.-K., JOHNSON R.K., LIVI G.P.;
RL   MOL. CELL. BIOL. 13:6012-6023(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JK-3D;
RM   94243030
RA   HELLIWELL S.B., WAGNER P., KUNZ J., DEUTER-REINHARD M., HENRIQUEZ R.,
RA   HALL M.N.;
RL   MOL. BIOL. CELL 5:105-118(1994).
CC   -!- FUNCTION: PHOSPHATIDYLINOSITOL 3-KINASE HOMOLOG REQUIRED FOR G1
CC       PROGRESSION. TARGET OF THE ANTIBIOTIC RAPAMYCIN.
CC   -!- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL = ADP +
CC       1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
CC   -!- IT MAY ACT ON ANOTHER SUBSTRATE OR PHOSPHORYLATE A DIFFERENT
CC       POSITION IN THE PHOSPHATIDYLINOSITOL RING.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
DR   EMBL; L19540; SCDRR1A.
DR   EMBL; X74857; SCTOR1.
DR   LISTA; SC01314; TOR1.
DR   PROSITE; PS00915; PI3_4_KINASE_1.
DR   PROSITE; PS00916; PI3_4_KINASE_2.
KW   TRANSFERASE; KINASE; CELL CYCLE.
FT   DOMAIN      441    447       ARG/LYS-RICH (BASIC).
FT   MUTAGEN    1972   1972       S->R,N: LOSS OF RAPAMYCIN SENSITIVITY.
FT   CONFLICT     58     58       G -> D (IN REF. 2).
FT   CONFLICT    115    115       I -> V (IN REF. 2).
FT   CONFLICT    133    133       N -> S (IN REF. 2).
FT   CONFLICT    231    231       A -> R (IN REF. 2).
FT   CONFLICT    675    675       T -> I (IN REF. 2).
FT   CONFLICT   1292   1292       G -> E (IN REF. 2).
FT   CONFLICT   1436   1436       G -> A (IN REF. 2).
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FT   CONFLICT   1469   1471       WGL -> GGS (IN REF. 2).
FT   CONFLICT   1590   1590       V -> I (IN REF. 2).
FT   CONFLICT   1632   1642       NDPSLPNTVKA -> TILVYQIRSKP (IN REF. 2).
FT   CONFLICT   1844   1844       L -> S (IN REF. 2).
FT   CONFLICT   2202   2202       Q -> H (IN REF. 2).
SQ   SEQUENCE   2470 AA;  281162 MW;  21744712 CN;

Initial Score     =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity  =     0%  Matches          =      0  Mismatches   =     8
Gaps              =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    RVAVLWHELWYEGLEDASRQFFVEHNIE
      1960    X 1970 X    1980
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7. US-08-121-713B-24 (1-8)
POLG_EMCVB GENOME POLYPROTEIN (COAT PROTEINS VP1 TO VP4; CORE

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ID   POLG_EMCVB     STANDARD;      PRT;  2292 AA.
AC   P17593;
DT   01-AUG-1990 (REL. 15, CREATED)
DT   01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   GENOME POLYPROTEIN (COAT PROTEINS VP1 TO VP4; CORE PROTEINS P2A TO
DE   P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C (EC 3.4.22.28)
DE   (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D (EC 2.7.7.48)).
OS   ENCEPHALOMYOCARDITIS VIRUS (STRAIN EMC-B NONDIABETOGENIC).
OC   VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; CARDIOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   89243189
RA   BAE Y.S., EUN H.M., YOON J.W.;
RL   VIROLOGY 170:282-287(1989).
CC   -!- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
CC       Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
DR   EMBL; M22457; EMCBCG.
DR   PIR; B31473; GNNYEB.
DR   HSSP; P12296; 1MEC.
KW   POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW   HYDROLASE; THIOL PROTEASE; MYRISTYLATION.
FT   PROPEP       1     67       LEADER PEPTIDE.
FT   CHAIN       68    137       COAT PROTEIN VP4 (RHO).
FT   CHAIN      138    393       COAT PROTEIN VP2 (BETA).
FT   CHAIN      394    624       COAT PROTEIN VP3 (GAMMA).
FT   CHAIN      625    901       COAT PROTEIN VP1 (ALPHA).
FT   CHAIN      902   1058       CORE PROTEIN P2A (G).
FT   CHAIN     1059   1194       CORE PROTEIN P2B (I).
FT   CHAIN     1195   1519       CORE PROTEIN P2C (F).
FT   CHAIN     1520   1607       CORE PROTEIN P3A.
FT   CHAIN     1608   1627       GENOME-LINKED PROTEIN VPG (H).
FT   CHAIN     1628   1832       PICORNAIN 3C (P22).
FT   CHAIN     1833   2292       RNA-DIRECTED RNA POLYMERASE P3D (E).
FT   LIPID       68     68       MYRISTATE (BY SIMILARITY).
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FT   ACT_SITE   1786   1786       PROTEASE (POTENTIAL).
FT   ACT_SITE   1804   1804       PROTEASE (POTENTIAL).
SQ   SEQUENCE   2292 AA;  255495 MW;  19494323 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    DAPLPCFQNNCLFLEKAGLQFRDNRTKE
          1470      1480
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8. US-08-121-713B-24 (1-8)
POLG_EMCVD GENOME POLYPROTEIN (COAT PROTEINS VP1 TO VP4; CORE

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ID   POLG_EMCVD      STANDARD;      PRT;  2292 AA.
AC   P17594;
DT   01-AUG-1990 (REL. 15, CREATED)
DT   01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   GENOME POLYPROTEIN (COAT PROTEINS VP1 TO VP4; CORE PROTEINS P2A TO
DE   P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C (EC 3.4.22.28)
DE   (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D (EC 2.7.7.48)).
OS   ENCEPHALOMYOCARDITIS VIRUS (STRAIN EMC-D DIABETOGENIC).
OC   VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; CARDIOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   89243189
RA   BAE Y.S., EUN H.M., YOON J.W.;
RL   VIROLOGY 170:282-287(1989).
CC   -!- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
CC       Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
DR   EMBL; M22458; EMCDCG.
DR   PIR; A31473; GNNYED.
DR   HSSP; P12296; 1MEC.
KW   POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW   HYDROLASE; THIOL PROTEASE; MYRISTYLATION.
FT   PROPEP        1     67       LEADER PEPTIDE.
FT   CHAIN        68    137       COAT PROTEIN VP4 (RHO).
FT   CHAIN       138    393       COAT PROTEIN VP2 (BETA).
FT   CHAIN       394    624       COAT PROTEIN VP3 (GAMMA).
FT   CHAIN       625    901       COAT PROTEIN VP1 (ALPHA).
FT   CHAIN       902   1058       CORE PROTEIN P2A (G).
FT   CHAIN      1059   1194       CORE PROTEIN P2B (I).
FT   CHAIN      1195   1519       CORE PROTEIN P2C (F).
FT   CHAIN      1520   1607       CORE PROTEIN P3A.
FT   CHAIN      1608   1627       GENOME-LINKED PROTEIN VPG (H).
FT   CHAIN      1628   1832       PICORNAIN 3C (P22).
FT   CHAIN      1833   2292       RNA-DIRECTED RNA POLYMERASE P3D (E).
FT   LIPID        68     68       MYRISTATE (BY SIMILARITY).
FT   ACT_SITE   1786   1786       PROTEASE (POTENTIAL).
FT   ACT_SITE   1804   1804       PROTEASE (POTENTIAL).
SQ   SEQUENCE   2292 AA;  255382 MW;  19455620 CN;
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Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    DAPLPCFQNNCLFLEKAGLQFRDNRTKE
          1470      1480
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9. US-08-121-713B-24 (1-8)
POLG_EMCV GENOME POLYPROTEIN (COAT PROTEINS VP1 TO VP4; CORE

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ID   POLG_EMCV       STANDARD;      PRT;  2290 AA.
AC   P03304;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   GENOME POLYPROTEIN (COAT PROTEINS VP1 TO VP4; CORE PROTEINS P2A TO
DE   P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C (EC 3.4.22.28)
DE   (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D (EC 2.7.7.48)).
OS   ENCEPHALOMYOCARDITIS VIRUS.
OC   VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; CARDIOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   84169586
RA   PALMENBERG A.C., KIRBY E.M., JANDA M.R., DRAKE N.L., DUKE G.M.,
RA   POTRATZ K.F., COLLETT M.S.;
RL   NUCLEIC ACIDS RES. 12:2969-2985(1984).
CC   -!- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
CC       Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC   -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC       EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC       VP3, AND VP4.
DR   EMBL; X00463; PIEMCY.
DR   PIR; A03906; GNNYE.
DR   HSSP; P12296; 1MEC.
KW   POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW   HYDROLASE; THIOL PROTEASE; MYRISTYLATION.
FT   PROPEP        1     67       LEADER PEPTIDE.
FT   CHAIN        68    136       COAT PROTEIN VP4 (RHO).
FT   CHAIN       137    391       COAT PROTEIN VP2 (BETA).
FT   CHAIN       392    622       COAT PROTEIN VP3 (GAMMA).
FT   CHAIN       623    910       COAT PROTEIN VP1 (ALPHA).
FT   CHAIN       911   1056       CORE PROTEIN P2A (G).
FT   CHAIN      1057   1192       CORE PROTEIN P2B (I).
FT   CHAIN      1193   1517       CORE PROTEIN P2C (F).
FT   CHAIN      1518   1605       CORE PROTEIN P3A.
FT   CHAIN      1606   1625       GENOME-LINKED PROTEIN VPG (H).
FT   CHAIN      1626   1830       PICORNAIN 3C (P22).
FT   CHAIN      1831   2290       RNA-DIRECTED RNA POLYMERASE P3D (E).
FT   LIPID        68     68       MYRISTATE (BY SIMILARITY).
FT   ACT_SITE   1784   1784       PROTEASE (POTENTIAL).
FT   ACT_SITE   1802   1802       PROTEASE (POTENTIAL).
SQ   SEQUENCE   2290 AA;  255756 MW;  19481048 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
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Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

   EAPLPCFQNNCLFLEKAGLQFRDNRTKE
 1460      1470      1480
```

10. US-08-121-713B-24 (1-8)
    POL1_GFLV   RNA1 POLYPROTEIN (253 KD PROTEIN) (CONTAINS: 63 KD

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 ID   POL1_GFLV      STANDARD;      PRT;  2284 AA.
 AC   P29149;
 DT   01-DEC-1992 (REL. 24, CREATED)
 DT   01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE   RNA1 POLYPROTEIN (253 KD PROTEIN) (CONTAINS: 63 KD PROTEASE COFACTOR,
 DE   72 KD MEMBRANE-BINDING PROTEIN, GENOME-LINKED PROTEIN (VPG), PROTEASE
 DE   (EC 3.4.22.-), RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48)).
 OS   GRAPEVINE FANLEAF VIRUS (GFLV).
 OC   VIRIDAE; SS-RNA NONENVELOPED VIRUSES; NEPOVIRIDAE.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RM   92013951
 RA   RITZENTHALER C., VIRY M., PINCK M., MARGIS R., FUCHS M., PINCK L.;
 RL   J. GEN. VIROL. 72:2357-2365(1991).
 CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 DR   EMBL; D00915; GFLRNA1.
 DR   PIR; JQ1373; GNVVGV.
 KW   POLYPROTEIN; TRANSMEMBRANE; HYDROLASE; PROTEASE; TRANSFERASE;
 KW   RNA-DIRECTED RNA POLYMERASE; ATP-BINDING.
 FT   CHAIN         1    568       63 KD PROTEASE COFACTOR (POTENTIAL).
 FT   CHAIN       569   1217       72 KD MEMBRANE-BINDING PROTEIN
 FT                                (POTENTIAL).
 FT   CHAIN      1218   1241       GENOME-LINKED PROTEIN (POTENTIAL).
 FT   CHAIN      1242   1460       CYSTEINE PROTEASE (POTENTIAL).
 FT   CHAIN      1461   2284       RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
 FT   NP_BIND     781    788       ATP (POTENTIAL).
 FT   ACT_SITE   1420   1420       CYSTEINE PROTEASE (POTENTIAL).
 SQ   SEQUENCE   2284 AA;  252930 MW;  20307487 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

   ISPNVAVKCCVARLEDGIPQFHFWSKYA
  1360      1370  X   1380
```

11. US-08-121-713B-24 (1-8)
    YCS2_YEAST   HYPOTHETICAL 251.0 KD PROTEIN IN CRY1-RBK1 INTERGE

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 ID   YCS2_YEAST     STANDARD;      PRT;  2167 AA.
 AC   P25356;
 DT   01-MAY-1992 (REL. 22, CREATED)
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 DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
 DT   01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
 DE   HYPOTHETICAL 251.0 KD PROTEIN IN CRY1-RBK1 INTERGENIC REGION.
 GN   YCR32W OR YCR591 OR YCR601.
 OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RM   92133166
 RA   WICKSTEED B.L., ROBERTS A.B., SAGLIOCCO F.A., BROWN A.J.P.;
 RL   YEAST 7:761-772(1991).
 RN   [2]
 RP   SEQUENCE FROM N.A.
 RM   92116648
 RA   RODRIGUEZ F., MARTEGANI E., MAURI I., ALBERGHINA L.;
 RL   YEAST 7:631-641(1991).
 RN   [3]
 RP   SEQUENCE OF 313-2167 FROM N.A.
 RM   91335897
 RA   JIA Y., SLONIMSKI P.P., HERBERT C.J.;
 RL   YEAST 7:413-424(1991).
 CC   -!- THIS PROTEIN IS ENCODED BY A NON-ESSENTIAL GENE.
 DR   EMBL; X59075; SCYCR59.
 DR   EMBL; X59720; SCCHRIII.
 DR   PIR; S15052; S15052.
 DR   PIR; S19444; S19444.
 DR   LISTA; SC01404; YCR32W.
 KW   HYPOTHETICAL PROTEIN.
 SQ   SEQUENCE   2167 AA;  250972 MW;  19698864 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

   TSNRIMTIEKHIYLEIKEGQFCISNDNY
        260 X     270
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12. US-08-121-713B-24 (1-8)
    MYSN_HUMAN   MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A (CELLULAR MYO

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 ID   MYSN_HUMAN     STANDARD;      PRT;  1961 AA.
 AC   P35579;
 DT   01-JUN-1994 (REL. 29, CREATED)
 DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE   MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A (CELLULAR MYOSIN HEAVY CHAIN,
 DE   TYPE A) (NMMHC-A).
 GN   MYH9.
 OS   HOMO SAPIENS (HUMAN).
 OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC   EUTHERIA; PRIMATES.
 RN   [1]
 RP   SEQUENCE OF 1-1337 FROM N.A.
 RM   92003925
 RA   TOOTHAKER L.E., GONZALEZ D.A., TUNG N., LEMONS R.S., LE BEAU M.M.,
 RA   ARNAOUT M.A., CLAYTON L.K., TENEN D.G.;
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RL   BLOOD 78:1826-1833(1991).
RN   [2]
RP   SEQUENCE OF 1-715 FROM N.A.
RM   91316803
RA   SIMONS M., WANG M., MCBRIDE O.W., KAWAMOTO S., YAMAKAWA K.,
RA   GDULA D., ADELSTEIN R.S., WEIR L.;
RL   CIRC. RES. 69:530-539(1991).
RN   [3]
RP   SEQUENCE OF 715-1961 FROM N.A.
RM   90138958
RA   SAEZ C.G., MYERS J.C., SHOWS T.B., LEINWAND L.A.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 87:1164-1168(1990).
CC   -!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,
CC       CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
CC       CAPPING.
CC   -!- SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY
CC       CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2
CC       REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC   -!- EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM)
CC       AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATTER BE SPLIT FURTHER INTO
CC       2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
CC   -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC       CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC       CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC   -!- SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY. STRONGEST
CC       TO OTHER NONMUSCLE MYOSINS.
DR   EMBL; M81105; HSMYH9.
DR   EMBL; M69180; HSMYOHCA.
DR   EMBL; M31013; HSMYONM.
DR   HSSP; P24733; 1SCM.
DR   MIM; 160775; 11TH EDITION.
KW   MYOSIN; COILED COIL; ACTIN-BINDING; ALKYLATION; ATP-BINDING;
KW   HEPTAD REPEAT PATTERN; MULTIGENE FAMILY.
FT   DOMAIN        1    835       GLOBULAR HEAD (S1).
FT   DOMAIN      836   1926       RODLIKE TAIL (S2 AND LMM DOMAINS).
FT   NP_BIND     174    181       ATP.
FT   DOMAIN      654    676       ACTIN-BINDING.
FT   MOD_RES     694    694       ALKYLATION (SH-1) (POTENTIAL).
FT   MOD_RES     704    704       ALKYLATION (SH-2) (POTENTIAL).
FT   CONFLICT     53     55       EAI -> RGH (IN REF. 2).
FT   CONFLICT    660    660       T -> S (IN REF. 2).
FT   CONFLICT    869    869       T -> M (IN REF. 3).
FT   CONFLICT    931    931       C -> Y (IN REF. 3).
FT   CONFLICT   1240   1241       KG -> GR (IN REF. 3).
SQ   SEQUENCE   1961 AA;  226600 MW;  15612344 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    ARALEEAMEQKAELERLNKQFRTEMEDL
        1490  X   1500      1510


13. US-08-121-713B-24 (1-8)
    MYSN_CHICK   MYOSIN HEAVY CHAIN, NONMUSCLE (NMMHC).
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ID   MYSN_CHICK     STANDARD;      PRT;  1959 AA.
AC   P14105;
DT   01-JAN-1990 (REL. 13, CREATED)
DT   01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   MYOSIN HEAVY CHAIN, NONMUSCLE (NMMHC).
OS   GALLUS GALLUS (CHICKEN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC   GALLIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=INTESTINAL EPITHELIUM;
RM   90046668
RA   SHOHET R.V., CONTI M.A., KAWAMOTO S., PRESTON Y.A., BRILL D.A.,
RA   ADELSTEIN R.S.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 86:7726-7730(1989).
CC   -!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,
CC       CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
CC       CAPPING.
CC   -!- SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY
CC       CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2
CC       REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC   -!- EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM)
CC       AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATTER BE SPLIT FURTHER INTO
CC       2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
CC   -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC       CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC       CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC   -!- SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY. STRONGEST
CC       TO OTHER NONMUSCLE MYOSINS.
DR   EMBL; M26510; GGMYHN.
DR   PIR; A33977; A33977.
DR   HSSP; P24733; 1SCM.
KW   MYOSIN; COILED COIL; ACTIN-BINDING; ALKYLATION; ATP-BINDING;
KW   HEPTAD REPEAT PATTERN; MULTIGENE FAMILY.
FT   DOMAIN        1    835       GLOBULAR HEAD (S1).
FT   DOMAIN      836   1926       RODLIKE TAIL (S2 AND LMM DOMAINS).
FT   NP_BIND     174    181       ATP.
FT   DOMAIN      654    676       ACTIN-BINDING.
FT   MOD_RES     694    694       ALKYLATION (SH-1) (POTENTIAL).
FT   MOD_RES     704    704       ALKYLATION (SH-2) (POTENTIAL).
SQ   SEQUENCE   1959 AA;  226502 MW;  15394260 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    ARALEEAIEQKAELERVNKQFRTEMEDL
        1490 X    1500


14. US-08-121-713B-24 (1-8)
    TRHY_HUMAN   TRICHOHYALIN.

ID   TRHY_HUMAN     STANDARD;      PRT;  1898 AA.
AC   Q07283;
DT   01-OCT-1994 (REL. 30, CREATED)
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DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   TRICHOHYALIN.
GN   THH OR TRHY OR THL.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   93280194
RA   LEE S.-C., KIM I.-G., MAREKOV L.N., O'KEEFE E.J., PARRY D.A.D.,
RA   STEINERT P.M.;
RL   J. BIOL. CHEM. 268:12164-12176(1993).
RN   [2]
RP   SEQUENCE OF 1731-1898 FROM N.A., AND CHARACTERIZATION.
RM   93315897
RA   O'KEEFE E.J., HAMILTON E.H., LEE S.-C., STEINERT P.M.;
RL   J. INVEST. DERMATOL. 101:65S-71S(1993).
CC   -!- FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES
CC       IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE
CC       INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR
CC       LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY
CC       ISODIPEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD, PROTEIN, TOGETHER
CC       WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN
CC       ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN
CC       ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
CC       DIFFERENTIATION.
CC   -!- SUBUNIT: MONOMER (PROBABLE).
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF
CC       THE EPIDERMIS.
CC   -!- TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUCH AS
CC       THE INNER ROOT SHEAT (IRS) OF HAIR FOLLICLES AND MEDULLA, AND IN
CC       THE FILIFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE).
CC   -!- DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND
CC       CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST
CC       ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS
CC       OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED
CC       ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS
CC       THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS.
CC       DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN
CC       THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
CC       DIFFERENT SPECIES.
CC   -!- PTM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE
CC       PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE.
CC   -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
CC       MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS IN THE N-TERMINUS.
DR   EMBL; L09190; HSTRHYAL.
DR   PIR; A45973; A45973.
DR   HSSP; P02633; 1BOC.
DR   MIM; 190370; 11TH EDITION.
KW   REPEAT; CALCIUM-BINDING.
FT   DOMAIN        1     91       S-100 LIKE.
FT   CA_BIND      22     33       SITE I (LOW AFFINITY) (POTENTIAL).
FT   CA_BIND      62     73       SITE II (HIGH AFFINITY) (POTENTIAL).
FT   DOMAIN      314    390       6 X 13 AA TANDEM REPEATS OF
FT                                R-R-E-Q-E-E-E-R-R-E-Q-Q-L.
FT   REPEAT      314    326       1-1 (APPROXIMATE).
FT   REPEAT      327    339       1-2 (APPROXIMATE).
FT   REPEAT      340    351       1-3 (APPROXIMATE).
FT   REPEAT      352    364       1-4.
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FT   REPEAT      365    377       1-5.
FT   REPEAT      378    390       1-6.
FT   DOMAIN      391    444       9 X 6 AA TANDEM REPEATS OF R-R-E-Q-Q-L.
FT   REPEAT      391    396       2-1.
FT   REPEAT      397    402       2-2.
FT   REPEAT      403    408       2-3.
FT   REPEAT      409    414       2-4.
FT   REPEAT      415    420       2-5.
FT   REPEAT      421    426       2-6.
FT   REPEAT      427    432       2-7.
FT   REPEAT      433    438       2-8.
FT   REPEAT      439    444       2-9.
FT   DOMAIN      444    702       9 X 28 AA APPROXIMATE TANDEM REPEATS.
FT   DOMAIN      923   1162       8 X 30 AA TANDEM REPEATS.
FT   REPEAT      923    952       4-1.
FT   REPEAT      953    982       4-2.
FT   REPEAT      983   1012       4-3.
FT   REPEAT     1013   1042       4-4.
FT   REPEAT     1043   1072       4-5.
FT   REPEAT     1073   1102       4-6.
FT   REPEAT     1103   1132       4-7.
FT   REPEAT     1133   1162       4-8.
FT   DOMAIN     1250   1849       23 X 26 AA APPROXIMATE TANDEM REPEATS.
FT   CONFLICT   1752   1752       F -> L (IN REF. 2).
FT   CONFLICT   1794   1801       QERDRQYR -> RSETGSTG (IN REF. 2).
FT   CONFLICT   1857   1857       Q -> K (IN REF. 2).
FT   CONFLICT   1880   1880       V -> G (IN REF. 2).
SQ   SEQUENCE   1898 AA;  247219 MW;  12293610 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions              =     0

            X      X
            XXXXXXXX

    EIQSQEGKGHGRLLEPGTHQFASVPVRS
      1860    X 1870 X    1880


15. US-08-121-713B-24 (1-8)
    MSAS_PENPA   6-METHYLSALICYLIC ACID SYNTHASE (EC 2.3.1.-) (MSAS

ID   MSAS_PENPA     STANDARD;      PRT;  1774 AA.
AC   P22367;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   6-METHYLSALICYLIC ACID SYNTHASE (EC 2.3.1.-) (MSAS).
OS   PENICILLIUM PATULUM (PENICILLIUM GRISEOFULVUM).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; PLECTOMYCETES; EUROTIALES.
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=DSM 62862;
RM   91006137
RA   BECK J., RIPKA S., SIEGNER A., SCHILTZ E., SCHWEIZER E.;
RL   EUR. J. BIOCHEM. 192:487-498(1990).
CC   -!- FUNCTION: THIS MULTIFUNCTIONAL ENZYME IS A POLYKETIDE SYNTHASE.
CC       IT CATALYSES A TOTAL OF 11 STEPS BY SEVEN DIFFERENT COMPONENT
CC       ENZYMES, IN THE BIOSYNTHESIS OF THE ANTIBIOTIC PATULIN.
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CC   -!- CATALYTIC ACTIVITY: ACETYL-COA + 3 MALONYL-COA + NADPH =
CC       6-METHYLSALICYLIC ACID + NADP(+) + 3 COA + 3 CO(2) + H(2)O.
CC   -!- PATHWAY: BIOSYNTHESIS OF PATULIN.
CC   -!- SUBUNIT: HOMOMULTIMER.
CC   -!- INDUCTION: IN THE LATE LOGARITHMIC GROWTH PHASE.
CC   -!- SIMILARITY: WITH MOST POLYKETIDE SYNTHASES, SPECIALLY WITH RAT
CC       FATTY ACID SYNTHASE, AND WITH OTHER ENZYMES SUCH AS LIPASES AND
CC       THIOLASES.
DR   EMBL; X55776; PPMSAS.
DR   PIR; S13178; S13178.
DR   PROSITE; PS00012; PHOSPHOPANTETHEINE.
DR   PROSITE; PS00606; B_KETOACYL_SYNTHASE.
KW   MULTIFUNCTIONAL ENZYME; OXIDOREDUCTASE; ANTIBIOTIC BIOSYNTHESIS;
KW   TRANSFERASE; NADP; PHOSPHOPANTETHEINE.
FT   DOMAIN      186    238       ACYLTRANSFERASE (AT).
FT   DOMAIN      642    676       ACETYL/MALONYL TRANSFERASES.
FT   DOMAIN     1403   1450       2-OXOACYL REDUCTASES.
FT   DOMAIN     1697   1758       2-OXOACYL SYNTHASE.
FT   DOMAIN     1697   1758       ACYL CARRIER.
FT   NP_BIND    1419   1424       NADP (POTENTIAL).
FT   ACT_SITE    204    204       BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT   ACT_SITE    653    653       MALONYLTRANSFERASE (BY SIMILARITY).
FT   BINDING    1732   1732       PHOSPHOPANTETHEINE (BY SIMILARITY).
SQ   SEQUENCE   1774 AA;  190732 MW;  15502921 CN;

Initial Score    =      8  Optimized Score  =      8  Significance =  7.42
Residue Identity =     0%  Matches          =      0  Mismatches   =     8
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             XXXXXXXX

    LKNTTSRGYFLDRLEDFDCQFFGISPKE
      90       100   X   110
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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq30asq.res made by  on Fri 19 May 95 8:42:39-PDT.


Query sequence being compared:US-08-121-713B-30 (1-7)
Number of sequences searched:                53402
Number of scores above cutoff:                3806

     Results of the initial comparison of US-08-121-713B-30 (1-7) with:
   Data bank : A-GeneSeq 18, all entries

100000-
       -
N      -
U50000*
M      -
B      -
E      -
R      -
       -
O      -                    *
F10000-
       -
S      -
E 5000-
Q      -
U      -
E      -
N      -
C      -
E      -
S 1000-
       -
       -
   500-
       -
       -
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       -
   100-
       -                    *
       -
    50-                                          *
       -
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       -
       -
       -
       -
    10-
       -
       -
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SEQ 30

Da data 121713

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     5-
      -
      -
      -
      -
      -
      -
     0-----------------------------------------------------------------------
       ||     |  |   |      |     |      | |    |  |  |      |      |
SCORE 0|     1  |   2      2     3      4 |    5  |  5      6      7
STDEV  1        2            3     4      5
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	0	1	1.23

Times:	CPU	Total Elapsed
	00:00:31.12	00:00:32.00

Number of residues: 6354270
Number of sequences searched: 53402
Number of scores above cutoff: 3806

Cut-off raised to 1.
Cut-off raised to 3.
Cut-off raised to 4.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

42 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. R13887	Inositol-3-phosphate binding	2749	7	7	5.71	0
2. R41043	CD4-EBA175 fusion protein.	1786	7	7	5.71	0
3. R36780	KRE5.	1365	7	7	5.71	0
4. P94265	Sequence of APH36.1 clone.	783	7	7	5.71	0
5. R33424	G6PD.	751	7	7	5.71	0
6. R41334	91 kD ISGF-3alpha.	739	7	7	5.71	0
7. R41335	84 kD ISGF-3alpha.	701	7	7	5.71	0
8. P70458	Sequence of gpD encoded by se	484	7	7	5.71	0
9. R25930	Human liver Type I iodothyron	249	7	7	5.71	0
10. R44510	Type I iodothyronine 5' deiod	249	7	7	5.71	0

11.	R33383	Cytokine mG-CSF.	208	7	7	5.71	0
12.	P90051	Human granulocyte colony stim	207	7	7	5.71	0
13.	P70161	Human G-CSF encoded by pBRG4	207	7	7	5.71	0
14.	P70163	Human G-CSF deduced from geno	207	7	7	5.71	0
15.	P71383	Sequence of human granulocyte	207	7	7	5.71	0
16.	P61340	Plasmid pBRG4 granulocyte CSF	207	7	7	5.71	0
17.	P71384	Sequence of human granulocyte	204	7	7	5.71	0
18.	P70731	Sequence encoded by human gra	204	7	7	5.71	0
19.	P61341	Plasmid pBRV2 insert encoding	204	7	7	5.71	0
20.	R33382	Cytokine hG-CSF.	204	7	7	5.71	0
21.	P95033	Granulocyte colony stimulatin	204	7	7	5.71	0
22.	P70162	Human G-CSF encoded by pBRV2	204	7	7	5.71	0
23.	P83163	Sequence of human granulocyte	204	7	7	5.71	0
24.	P70730	Sequence encoded by human gra	186	7	7	5.71	0
25.	R59511	Sequence of the light chain v	133	7	7	5.71	0
26.	R10920	kappa light chain variable re	132	7	7	5.71	0
27.	R37716	Mouse 4C10 anti-idiotype Ab l	132	7	7	5.71	0
28.	P90543	Amino acids sequence of a V c	131	7	7	5.71	0
29.	R04132	Anti-Leu 3a light chain varia	131	7	7	5.71	0
30.	R05089	Light chain variable domain o	131	7	7	5.71	0
31.	R28668	p12-k2.	131	7	7	5.71	0
32.	R29008	p64-k4 protein product.	131	7	7	5.71	0
33.	R30881	Antibody 4A2 light chain cons	131	7	7	5.71	0
34.	R32123	Anti-CD4 antibody MT 3.10 lig	131	7	7	5.71	0
35.	R06375	Anti-Tac light chain variable	126	7	7	5.71	0
36.	R24108	Humanised anti-Tac antibody l	126	7	7	5.71	0
37.	R04938	Chelate-specific light chain	110	7	7	5.71	0
38.	R05038	Metal chelate specific light	110	7	7	5.71	0
39.	R54136	CHA255 light chain variable r	110	7	7	5.71	0
40.	R10540	Eukaryotic signal peptide enc	20	7	7	5.71	0
41.	R54141	CHA255 light chain variable r	9	7	7	5.71	0
42.	R65508	Endothelin antagonist cyclic	5	7	7	5.71	0

The list of other best scores is:

Sequence	Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
		**** 3 standard deviations above mean ****					
43.	P50687	Hepatitus B virus antigenic p	16	4	4	3.26	0
44.	R37946	HCV NS-4 type 1 region 2 (171	17	4	4	3.26	0
45.	R26013	Influenza fusion peptide #10.	22	4	4	3.26	0

1. US-08-121-713B-30 (1-7)
R13887 Inositol-3-phosphate binding peptide.

ID R13887 standard; Protein; 2749 AA.
AC R13887;
DT 27-NOV-1991 (first entry)
DE Inositol-3-phosphate binding peptide.
KW I-3-P; transformation; inositol.
PN J03183482-A.
PD 09-AUG-1991.
PF 14-DEC-1989; 324256.
PR 14-DEC-1989; JP-324256.
PA (KYOW) KYOWA HAKKO KOGYO KK.
DR WPI; 91-277584/38.
DR N-PSDB; Q13593.
PT New polypeptide having binding affinity to inositol-3-phosphate -

PT prepd. by culturing cell contg. recombinant plasmid comprising
PT DNA and vector DNA
PS Disclosure; Fig 2(1-3); 11pp; Japanese.
CC The sequence encoding this peptide may be included in a
CC plasmid/vector for transformation of a host cell and mass-prodn.
CC of the peptide.
SQ Sequence 2749 AA;
SQ 146A; 155R; 144N; 154D; 0 B; 60 C; 128Q; 229E; 0 Z; 142G; 71 H;
SQ 155I; 314L; 167K; 69 M; 123F; 99 P; 180S; 136T; 21 W; 71 Y; 185V;

Initial Score = 7 Optimized Score = 7 Significance = 5.71
Residue Identity = 28% Matches = 2 Mismatches = 5
Gaps = 0 Conservative Substitutions = 0

```
            X     X
            XWXXXLX
             |    |
   GTLEPHWSGLLWTAMLISLAIVIALPK
       2310 X    2320
```

2. US-08-121-713B-30 (1-7)
R41043 CD4-EBA175 fusion protein.

ID R41043 standard; protein; 1786 AA.
AC R41043;
DT 22-MAR-1994 (first entry)
DE CD4-EBA175 fusion protein.
KW Merozoite; Erythrocyte Binding Antigen 175; malaria; HIV; env;
KW human immunodeficiency virus; envelope glycoprotein; hybrid protein;
KW red blood cell; erythrocyte; AIDS; molecular machine.
OS Chimeric Homo sapiens.
OS Chimeric Plasmodium falciparum.
FH Key Location/Qualifiers
FT Region 1..371
FT /note= "residues 1-371 of CD4"
FT Region 372..1786
FT /note= "residues 20-1435 of EBA-175"
PN WO9318160-A.
PD 16-SEP-1993.
PF 10-MAR-1993; G00505.
PR 11-MAR-1992; GB-005276.
PR 08-JUL-1992; GB-014481.
PR 24-JUL-1992; GB-015829.
PR 16-SEP-1992; GB-019562.
PR 03-MAR-1993; GB-004311.
PA (PREN/) PRENDERGAST K F.
PI Prendergast KF;
DR WPI; 93-303474/38.
PT Anti-viral fusion peptide(s) - comprise viral-binding component
PT and malaria merozoite red cell binding component, for treating
PT e.g. HIV, and hepatitis
PS Claim 9; Page 44-47; 69pp; English.
CC The hybrid protein NH2-CD4(1-371)-EBA175(20-1435)-COOH is a
CC specifically claimed example of a fusion protein of the invention;
CC it comprises at least part of the CD4 molecule fused to a peptide
CC from a malarial parasite merozoite protein with affinity for red
CC blood cells. The fusion protein can bind free HIV in the blood to
CC red blood cells and consequently reduce viral titre, prevent
CC transmission of the virus and improve safety of blood transfusions.

```
SQ   Sequence   1786 AA;
SQ   47 A; 65 R; 163N; 126D; 0  B; 41 C; 63 Q; 169E; 0  Z; 73 G; 40 H;
SQ   103I; 134L; 202K; 29 M; 55 F; 51 P; 160S; 98 T; 28 W; 54 Y; 85 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
    KEWWNEFREKLWEAMLSEHKNNINNCK
     640       650  X    660
```

3. US-08-121-713B-30 (1-7)
R36780 KRE5.

```
ID   R36780 standard; Protein; 1365 AA.
AC   R36780;
DT   16-JUL-1993  (first entry)
DE   KRE5.
KW   Yeast; cell wall; beta-glucan; assembly; pathway; KRE1; KRE5; growth;
KW   secretory; O-linked mannose; (1>6)-beta-glucan; epistasis; morphology;
KW   hydrophilic; glycoprotein; COOH-terminal; endoplasmic reticulum; ER;
KW   retention signal; antifungal agent.
OS   Saccharomyces cerevisiae.
PN   US5194600-A.
PD   16-MAR-1993.
PF   05-MAR-1990; 488316.
PR   05-MAR-1990; US-488316.
PA   (ROYA-) ROYAL INST ADVANCEMENT LEARNING.
PI   Boone C,  Bussey H,  Hill K,  Meaden P,  Sommer SS;
DR   WPI; 93-109384/13.
DR   N-PSDB; Q38899.
PT   New DNA encoding genes which participate in beta-glucan assembly
PT   - useful for producing mutants for in=vivo screening of
PT   antifungal agents and providing tools for in-vitro screening
PS   Claim 1; Columns 38-44; 24pp; English.
CC   The sequences given in R34785 and R36780 represent proteins which
CC   participate in a yeast cell wall beta-glucan assembly pathway.
CC   These proteins represent KRE1 and KRE5 respectively, and are
CC   essential for normal cell growth.  KR1 is a Ser/Thr rich protein
CC   that is directed into the yeast secretory pathway, where it is
CC   highly modified, probably through addition of O-linked mannose
CC   residues.  Gene disruption of the KRE1 locus leads to a 40% reduced
CC   level of cell wall (1>6)-beta-glucan.  Mutations at KRE5 also caused
CC   defects in cell wall (1>6)-beta-glucan production and appears to be
CC   epistatic to KRE1.  KRE5 is a large hydrophilic secretory glyco-
CC   protein which contains the COOH-terminal endoplasmic reticulum (ER)
CC   retention signal (His-Asp-Glu-Leu).  Deletion of the KRE5 gene results
CC   in cells with aberant morphology and extremly compromised growth.
CC   KRE1 and KRE5 are useful as tools for the in vitro screening of anti-
CC   fungal agents which inhibit fungi pathogenic to plants and animals.
CC   The genes can be used to produce mutants for in vivo screening of
CC   antifungal agents.
SQ   Sequence   1365 AA;
SQ   43 A; 56 R; 81 N; 98 D; 0  B; 12 C; 51 Q; 92 E; 0  Z; 60 G; 23 H;
SQ   114I; 166L; 92 K; 25 M; 66 F; 60 P; 121S; 61 T; 13 W; 55 Y; 76 V;
```



```
Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
    MSGDGYWKEGYWEKMLRENNLEFYSTE
 1230      1240      1250
```

4. US-08-121-713B-30 (1-7)
P94265 Sequence of APH36.1 clone.

```
ID   P94265 standard; protein; 783 AA.
AC   P94265;
DT   24-JUN-1990  (first entry)
DE   Sequence of APH36.1 clone.
KW   Clone APH36.1; acyl-peptide hydrolase.
OS   Rattus rattus.
FH   Key             Location/Qualifiers
FT   Protein         1..721
FT   /label=claimed protein
FT   Active-site     580..587
FT   Region          130.
FT   /note="potential site of glycosylation"
FT   Region          131.
FT   /note="potential site of glycosylation"
FT   Region          132.
FT   /note="potential site of glycosylation"
FT   Region          229.
FT   /note="potential site of glycosylation"
FT   Region          230.
FT   /note="potential site of glycosylation"
FT   Region          231.
FT   /note="potential site of glycosylation"
FT   Region          239.
FT   /note="potential site of glycosylation"
FT   Region          240.
FT   /note="potential site of glycosylation"
FT   Region          241.
FT   /note="potential site of glycosylation"
PN   EP-303997-A.
PD   22-FEB-1989.
PF   13-AUG-1988; 113186.
PR   21-AUG-1987; US-087936.
PA   (GEHO-) The General Hospital Corp.
PI   Smith JA;
DR   WPI; 89-055444/08.
DR   N-PSDB; N91052.
PT   Recombinant acyl-peptide hydrolase -used to catalyse hydrolysis of N-acyl
PT   peptide(s) or reaction of N-acetyl amino acid donor and acceptor protein.
PS   Disclosure; pp; English.
CC   Sequence contains the claimed sequence of acyl-peptide hydrolase (APH)
CC   (claim 1, page 11).  APH can be used to catalyse the hydrolysis of the
CC   N-terminal acyl amino acid of an acylated polypeptide, or the reaction
CC   between a derivatised N alpha-acetyl amino acid donor and acceptor with
CC   a free alpha-NH2.  It can also be used to make refractory proteins
CC   susceptible to Edman sequencing or th reduce degradation of proteins to
CC   be used therapeutically.
```

```
 SQ   Sequence   783 AA;
 SQ   50 A;  39 R;  18 N;  40 D;  0 B;  20 C;  37 Q;  44 E;  0 Z;  57 G;  19 H;
 SQ   24 I;  81 L;  39 K;  21 M;  31 F;  53 P;  73 S;  33 T;  19 W; 24 Y; 61 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
    YSNSCLPDLNVWEEMLDKSPIKYIPQV
         640  X    650
```

5. US-08-121-713B-30 (1-7)
   R33424 G6PD.

```
 ID   R33424 standard; Protein; 751 AA.
 AC   R33424;
 DT   27-JUL-1993  (first entry)
 DE   G6PD.
 KW   Polymerase chain reaction; glucose-6-phosphate dehydrogenase; PCR;
 KW   E. coli; G6PD; drug; transformation; primer; amplify.
 OS   Plasmodium falciparum.
 PN   WO9306125-A.
 PD   01-APR-1993.
 PF   21-SEP-1992; U07807.
 PR   20-SEP-1991; US-762137.
 PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
 PI   Kaslow DC,  Shahabuddin M;
 DR   WPI; 93-117467/14.
 DR   N-PSDB; Q33424.
 PT   DNA segments encoding Plasmodium falciparum G6PD obtd. by PCR -
 PT   used to express proteins and raise antibodies for diagnosis and
 PT   treatment of malaria
 PS   Claim 2; Fig 2; 36pp; English.
 CC   This sequence represents Plasmodium falciparum glucose-6-phosphate
 CC   dehydrogenase (G6PD).  The DNA encoding this sequence was isolated
 CC   using the primers given in Q38806-07.  The amplified sequence was
 CC   used in the production of transformed E. coli which produce a
 CC   recombinant P. falciparum G6PD.  These transformed cells can be used
 CC   in a method of screening drugs for activity against P. falciparum
 CC   G6PD.
 SQ   Sequence   751 AA;
 SQ   15 A; 14 R; 85 N; 44 D; 0  B; 18 C; 17 Q; 52 E; 0  Z; 26 G; 11 H;
 SQ   69 I; 73 L; 80 K; 15 M; 41 F; 22 P; 50 S; 36 T; 4  W; 53 Y; 26 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
    FLLNSKDKLDLWKNMLIKSYIEVNYNL
     80        90   X   100
```

6. US-08-121-713B-30 (1-7)

R41334 91 kD ISGF-3alpha.

```
 ID   R41334 standard; Protein; 739 AA.
 AC   R41334;
 DT   22-APR-1994  (first entry)
 DE   91 kD ISGF-3alpha.
 KW   113 kD; 91 kD; 84 kD; ISGF-3alpha; interferon-related; receptor;
 KW   recognition factor; gene family; translation protein; tyrosine;
 KW   DNA binding protein; interferon-gamma; hairy cell leukaemia;
 KW   interferon therapy; chronic viral hepatitis; phosphorylation;
 KW   adjuvant therapy; tyrosine kinase.
 OS   Homo sapiens.
 PN   WO9319179-A.
 PD   30-SEP-1993.
 PF   19-MAR-1993; U02569.
 PR   19-MAR-1992; US-854296.
 PR   23-NOV-1992; US-980498.
 PA   (UYRQ ) UNIV ROCKEFELLER.
 PI   Darnell JE,  Fu X,  Schindler CW,  Shuai K;
 DR   WPI; 93-320745/40.
 DR   N-PSDB; Q49165.
 PT   Interferon receptor recognition factors - useful e.g. to treat
 PT   viral hepatitis, hairy cell leukaemia and to potentiate interferon
 PT   effects
 PS   Claim 17; Fig 2; 131pp; English.
 CC   The sequences given in R41333-35 represent the 113 kD, 91 kD and 84 kD
 CC   ISGF-3alpha proteins respectively.  ISGF-3alpha is an interferon-
 CC   related receptor recognition factor which comprises several
 CC   substituents.  The 113 kD, and the 91 and 84 kD proteins are derived
 CC   from two different but related genes.  It is clear that a gene
 CC   family exists and further members are likely to be found.  The 91 kD
 CC   protein has the capability of acting as a translation protein and as
 CC   a DNA binding protein in response to interferon-gamma stimulation.
 CC   These proteins participate in rapid phosphorylation and dephosphory-
 CC   lation during the course of, and as part of their activity.  This
 CC   phosphorylation takes place in an interferon-dependant manner on
 CC   specified tyrosine residues.  These proteins may be used in
 CC   conjunction with interferon therapy eg. to treat chronic viral
 CC   hepatitis, hairy cell leukaemia and for use with interferon in
 CC   adjuvant therapy.
 SQ   Sequence   739 AA;
 SQ   26 A; 34 R; 44 N; 38 D; 0  B; 10 C; 53 Q; 64 E; 0  Z; 27 G; 16 H;
 SQ   36 I; 89 L; 55 K; 19 M; 33 F; 35 P; 49 S; 35 T; 14 W; 18 Y; 44 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
    SQLPSGWASILWYNMLVAEPRNLSFFL
          460       470
```

7. US-08-121-713B-30 (1-7)
   R41335 84 kD ISGF-3alpha.

```
 ID   R41335 standard; Protein; 701 AA.
 AC   R41335;
```

```
DT   22-APR-1994  (first entry)
DE   84 kD ISGF-3alpha.
KW   113 kD; 91 kD; 84 kD; ISGF-3alpha; interferon-related; receptor;
KW   recognition factor; gene family; translation protein; tyrosine;
KW   DNA binding protein; interferon-gamma; hairy cell leukaemia;
KW   interferon therapy; chronic viral hepatitis; phosphorylation;
KW   adjuvant therapy; tyrosine kinase.
OS   Homo sapiens.
PN   WO9319179-A.
PD   30-SEP-1993.
PF   19-MAR-1993; U02569.
PR   19-MAR-1992; US-854296.
PR   23-NOV-1992; US-980498.
PA   (UYRQ ) UNIV ROCKEFELLER.
PI   Darnell JE,  Fu X,  Schindler CW,  Shuai K;
DR   WPI; 93-320745/40.
DR   N-PSDB; Q49166.
PT   Interferon receptor recognition factors - useful e.g. to treat
PT   viral hepatitis, hairy cell leukaemia and to potentiate interferon
PT   effects
PS   Claim 17; Fig 3; 131pp; English.
CC   The sequences given in R41333-35 represent the 113 kD, 91 kD and 84 kD
CC   ISGF-3alpha proteins respectively.  ISGF-3alpha is an interferon-
CC   related receptor recognition factor which comprises several
CC   substituents.  The 113 kD, and the 91 and 84 kD proteins are derived
CC   from two different but related genes.  It is clear that a gene
CC   family exists and further members are likely to be found.  The 91 kD
CC   protein has the capability of acting as a translation protein and as
CC   a DNA binding protein in response to interferon-gamma stimulation.
CC   These proteins participate in rapid phosphorylation and dephosphory-
CC   lation during the course of, and as part of their activity.  This
CC   phosphorylation takes place in an interferon-dependant manner on
CC   specified tyrosine residues.  These proteins may be used in
CC   conjunction with interferon therapy eg. to treat chronic viral
CC   hepatitis, hairy cell leukaemia and for use with interferon in
CC   adjuvant therapy.
SQ   Sequence   701 AA;
SQ   26 A; 33 R; 42 N; 35 D; 0  B; 10 C; 52 Q; 60 E; 0  Z; 26 G; 15 H;
SQ   35 I; 85 L; 55 K; 16 M; 31 F; 32 P; 44 S; 32 T; 14 W; 18 Y; 40 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
    SQLPSGWASILWYNMLVAEPRNLSFFL
          460       470
```

8. US-08-121-713B-30 (1-7)
   P70458 Sequence of gpD encoded by segment of Xanthomonas

```
ID   P70458 standard; protein; 484 AA.
AC   P70458;
DT   13-FEB-1991  (first entry)
DE   Sequence of gpD encoded by segment of Xanthomonas campestris DNA
DE   that contains a gene cluster that directs Xanthan biosynthesis.
KW   Thickening agent; oil recovery; drilling fluid.
```



```
OS   Xanthomonas campestris.
PN   WO8705938-A.
PD   08-OCT-1987.
PF   24-MAR-1987; U00604.
PR   23-MAR-1987; US-029530.
PA   (GETT-) Getty Sci Dev Co.
PI   Capage MA, Doherty DH, Betlach MR, Vanderslice RW.
DR   WPI; 87-291651/41.
PT   Recombinant DNA prodn. of xanthan gum or its variants - by
PT   transforming host cells with vector contg. DNA coding for enzymes
PT   involved in polysaccharide synthesis
PS   Example; Fig 12; 149pp; English.
CC   Virtually all of the segment of Xanthomonas campestris DNA that
CC   contains a gene cluster that directs Xanthan biosynthesis (N70753),
CC   codes for protein products. Each gene is designated by a letter (see
CC   Fig 11) and its protein product is designated by that letter
CC   preceded by 'gp' (P70455-67).
SQ   Sequence   484 AA;
SQ   33 A; 40 R; 15 N; 21 D; 0  B; 2  C; 23 Q; 13 E; 0  Z; 41 G; 12 H;
SQ   26 I; 61 L; 15 K; 13 M; 22 F; 21 P; 26 S; 21 T; 10 W; 19 Y; 50 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
    KILAVIAILMGLWPLMLAIAVGVKMSSP
    300       310   X   320
```

9. US-08-121-713B-30 (1-7)
   R25930 Human liver Type I iodothyronine 5' deiodinase.

```
ID   R25930 standard; Protein; 249 AA.
AC   R25930;
DT   27-JAN-1993  (first entry)
DE   Human liver Type I iodothyronine 5' deiodinase.
KW   thyroid hormone; SeCys; selenocysteine; thyroxine;
KW   3,3',5-triiodothyronine; ITDI.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Modified_site   126
FT   /label= OTHER
FT   /note= "Selenocysteine"
PN   WO9213077-A.
PD   06-AUG-1992.
PF   29-JAN-1992; U00740.
PR   29-JAN-1991; US-647657.
PR   03-SEP-1991; US-757024.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PI   Berry MA, Larsen PR;
DR   WPI; 92-284662/34.
DR   N-PSDB; Q26751.
PT   Type I iodo:thyronine 5' de-iodinase and DNA encoding it - for
PT   treatment and diagnosis of thyroid function related diseases;
PT   also for diagnosis of thyroid cancer
PS   Claim 2; Fig 4B; 104pp; English.
CC   A 2.1kb cDNA for 5'-deiodinase was isolated from a rat liver
```

```
CC   library by expression in Xenopus oocytes (see Q26750). The clone
CC   was used to probe a human cDNA library and a gene encoding the
CC   complete human ITDI enzyme was isolated. The UGA codon at
CC   nucleotide 382 encodes the rare amino acid selenocysteine. The
CC   selenocysteine insertion sequence (SECIS) in the 3'-UTR has 66%
CC   homology to the SECIS downstream of the rat ITDI gene. The
CC   presence of SeCys is essential for full activity.
SQ   Sequence   249 AA;
SQ   13 A; 16 R; 14 N; 10 D; 0  B; 4  C; 14 Q; 13 E; 0  Z; 14 G; 7  H;
SQ   12 I; 30 L; 11 K; 7  M; 15 F; 14 P; 13 S; 8  T; 8  W; 6  Y; 19 V;
SQ   1 Others;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

          X     X
          XWXXXLX
           |    |
   MGLPQPGLWLKRLWVLLEVAVHVV
           10   X    20
```

10. US-08-121-713B-30 (1-7)
    R44510 Type I iodothyronine 5' deiodinase.

```
ID   R44510 standard; Protein; 249 AA.
AC   R44510;
DT   16-JUN-1994  (first entry)
DE   Type I iodothyronine 5' deiodinase.
KW   Type I; iodothyronine; 5'; deiodinase; 3' untranslated region;
KW   selenocysteine; transient expression assay; antibody; diagnosis;
KW   thyroid; function; selenocysteine insertion sequence; reporter gene;
KW   transfection; efficiency; promoter.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Misc_difference 126
FT   /label= OTHER
FT   /note= "Selenocysteine"
PN   US5272078-A.
PD   21-DEC-1993.
PF   29-JAN-1991; 647657.
PR   29-JAN-1991; US-647657.
PR   03-SEP-1991; US-757024.
PR   29-JAN-1992; US-828790.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PI   Berry MJ,  Larsen PR;
DR   WPI; 93-413408/51.
DR   N-PSDB; Q53466.
PT   DNA encoding the type I iodo-thyronine 5'-deiodinase and mutants
PT   of this - has a seleno-cysteine site which may be used to study
PT   thyroid hormone and in diagnosis of thyroid cancer
PS   Claim 2; Fig 4B; 49pp; English.
CC   This sequence represents a type I iodothyronine 5' deiodinase.  The
CC   gene encoding this protein contains in the 3' untranslated region a
CC   sequence which causes inclusion of a selenocysteine residue at a TGA
CC   codon within the deiodinase gene.  This protein and antibodies
CC   reacting with it, are useful in the diagnosis and treatment of
CC   disease states related to thyroid function.  Mutant reporter genes
CC   based on the deiodinase gene sequence containing Cys in place of
```



```
CC   selenocysteine, may be used for monitoring transfection efficiencies
CC   or in the study of heterologous promoter function in transient
CC   expression assays.  Characterisation of the selenocysteine insertion
CC   sequence is useful to effect incorporation of selenocysteine into
CC   peptides or proteins to study the effects of the presence of
CC   selenocysteine on the properties of such proteins.
SQ   Sequence   249 AA;
SQ   13 A; 16 R; 14 N; 10 D; 0  B; 4  C; 14 Q; 13 E; 0  Z; 14 G; 7  H;
SQ   12 I; 30 L; 11 K; 7  M; 15 F; 14 P; 13 S; 8  T; 8  W; 6  Y; 19 V;
SQ   1 Others;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

          X     X
          XWXXXLX
           |    |
   MGLPQPGLWLKRLWVLLEVAVHVV
           10   X    20
```

11. US-08-121-713B-30 (1-7)
    R33383 Cytokine mG-CSF.

```
ID   R33383 standard; peptide; 208 AA.
AC   R33383;
DT   15-JUL-1993  (first entry)
DE   Cytokine mG-CSF.
KW   Cytokine; family; leukemia inhibitory factor; LIF; interleukin-6; OSM;
KW   granulocyte colony stimulating factor; G-CSF; oncostatin-M; hybrid;
KW   IL-6; alpha-helix.
OS   Mus musculus.
PN   WO9305169-A.
PD   18-MAR-1993.
PF   24-AUG-1992; U07112.
PR   30-AUG-1991; US-753178.
PA   (HUTC-) HUTCHINSON CANCER RES CENT FRED.
PI   Rose TM,  Todaro GJ;
DR   WPI; 93-100991/12.
PT   Hybrid cytokine(s) contg. four helical regions - derived from
PT   LIF, G-CSF, IL-6 or oncostatin-M, useful for treating Kaposi's
PT   sarcoma, rheumatoid arthritis, malignancies etc.
PS   Disclosure; Fig 1; 41pp; English.
CC   The sequences in R33378-85 cytokines derived from the cytokine
CC   family members leukemia inhibitory factor (LIF), granulocyte colony
CC   stimulating factor (G-CSF), interleukin-6 (IL-6) and oncostatin-M
CC   (OSM).  These cytokins were used in the production of hybrid
CC   cytokines which have unique physiological properties.  The hybrid
CC   cytokines comprise a first, second, third and fourth alpha-helical
CC   region derived from the corresponding region of one of the cytokines
CC   given each derived from a factor different from that which at least
CC   one additional region of the cytokine is derived.
SQ   Sequence   208 AA;
SQ   24 A; 8  R; 2  N; 2  D; 0  B; 5  C; 21 Q; 7  E; 0  Z; 12 G; 5  H;
SQ   5  I; 43 L; 5  K; 5  M; 5  F; 12 P; 21 S; 9  T; 3  W; 4  Y; 10 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0
```

```
            X     X
            XWXXXLX
              |   |
    RMKLMALQLLLWQSALWSGREAVPLVT
    10        20    X   30
```

12. US-08-121-713B-30 (1-7)
    P90051 Human granulocyte colony stimulating factor

```
 ID   P90051 standard; protein;  207 AA.
 AC   P90051;
 DT   1-NOV-1989  (first entry)
 DE   Human granulocyte colony stimulating factor
 KW   Human granulocyte colony stimulating factor; prevents
 KW   Pseudomonas aeruginosa; Listeria; Candida.
 OS   Homo sapiens (Human)
 PN   J01110629-A.
 PD   11-MAY-1989.
 PF   07-FEB-1986; 501027.
 PR   07-FEB-1986; JP-501027.
 PA   (CHUS) Chugai Pharmaceutical KK.
 DR   WPI; 89-169399/23.
 PT   Agent for preventing infection caused eg by
 PT   Pseudomonas aeruginosa - contg. human granulocyte
 PT   colony stimulating factors.
 PS   Disclosure; fig 3; 57pp; Japanese.
 CC   Human granulocyte colony stimulating factor (h-G-CSF)
 CC   used as active ingredient for preventing infection by Pseudomonas
 CC   aeruginosa, Candida and Listeria.  h-G-CSF is pref.
 CC   a neutrophil obtd. from, eg CHU-1 or CHU-2.  h-G-CSF
 CC   has mol. wt. approx. 19 kD, isoelectric point approx.
 CC   5.5,5.8 or 6.1, max. absorption at 280 nm, min. at 250 nm.
 CC   Part of h-G-CSF (amino acids 1 - 175)
 CC   can also be used as active agent.
 CC
 SQ   Sequence   207 AA;
 SQ   24 A;  5 R;  0 N;  4 D;  0 B;  5 C;  21 Q;  10 E;  0 Z;  15 G;  6 H;
 SQ   4 I;  39 L;  5 K;  6 M;  6 F;  15 P;  17 S;  9 T;  4 W;  3 Y;  9 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0
```

```
            X     X
            XWXXXLX
              |   |
    PMKLMALQLLLWHSALWTVQEATPLGP
    10        20    X   30
```

13. US-08-121-713B-30 (1-7)
    P70161 Human G-CSF encoded by pBRG4 insert.

```
 ID   P70161 standard; Protein; 207 AA.
 AC   P70161;
 DT   25-APR-1991  (first entry)
 DE   Human G-CSF encoded by pBRG4 insert.
 KW   Human granulocyte colony stimulating factor; G-CSF; leukaemia; ss.
```



```
 OS   Homo sapiens.
 PN   EP-220520-A.
 PD   06-MAY-1987.
 PF   30-SEP-1986; 113446.
 PR   30-SEP-1985; JP-217150.
 PR   17-JUL-1986; JP-166710.
 PR   17-JUL-1986; JP-166709.
 PA   (CHUS) Chugai Seiyaku KK.
 PI   Yamzaki T, Nagata S, Tsuchiya M.
 DR   WPI; 87-124182/18.
 DR   N-PSDB; N70222.
 PT   Polypeptide with human granulocyte colony stimulating factor
 PT   activity - is obtd. by cultivating transformant formed by
 PT   recombinant DNA procedures.
 PS   Disclosure; Fig 3; 73pp; English.
 CC   The plasmid was isolated from a cDNA prepd. from CHU-2 cells, a
 CC   human oral cavity tumour cell line, using a 600 bp insert from
 CC   pHCS-1 (N70221) as a probe.  The plasmid was used to prepare
 CC   recombinant expression plasmids for the prodn. of h G-CSF.
 CC   See also P70162 and P70163.
 SQ   Sequence   207 AA;
 SQ   24 A;  5 R;  0 N;  4 D;  0 B;  5 C;  20 Q;  11 E;  0 Z;  15 G;  6 H;
 SQ   4 I;  39 L;  5 K;  6 M;  6 F;  15 P;  17 S;  9 T;  4 W;  3 Y;  9 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0
```

```
            X     X
            XWXXXLX
              |   |
    PMKLMALQLLLWHSALWTVQEATPLGP
    10        20    X   30
```

14. US-08-121-713B-30 (1-7)
    P70163 Human G-CSF deduced from genomic DNA.

```
 ID   P70163 standard; Protein; 207 AA.
 AC   P70163;
 DT   10-MAR-1993  (revised)
 DT   25-APR-1991  (first entry)
 DE   Human G-CSF deduced from genomic DNA.
 KW   Human granulocyte colony stimulating factor; G-CSF; leukaemia; ss.
 OS   Homo sapiens.
 PN   EP-220520-A.
 PD   06-MAY-1987.
 PF   30-SEP-1986; 113446.
 PR   30-SEP-1985; JP-217150.
 PR   17-JUL-1986; JP-166710.
 PR   17-JUL-1986; JP-166709.
 PA   (CHUS) Chugai Seiyaku KK.
 PI   Yamzaki T, Nagata S, Tsuchiya M.
 DR   WPI; 87-124182/18.
 DR   N-PSDB; N70224.
 PT   Polypeptide with human granulocyte colony stimulating factor
 PT   activity - is obtd. by cultivating transformant formed by
 PT   recombinant DNA procedures.
 PS   Disclosure; Fig 5; 73pp; English.
 CC   The plasmid was isolated from a human chromosomal DNA library using
```

```
 CC   using a 600 bp insert pHCS-1 isolated from a cDNA library prepd.
 CC   from CHU-2 cells, a human oral cavity tumour cell line.
 CC   The plasmid was used to prepare recombinant expression plasmids for
 CC   the prodn. of h G-CSF.
 CC   See also P70161 and P70162.
 SQ   Sequence   207 AA;
 SQ   24 A; 5  R; 0  N; 4  D; 0  B; 5  C; 20 Q; 11 E; 0  Z; 15 G; 6  H;
 SQ   4  I; 39 L; 5  K; 6  M; 6  F; 15 P; 17 S; 9  T; 4  W; 3  Y; 9  V;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

            X     X
            XWXXXLX
              |   |
    PMKLMALQLLLWHSALWTVQEATPLGP
    10        20    X   30


15. US-08-121-713B-30 (1-7)
    P71383       Sequence of human granulocyte colony stimulating f

 ID   P71383 standard; Protein; 207 AA.
 AC   P71383;
 DT   23-APR-1991  (first entry)
 DE   Sequence of human granulocyte colony stimulating factor (hGCSF)
 DE   in pBRG4.
 KW   Leukopenia therapy; neutropenia; eosinopenia; lymphopenia.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   Peptide         1..30
 FT   Protein         31..208
 FT   /note= "claimed; N-terminal Met optionl"
 FT   Misc_difference 66..68
 FT   /note= "optional in claim"
 PN   EP-217404-A.
 PD   08-APR-1987.
 PF   03-OCT-1986; 113671.
 PR   04-OCT-1985; JP-220450.
 PR   02-JUN-1986; JP-125660.
 PA   (CHUS ) CHUGAI SEIYAKU KK.
 PI   Tamura M, Nomura H, Hattori K, Ono M;
 DR   WPI; 87-095431/14.
 DR   N-PSDB; N71319.
 PT   Leukopenia treating agent esp. for producing fully mature
 PT   neutrophiles - contains human granulocyte colony stimulating
 PT   factor obtd. by recombinant DNA methods etc.
 PS   Disclosure; Fig 2; 34pp; English.
 CC   The hGCSF has the following properties: (i) mol. wgt. 19000 +/- 1000
 CC   (by SDS-PAGE); (ii) isoelectric pt. at 5.5, 5.8 or 6.1 each +/- 0.1;
 CC   (iii) UV max. absorption at 280nm and min. at 250nm. Prodn. of the
 CC   gene, vector etc. is described in JP 269455, 269456, 270838 and
 CC   270839, each of 1985.
 SQ   Sequence   207 AA;
 SQ   24 A; 5  R; 0  N; 4  D; 0  B; 5  C; 20 Q; 11 E; 0  Z; 15 G; 6  H;
 SQ   4  I; 39 L; 5  K; 6  M; 6  F; 15 P; 17 S; 9  T; 4  W; 3  Y; 9  V;

Initial Score    =      7  Optimized Score  =      7  Significance =  5.71
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
```



```
Gaps             =      0  Conservative Substitutions              =     0

            X     X
            XWXXXLX
              |   |
    PMKLMALQLLLWHSALWTVQEATPLGP
    10        20    X   30
> O <
O| |O  IntelliGenetics
> O <

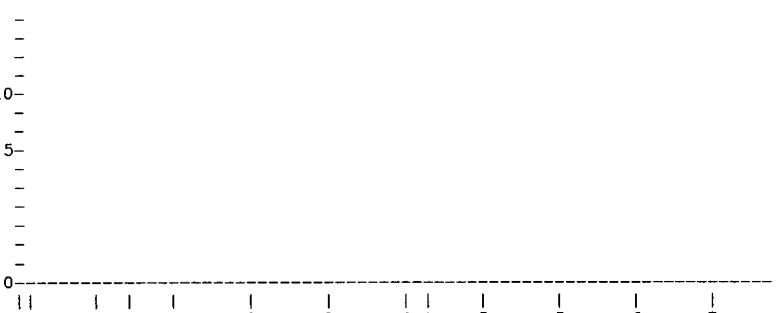
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq30pir.res made by  on Fri 19 May 95 8:49:28-PDT.


Query sequence being compared:US-08-121-713B-30 (1-7)
Number of sequences searched:                75511
Number of scores above cutoff:                4165

     Results of the initial comparison of US-08-121-713B-30 (1-7) with:
   Data bank : PIR 43, all entries

100000-
      -
N     -
U50000-
M     *                          *
B     -
E     -
R     -
      -
O     -
F10000-
      -
S     -
E 5000-
Q     -
U     -
E     -
N     -
C     -
E     -
S 1000-
      -
      -
   500-
      -                                    *
      -
      -
      -
      -
      -                                                              *
   100-
      -
      -
    50-
      -
      -
```



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	1	1.52

Times:	CPU	Total Elapsed
	00:01:15.00	00:01:16.00

Number of residues: 22468834
Number of sequences searched: 75511
Number of scores above cutoff: 4165

Cut-off raised to 1.
Cut-off raised to 3.
Cut-off raised to 4.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

120 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. ACMSIT	inositol-trisphosphate recept	2749	7	7	3.94	0
2. A36579	inositol 1,4,5-triphosphate r	2749	7	7	3.94	0
3. B36579	inositol 1,4,5-triphosphate r	2734	7	7	3.94	0

4. A40743	IP3 receptor, XIP3R - African	2693	7	7	3.94	0
5. A46692	DNA polymerase epsilon cataly	2257	7	7	3.94	0
6. RRXPLC	RNA-directed RNA polymerase (	2210	7	7	3.94	0
7. BWASBE	bimE protein - Emericella nid	2073	7	7	3.94	0
8. A40262	210K nuclear DNA-binding prot	1872	7	7	3.94	0
9. S23810	collagen alpha 1(XVI) chain p	1603	7	7	3.94	0
10. A44604	polycystic kidney disease pro	1594	7	7	3.94	0
11. I48216	neurexin III-alpha membrane-b	1578	7	7	3.94	0
12. A48218	neurexin III-alpha membrane-b	1575	7	7	3.94	0
13. B48218	neurexin III-alpha membrane-b	1471	7	7	3.94	0
14. C48218	neurexin III-alpha membrane-b	1468	7	7	3.94	0
15. A45665	adult-specific brush border e	1458	7	7	3.94	0
16. A48216	neurexin III-alpha secreted t	1438	7	7	3.94	0
17. A37793	erythrocyte-binding antigen 1	1435	7	7	3.94	0
18. B48216	neurexin III-alpha secreted t	1435	7	7	3.94	0
19. S11561	EBA-175 protein - Plasmodium	1426	7	7	3.94	0
20. G48216	neurexin III-alpha secreted t	1399	7	7	3.94	0
21. H48216	neurexin III-alpha secreted t	1396	7	7	3.94	0
22. C48216	neurexin III-alpha secreted t	1395	7	7	3.94	0
23. D48216	neurexin III-alpha secreted t	1392	7	7	3.94	0
24. E48216	neurexin III-alpha secreted t	1378	7	7	3.94	0
25. F48216	neurexin III-alpha secreted t	1375	7	7	3.94	0
26. BVBYK5	KRE5 protein precursor - yeas	1365	7	7	3.94	0
27. S46122	SNF2 protein homolog - yeast	1143	7	7	3.94	0
28. S37837	suppressor protein SPT23 - ye	1082	7	7	3.94	0
29. S40259	glucose-6-phosphate 1-dehydro	910	7	7	3.94	0
30. S40725	hypothetical protein - Caenor	856	7	7	3.94	0
31. YFBSB	phenylalanine--tRNA ligase (E	804	7	7	3.94	0
32. S30059	probable transport protein AL	745	7	7	3.94	0
33. A46159	ISGF-3 91 kda component=inter	739	7	7	3.94	0
34. S27830	glucose-6-phosphate 1-dehydro	736	7	7	3.94	0
35. S47044	mALDP protein - mouse	736	7	7	3.94	0
36. S07624	acylaminoacyl-peptidase (EC 3	732	7	7	3.94	0
37. A46265	photosystem 1 reaction center	730	7	7	3.94	0
38. A49931	peptidyl-dipeptidase A (EC 3.	681	7	7	3.94	0
39. S14870	dipeptidyl carboxypeptidase -	681	7	7	3.94	0
40. A42297	peptidyl dipeptidase (EC 3.4.	680	7	7	3.94	0
41. S43341	starch (bacterial glycogen) s	608	7	7	3.94	0
42. JX0225	cytochrome P450 CYP10 - great	545	7	7	3.94	0
43. S21961	APG protein - Arabidopsis tha	534	7	7	3.94	0
44. A32431	cytochrome-c oxidase (EC 1.9.	521	7	7	3.94	0
45. DNETU2	NADH dehydrogenase (ubiquinon	515	7	7	3.94	0

1. US-08-121-713B-30 (1-7)
   ACMSIT inositol-trisphosphate receptor - mouse

ENTRY	ACMSIT #type complete
TITLE	inositol-trisphosphate receptor - mouse
ALTERNATE_NAMES	inositol-1,4,5-triphosphate-binding protein P400; membrane-associated glycoprotein P400
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Nov-1994
ACCESSIONS	S04844; S06796
REFERENCE	S04844
#authors	Furuichi, T.; Yoshikawa, S.; Mikoshiba, K.
#journal	Nucleic Acids Res. (1989) 17:5385-5386
#title	Nucleotide sequence of cDNA encoding P400 protein in the mouse cerebellum.

```
    #cross-references MUID:89345101
    #accession     S04844
       ##molecule_type mRNA
       ##residues      1-2749 ##label FUR
       ##cross-references EMBL:X15373
       ##note          translation of nucleotide sequence not given
 REFERENCE         S06796
    #authors       Furuichi, T.; Yoshikawa, S.; Miyawaki, A.; Wada, K.; Maeda,
                     N.; Mikoshiba, K.
    #journal       Nature (1989) 342:32-38
    #title         Primary structure and functional expression of the inositol
                     1,4,5-trisphosphate-binding protein P(400).
    #cross-references MUID:90044039
    #accession     S06796
       ##molecule_type mRNA
       ##residues      1-2749 ##label FU2
       ##cross-references EMBL:X15373
       ##note          the nucleotide sequence is not given in this paper
 CLASSIFICATION    #superfamily inositol-trisphosphate receptor
 KEYWORDS          glycoprotein; phosphoprotein; receptor; transmembrane protein
 FEATURE
    890-907            #domain transmembrane #status predicted #label TM1\
    1960-1976          #domain transmembrane #status predicted #label TM2\
    2276-2294          #domain transmembrane #status predicted #label TM3\
    2308-2326          #domain transmembrane #status predicted #label TM4\
    2334-2350          #domain transmembrane #status predicted #label TM5\
    2352-2372          #domain transmembrane #status predicted #label TM6\
    2391-2407          #domain transmembrane #status predicted #label TM7\
    2440-2462          #domain transmembrane #status predicted #label TM8\
    2570-2589          #domain transmembrane #status predicted #label TM9\
    1588,1755          #binding_site phosphate (Ser) (covalent) #status
                         predicted\
    2475,2503,2622,
    2710               #binding_site carbohydrate (Asn) (covalent) #status
                         predicted
 SUMMARY           #length 2749  #molecular-weight 313195  #checksum 2330
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XWXXXLX
              |   |
    GTLEPHWSGLLWTAMLISLAIVIALPK
         2310 X    2320


2. US-08-121-713B-30 (1-7)
   A36579       inositol 1,4,5-triphosphate receptor 1 - rat

 ENTRY             A36579     #type complete
 TITLE             inositol 1,4,5-triphosphate receptor 1 - rat
 ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
 DATE              08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change
                     18-Jun-1993
 ACCESSIONS        A36579
 REFERENCE         A36579
    #authors       Mignery, G.A.; Newton, C.L.; Archer III, B.T.; Suedhof, T.C.
```



```
    #journal       J. Biol. Chem. (1990) 265:12679-12685
    #title         Structure and expression of the rat inositol 1,4,
                     5-trisphosphate receptor.
    #cross-references MUID:90324264
    #accession     A36579
       ##status        preliminary
       ##molecule_type mRNA
       ##residues      1-2749 ##label MIG
       ##cross-references GB:J05510
 CLASSIFICATION    #superfamily inositol-trisphosphate receptor
 SUMMARY           #length 2749  #molecular-weight 313134  #checksum 2229
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XWXXXLX
              |   |
    GTLEPHWSGLLWTAMLISLAIVIALPK
         2310 X    2320


3. US-08-121-713B-30 (1-7)
   B36579       inositol 1,4,5-triphosphate receptor 2 - rat

 ENTRY             B36579     #type complete
 TITLE             inositol 1,4,5-triphosphate receptor 2 - rat
 ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
 DATE              08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change
                     18-Jun-1993
 ACCESSIONS        B36579
 REFERENCE         A36579
    #authors       Mignery, G.A.; Newton, C.L.; Archer III, B.T.; Suedhof, T.C.
    #journal       J. Biol. Chem. (1990) 265:12679-12685
    #title         Structure and expression of the rat inositol 1,4,
                     5-trisphosphate receptor.
    #cross-references MUID:90324264
    #accession     B36579
       ##status        preliminary
       ##molecule_type mRNA
       ##residues      1-2734 ##label MIG
       ##cross-references GB:J05510
 CLASSIFICATION    #superfamily inositol-trisphosphate receptor
 SUMMARY           #length 2734  #molecular-weight 311368  #checksum 6817
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XWXXXLX
              |   |
    GTLEPHWSGLLWTAMLISLAIVIALPK
    2290      2300  X   2310


4. US-08-121-713B-30 (1-7)
```

```
   A40743       IP3 receptor, XIP3R - African clawed frog

 ENTRY            A40743     #type complete
 TITLE            IP3 receptor, XIP3R - African clawed frog
 ORGANISM         #formal_name Xenopus laevis #common_name African clawed frog
 DATE             03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change
                    18-Nov-1994
 ACCESSIONS       A40743
 REFERENCE        A40743
    #authors      Kume, S.; Muto, A.; Aruga, J.; Nakagawa, T.; Michikawa, T.;
                    Furuichi, T.; Nakade, S.; Okano, H.; Mikoshiba, K.
    #journal      Cell (1993) 73:555-570
    #title        The Xenopus IP3 receptor: structure, function, and
                    localization in oocytes and eggs.
    #cross-references MUID:93258819
    #contents     oocytes and eggs
    #accession    A40743
       ##status         preliminary
       ##molecule_type mRNA
       ##residues       1-2693 ##label KUM
       ##cross-references NCBIP:131713
       ##note           sequence extracted from NCBI backbone
       ##note           sequence not compared to nucleotide translation
 SUMMARY          #length 2693  #molecular-weight 306670  #checksum 918
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
    GTLDSRLSGLLWTAMLVSLAIVIVLPK
  2250      2260    X 2270


5. US-08-121-713B-30 (1-7)
   A46692       DNA polymerase epsilon catalytic subunit - human

 ENTRY            A46692     #type complete
 TITLE            DNA polymerase epsilon catalytic subunit - human
 ORGANISM         #formal_name Homo sapiens #common_name man
 DATE             21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
                    18-Nov-1994
 ACCESSIONS       A46692
 REFERENCE        A46692
    #authors      Kesti, T.; Frantti, H.; Syvaoja, J.E.
    #journal      J. Biol. Chem. (1993) 268:10238-10245
    #title        Molecular cloning of the cDNA for the catalytic subunit of
                    human DNA polymerase epsilon.
    #contents     HeLa cells
    #accession    A46692
       ##status         preliminary
       ##molecule_type nucleic acid; protein
       ##residues       1-2257 ##label KES
       ##cross-references NCBIN:131270; NCBIP:131271
       ##note           sequence inconsistent with the nucleotide translation
       ##note           sequence extracted from NCBI backbone
 SUMMARY          #length 2257  #molecular-weight 257967  #checksum 1781
```



```
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
    FHSLTISFSRCWEFLLWMDPSNYGGIK
         1880      1890


6. US-08-121-713B-30 (1-7)
   RRXPLC       RNA-directed RNA polymerase (EC 2.7.7.48) - lympho

 ENTRY            RRXPLC     #type complete
 TITLE            RNA-directed RNA polymerase (EC 2.7.7.48) - lymphocytic
                    choriomeningitis virus (strain Armstrong 53b)
 ORGANISM         #formal_name lymphocytic choriomeningitis virus
 DATE             31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change
                    17-Feb-1994
 ACCESSIONS       A30181
 REFERENCE        A30181
    #authors      Salvato, M.; Shimomaye, E.; Oldstone, M.B.A.
    #journal      Virology (1989) 169:377-384
    #title        The primary structure of the lymphocytic choriomeningitis
                    virus L gene encodes a putative RNA polymerase.
    #cross-references MUID:89204909
    #accession    A30181
       ##molecule_type genomic RNA
       ##residues       1-2210 ##label SAL
 GENETICS
    #map_position segment L
 CLASSIFICATION   #superfamily arenavirus RNA-directed RNA polymerase
 KEYWORDS         nucleotidyltransferase
 SUMMARY          #length 2210  #molecular-weight 254529  #checksum 7158
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
    NPKAFKSLKDLWDYMLNYTKGVLEFSI
  1930      1940    X 1950


7. US-08-121-713B-30 (1-7)
   BWASBE       bimE protein - Emericella nidulans

 ENTRY            BWASBE     #type complete
 TITLE            bimE protein - Emericella nidulans
 ORGANISM         #formal_name Emericella nidulans, Aspergillus nidulans
 DATE             31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
                    09-Sep-1994
 ACCESSIONS       A37879
 REFERENCE        A37879
```

```
    #authors      Engle, D.B.; Osmani, S.A.; Osmani, A.H.; Rosborough, S.;
                    Xiang, X.; Morris, N.R.
    #journal      J. Biol. Chem. (1990) 265:16132-16137
    #title        A negative regulator of mitosis in Aspergillus is a putative
                    membrane-spanning protein.
    #cross-references MUID:90375468
    #accession    A37879
       ##molecule_type mRNA
       ##residues      1-2073 ##label ENG
       ##cross-references GB:J05607
       ##note          in addition to three predicted transmembrane domains,
                        there are several potential N-glycosylation sites,
                        five possible sites for phosphorylation by
                        cAMP-dependent protein kinase and one for casein
                        kinase, and one sequence that resembles a nuclear
                        localization signal
 COMMENT    This protein is part of a regulatory pathway that includes the nimA
              protein kinase. It is required to prevent premature entry into
              mitosis. Mutations to this protein both cause cells to enter
              mitosis and prevent them from leaving mitosis.
 GENETICS
    #gene         bimE
 CLASSIFICATION   #superfamily bimE protein
 KEYWORDS         cell cycle control; mitosis; transmembrane protein
 FEATURE
    1623-1643          #domain transmembrane #status predicted #label TM1\
    1685-1703          #domain transmembrane #status predicted #label TM2\
    1746-1764          #domain transmembrane #status predicted #label TM3
 SUMMARY          #length 2073  #molecular-weight 229177  #checksum 7408
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XWXXXLX
              |   |
    SSSGSYVDTESWESMLEQESGSAGVVA
        850   X   860       870


8. US-08-121-713B-30 (1-7)
   A40262       210K nuclear DNA-binding protein CCG1 - human

 ENTRY            A40262     #type complete
 TITLE            210K nuclear DNA-binding protein CCG1 - human
 ORGANISM         #formal_name Homo sapiens #common_name man
 DATE             17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change
                    02-Dec-1994
 ACCESSIONS       A40262; S03005; S00830
 REFERENCE        A40262
    #authors      Sekiguchi, T.; Nohiro, Y.; Nakamura, Y.; Hisamoto, N.;
                    Nishimoto, T.
    #journal      Mol. Cell. Biol. (1991) 11:3317-3325
    #title        The human CCG1 gene, essential for progression of the G-1
                    phase, encodes a 210-kilodalton nuclear DNA-binding
                    protein.
    #cross-references MUID:91246200
    #accession    A40262
```



```
       ##molecule_type mRNA
       ##residues      1-1872 ##label SEK
       ##cross-references GB:D90359
       ##note          nucleotide sequence not complete in this paper
 REFERENCE        S03005
    #authors      Sekiguchi, T.; Miyata, T.; Nishimoto, T.
    #submission   submitted to the EMBL Data Library, February 1988
    #accession    S03005
       ##molecule_type mRNA
       ##residues      'MYR',60-1583,'DN',1586,'CSSKANDIVCLIQYCSSQI',1606,
                        'ELRF' ##label SE2
       ##cross-references EMBL:X07024
       ##note          this sequence has been revised in reference A40262
 REFERENCE        S00830
    #authors      Sekiguchi, T.; Miyata, T.; Nishimoto, T.
    #journal      EMBO J. (1988) 7:1683-1687
    #title        Molecular cloning of the cDNA of human X chromosomal gene
                   (CCG1) which complements the temperature-sensitive G1
                   mutants, tsBN462 and ts13, of the BHK cell line.
    #cross-references MUID:89005056
    #accession    S00830
       ##molecule_type DNA
       ##residues      1351-1358;1365-1583,'DN',1586,'CSSKANDIVCLIQYCSSQI',
                        1606,'ELRF' ##label SE3
       ##cross-references EMBL:X07024
 GENETICS
    #gene         GDB:CCG1
    #map_position Xq13.1
 CLASSIFICATION   #superfamily bromodomain homology
 FEATURE
    1405-1460          #domain bromodomain homology #label BRO1\
    1528-1583          #domain bromodomain homology #label BRO2
 SUMMARY          #length 1872  #molecular-weight 212675  #checksum 1180
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XWXXXLX
              |   |
    VAEWRYGPARLWYDMLGVPEDGSGFDY
    340       350   X   360


9. US-08-121-713B-30 (1-7)
   S23810       collagen alpha 1(XVI) chain precursor - human

 ENTRY            S23810     #type complete
 TITLE            collagen alpha 1(XVI) chain precursor - human
 ORGANISM         #formal_name Homo sapiens #common_name man
 DATE             28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change
                    28-Oct-1994
 ACCESSIONS       S23810; S08012
 REFERENCE        S23810
    #authors      Pan, T.C.; Zhang, R.Z.; Mattei, M.G.; Timpl, R.; Chu, M.L.
    #journal      Proc. Natl. Acad. Sci. U.S.A. (1992) 89:6565-6569
    #title        Cloning and chromosomal location of human alphal(XVI)
                    collagen.
```

```
    #cross-references MUID:92335339
    #accession     S23810
       ##molecule_type mRNA
       ##residues      1-1603 ##label PAN
       ##cross-references EMBL:M92642
 REFERENCE         S08012
    #authors       Kimura, S.
    #submission    submitted to the EMBL Data Library, April 1989
    #description   Partial nucleotide and amino acid sequence of a collagen-like
                    protein from human placenta.
    #accession     S08012
       ##molecule_type mRNA
       ##residues      403-419,'GR',421-536,'P',538-846,'VM' ##label KIM
       ##cross-references EMBL:X14963
 CLASSIFICATION    #superfamily collagen alpha chain
 KEYWORDS          cell binding; extracellular matrix; glycoprotein;
                     hydroxylysine; hydroxyproline
 FEATURE
    1-21               #domain signal sequence #status predicted #label SIG\
    22-1603            #product collagen alpha 1(XVI) chain #status predicted
                         #label MAT\
    334-360            #domain collagenous COL10 #label CO10\
    375-505            #domain collagenous COL9 #label COL9\
    521-554            #domain collagenous COL8 #label COL8\
    539-541            #region cell attachment (R-G-D) motif\
    572-630            #domain collagenous COL7 #label COL7\
    652-722            #domain collagenous COL6 #label COL6\
    738-875            #domain collagenous COL5 #label COL5\
    887-938            #domain collagenous COL4 #label COL4\
    973-987            #domain collagenous COL3 #label COL3\
    1005-1007          #region cell attachment (R-G-D) motif\
    1011-1432          #domain collagenous COL2 #label COL2\
    1226-1228          #region cell attachment (R-G-D) motif\
    1472-1577          #domain collagenous COL1 #label COL1\
    47,327             #binding_site carbohydrate (Asn) (covalent) #status
                         predicted
 SUMMARY           #length 1603  #molecular-weight 157693  #checksum 1714
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

           X     X
           XWXXXLX
            |   |
    MWVSWAPGLWLLGLWATFGHGANTG
           10    X   20


10. US-08-121-713B-30 (1-7)
    A44604        polycystic kidney disease protein 1 - human (fragm

 ENTRY             A44604      #type fragment
 TITLE             polycystic kidney disease protein 1 - human (fragment)
 ORGANISM          #formal_name Homo sapiens #common_name man
 DATE              17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change
                     17-Jul-1994
 ACCESSIONS        A44604
 REFERENCE         A44604
```



```
    #authors       Ward, C.J.; Peral, B.; Hughes, J.; Thomas, S.; Gamble, V.;
                     MacCarthy, A.B.; Sloane-Stanley, J.; Buckle, V.J.; Kearney,
                     L.; Higgs, D.R.; Ratcliffe, P.J.; Harris, P.C.; Roelfsema,
                     J.H.; Spruit, L.; Saris, J.J.; Dauwerse, H.G.; Peters,
                     D.J.M.; Breuning, M.H.; Nellist, M.; Brook-Carter, P.T.;
                     Maheshwar, M.M.; Cordeiro, I.; Santos, H.; Cabral, P.;
                     Sampson, J.R.; Janssen, B.; Hesseling-Janssen, A.L.W.; van
                     den Ouweland, A.M.W.; Eussen, B.; Verhoef, S.; Lindhout,
                     D.; Halley, D.J.J.
    #journal       Cell (1994) 77:881-894
    #title         The polycystic kidney disease 1 gene encodes a 14 kb
                     transcript and lies within a duplicated region on
                     chromosome 16.
    #accession     A44604
       ##status        preliminary
       ##molecule_type mRNA
       ##residues      1-1594 ##label WAR
       ##cross-references GB:L33243
 SUMMARY           #length 1594  #checksum 7489
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =     28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

           X     X
           XWXXXLX
            |   |
    WHLSPLLCVGLWALRLWGALRLGAVIL
          1300      1310


11. US-08-121-713B-30 (1-7)
    I48216        neurexin III-alpha membrane-bound type 1 precursor

 ENTRY             I48216      #type complete
 TITLE             neurexin III-alpha membrane-bound type 1 precursor - rat
 ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
 DATE              26-May-1994 #sequence_revision 26-May-1994 #text_change
                     26-May-1994
 ACCESSIONS        I48216
 REFERENCE         A48216
    #authors       Ushkaryov, Y.A.; Suedhof, T.C.
    #journal       Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6410-6414
    #title         Neurexin IIIalpha: extensive alternative splicing generates
                     membrane-bound and soluble forms.
    #accession     I48216
       ##status        preliminary
       ##molecule_type mRNA
       ##residues      1-1578 ##label USH
       ##cross-references GB:L14851
 GENETICS
    #introns       1372/1
 KEYWORDS          alternative splicing; brain; cell surface component;
                     receptor; repeat; transmembrane protein
 FEATURE
    1-27               #domain signal sequence #status predicted #label SIG
 SUMMARY           #length 1578  #molecular-weight 174212  #checksum 5082
 SEQUENCE
```

```
Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
               |   |
    NRAGLILPTELWTAMLNYGYVGCIRDL
          600 X     610
```

12. US-08-121-713B-30 (1-7)
    A48218 neurexin III-alpha membrane-bound type 2 precursor

```
 ENTRY            A48218     #type complete
 TITLE            neurexin III-alpha membrane-bound type 2 precursor - rat
 ORGANISM         #formal_name Rattus norvegicus #common_name Norway rat
 DATE             26-May-1994 #sequence_revision 26-May-1994 #text_change
                    26-May-1994
 ACCESSIONS       A48218
 REFERENCE        A48216
    #authors      Ushkaryov, Y.A.; Suedhof, T.C.
    #journal      Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6410-6414
    #title        Neurexin IIIalpha: extensive alternative splicing generates
                    membrane-bound and soluble forms.
    #accession    A48218
       ##status        preliminary
       ##molecule_type mRNA
       ##residues      1-1575 ##label USH
       ##cross-references GB:L14851
 GENETICS
    #introns      1369/1
 KEYWORDS         alternative splicing; brain; cell surface component;
                    receptor; repeat; transmembrane protein
 FEATURE
    1-27              #domain signal sequence #status predicted #label SIG
 SUMMARY          #length 1575  #molecular-weight 173911  #checksum 6342
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
               |   |
    NRAGLILPTELWTAMLNYGYVGCIRDL
          600 X     610
```

13. US-08-121-713B-30 (1-7)
    B48218 neurexin III-alpha membrane-bound type 3 precursor

```
 ENTRY            B48218     #type complete
 TITLE            neurexin III-alpha membrane-bound type 3 precursor - rat
 ORGANISM         #formal_name Rattus norvegicus #common_name Norway rat
 DATE             26-May-1994 #sequence_revision 26-May-1994 #text_change
                    26-May-1994
 ACCESSIONS       B48218
 REFERENCE        A48216
```



```
    #authors      Ushkaryov, Y.A.; Suedhof, T.C.
    #journal      Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6410-6414
    #title        Neurexin IIIalpha: extensive alternative splicing generates
                    membrane-bound and soluble forms.
    #accession    B48218
       ##status        preliminary
       ##molecule_type mRNA
       ##residues      1-1471 ##label USH
       ##cross-references GB:L14851
 GENETICS
    #introns      1372/1
 KEYWORDS         alternative splicing; brain; cell surface component;
                    receptor; repeat; transmembrane protein
 FEATURE
    1-27              #domain signal sequence #status predicted #label SIG
 SUMMARY          #length 1471  #molecular-weight 162434  #checksum 183
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
               |   |
    NRAGLILPTELWTAMLNYGYVGCIRDL
          600 X     610
```

14. US-08-121-713B-30 (1-7)
    C48218 neurexin III-alpha membrane-bound type 4 precursor

```
 ENTRY            C48218     #type complete
 TITLE            neurexin III-alpha membrane-bound type 4 precursor - rat
 ORGANISM         #formal_name Rattus norvegicus #common_name Norway rat
 DATE             26-May-1994 #sequence_revision 26-May-1994 #text_change
                    26-May-1994
 ACCESSIONS       C48218
 REFERENCE        A48216
    #authors      Ushkaryov, Y.A.; Suedhof, T.C.
    #journal      Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6410-6414
    #title        Neurexin IIIalpha: extensive alternative splicing generates
                    membrane-bound and soluble forms.
    #accession    C48218
       ##status        preliminary
       ##molecule_type mRNA
       ##residues      1-1468 ##label USH
       ##cross-references GB:L14851
 GENETICS
    #introns      1369/1
 KEYWORDS         alternative splicing; brain; cell surface component;
                    receptor; repeat; transmembrane protein
 FEATURE
    1-27              #domain signal sequence #status predicted #label SIG
 SUMMARY          #length 1468  #molecular-weight 162134  #checksum 408
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0
```

```
              X     X
              XWXXXLX
               |   |
    NRAGLILPTELWTAMLNYGYVGCIRDL
          600 X     610
```

15. US-08-121-713B-30 (1-7)
    A45665 adult-specific brush border esterase/phospholipase

```
 ENTRY            A45665     #type complete
 TITLE            adult-specific brush border esterase/phospholipase (EC
                    3.-.-.-) precursor - rabbit
 ORGANISM         #formal_name Oryctolagus cuniculus #common_name domestic
                    rabbit
 DATE             03-May-1994 #sequence_revision 03-May-1994 #text_change
                    03-May-1994
 ACCESSIONS       A45665
 REFERENCE        A45665
    #authors      Boll, W.; Schmid-Chanda, T.; Semenza, G.; Mantei, N.
    #journal      J. Biol. Chem. (1993) 268:12901-12911
    #title        Messenger RNAs expressed in intestine of adult but not baby
                    rabbits. Isolation of cognate cDNAs and characterization of
                    a novel brush border protein with esterase and
                    phospholipase activity.
    #accession    A45665
       ##status        preliminary
       ##molecule_type mRNA
       ##residues      1-1458 ##label BOL
       ##cross-references GB:Z12841
 SUMMARY          #length 1458  #molecular-weight 161343  #checksum 2780
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.94
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

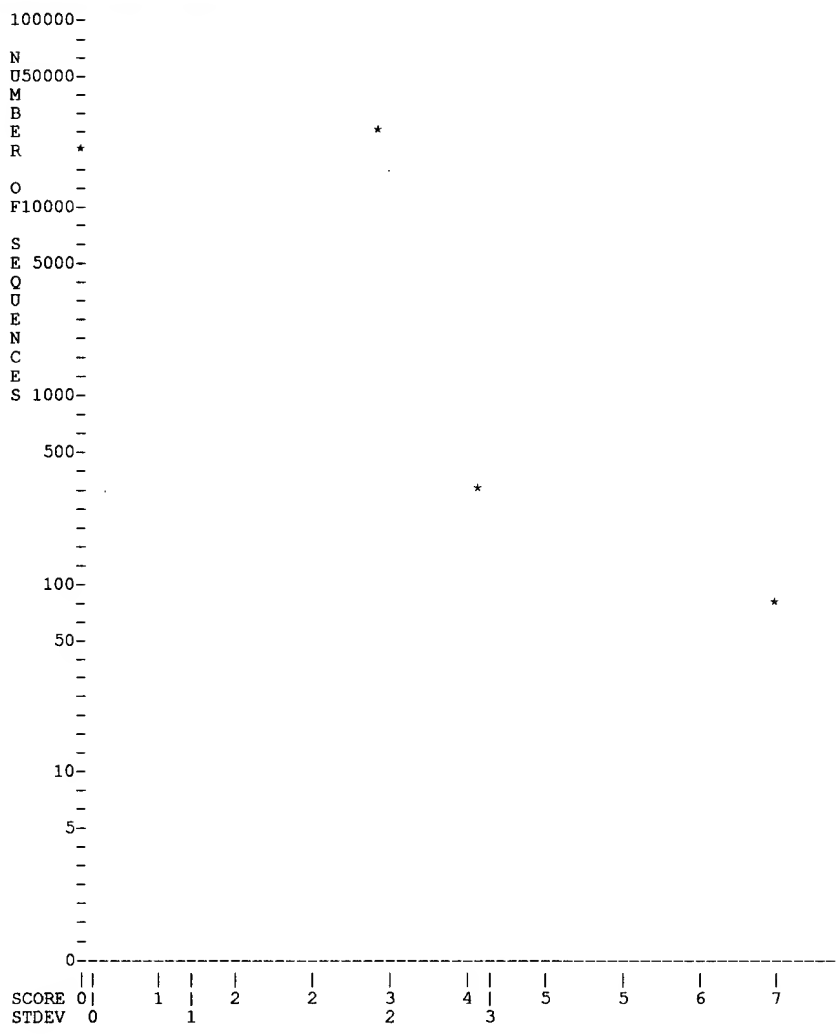
              X     X
              XWXXXLX
               |   |
    SKAHAHAASALWNNMLEPVGQKTTHND
    660       670   X   680
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq30spt.res made by  on Fri 19 May 95 9:00:53-PDT.


Query sequence being compared:US-08-121-713B-30 (1-7)
Number of sequences searched:                43470
Number of scores above cutoff:                4001

      Results of the initial comparison of US-08-121-713B-30 (1-7) with:
   Data bank : Swiss-Prot 31, all entries
```

PARAMETERS

```
Similarity matrix      Unitary     K-tuple                    2
Mismatch penalty             1     Joining penalty           20
```

Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	4	1.50

Times:	CPU	Total Elapsed
	00:00:43.06	00:00:44.00

Number of residues: 15335248
Number of sequences searched: 43470
Number of scores above cutoff: 4001

Cut-off raised to 1.
Cut-off raised to 3.
Cut-off raised to 4.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

71 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. IP3R_MOUSE	INOSITOL 1,4,5-TRISPHOSPHATE-	2749	7	7	3.99	0
2. IP3R_RAT	INOSITOL 1,4,5-TRISPHOSPHATE-	2749	7	7	3.99	0
3. DPOE_HUMAN	DNA POLYMERASE EPSILON, CATAL	2257	7	7	3.99	0
4. RRPO_LYCVA	RNA POLYMERASE (EC 2.7.7.48).	2210	7	7	3.99	0
5. BIME_EMENI	NEGATIVE REGULATOR OF MITOSIS	2073	7	7	3.99	0
6. CCG1_HUMAN	TRANSCRIPTION INITIATION FACT	1872	7	7	3.99	0
7. CA1F_HUMAN	COLLAGEN ALPHA 1(XVI) CHAIN P	1603	7	7	3.99	0
8. PHLX_RABIT	PHOSPHOLIPASE ADRAB-B PRECURS	1458	7	7	3.99	0
9. EBA1_PLAFC	ERYTHROCYTE-BINDING ANTIGEN E	1426	7	7	3.99	0
10. KRE5_YEAST	KILLER TOXIN-RESISTANCE PROTE	1365	7	7	3.99	0
11. YB95_YEAST	HYPOTHETICAL 132.7 KD HELICAS	1143	7	7	3.99	0
12. SP23_YEAST	SPT23 PROTEIN.	1082	7	7	3.99	0
13. PPS3_BACSU	PEPTIDE SYNTHETASE 3 (FRAGMEN	859	7	7	3.99	0
14. YLH5_CAEEL	PUTATIVE ABC TRANSPORTER C48B	856	7	7	3.99	0
15. SYFB_BACSU	PHENYLALANYL-TRNA SYNTHETASE	804	7	7	3.99	0
16. APRF_HUMAN	ACUTE-PHASE RESPONSE FACTOR.	770	7	7	3.99	0
17. ALD_HUMAN	ADRENOLEUKODYSTROPHY PROTEIN	745	7	7	3.99	0
18. ACPH_RAT	ACYLAMINO-ACID-RELEASING ENZY	732	7	7	3.99	0
19. DCP_ECOLI	DIPEPTIDYL CARBOXYPEPTIDASE (	680	7	7	3.99	0
20. DCP_SALTY	DIPEPTIDYL CARBOXYPEPTIDASE (	680	7	7	3.99	0
21. APG_ARATH	ANTER-SPECIFIC PROLINE-RICH P	534	7	7	3.99	0
22. YJCC_ECOLI	HYPOTHETICAL 60.8 KD PROTEIN	528	7	7	3.99	0
23. COX1_APIME	CYTOCHROME C OXIDASE POLYPEPT	521	7	7	3.99	0
24. NU2M_BETVU	NADH-UBIQUINONE OXIDOREDUCTAS	515	7	7	3.99	0
25. NUOM_ECOLI	NADH DEHYDROGENASE I CHAIN M	509	7	7	3.99	0
26. PCD6_MOUSE	PROTEIN PCD-6 (FRAGMENT).	500	7	7	3.99	0
27. YPUM_RHOCA	HYPOTHETICAL 50.4 KD PROTEIN	477	7	7	3.99	0

28. PRI1_MOUSE	DNA PRIMASE 49 KD SUBUNIT (EC	417	7	7	3.99	0
29. CVAA_ECOLI	COLICIN V SECRETION PROTEIN C	413	7	7	3.99	0
30. YBL2_SFV3L	BEL-2 PROTEIN.	388	7	7	3.99	0
31. YGIC_ECOLI	HYPOTHETICAL 45.0 KD PROTEIN	386	7	7	3.99	0
32. CAR2_DICDI	CYCLIC AMP RECEPTOR 2.	375	7	7	3.99	0
33. YEJP_ECOLI	HYPOTHETICAL 39.1 KD PROTEIN	350	7	7	3.99	0
34. YIFC_ECOLI	HYPOTHETICAL 39.6 KD PROTEIN	349	7	7	3.99	0
35. SUR4_YEAST	SUR4 PROTEIN (SRE1 PROTEIN).	345	7	7	3.99	0
36. YIBD_ECOLI	HYPOTHETICAL 40.5 KD PROTEIN	344	7	7	3.99	0
37. TRAU_ECOLI	TRAU PROTEIN PRECURSOR.	330	7	7	3.99	0
38. UPAR_MOUSE	UROKINASE PLASMINOGEN ACTIVAT	327	7	7	3.99	0
39. SYPH_HUMAN	SYNAPTOPHYSIN (MAJOR SYNAPTIC	313	7	7	3.99	0
40. SYPH_BOVIN	SYNAPTOPHYSIN (MAJOR SYNAPTIC	307	7	7	3.99	0
41. SYPH_RAT	SYNAPTOPHYSIN (MAJOR SYNAPTIC	307	7	7	3.99	0
42. YHBJ_ECOLI	HYPOTHETICAL 32.5 KD PROTEIN	284	7	7	3.99	0
43. YFI1_STRPA	HYPOTHETICAL 29.9 KD PROTEIN	280	7	7	3.99	0
44. YPU2_RHOCA	HYPOTHETICAL 30.4 KD PROTEIN	274	7	7	3.99	0
45. NODJ_RHILT	NODULATION PROTEIN J.	262	7	7	3.99	0

1. US-08-121-713B-30 (1-7)
IP3R_MOUSE INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE

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ID   IP3R_MOUSE      STANDARD;      PRT;  2749 AA.
AC   P11881;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 1 RECEPTOR
DE   (INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN P(400)) (TYPE 1 INSP3
DE   RECEPTOR).
GN   INSP3R.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CERBELLA PURKINJE NEURONS;
RM   90044039
RA   FURUICHI T., YOSHIKAWA S., MIYAWAKI A., WADA K., MAEDA N.,
RA   MIKOSHIBA K.;
RL   NATURE 342:32-38(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR; TISSUE=CEREBELLUM;
RM   89345101
RA   FURUICHI T., YOSHIKAWA S., MIKOSHIBA K.;
RL   NUCLEIC ACIDS RES. 17:5385-5386(1989).
RN   [3]
RP   ALTERNATIVE SPLICING.
RM   91296797
RA   NAKAGAWA T., OKANO H., FURUICHI T., ARUGA J., MIKOSHIBA K.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 88:6244-6248(1991).
CC   -!- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND
CC       MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
CC       THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL
CC       EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-
CC       BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE
CC       PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
CC   -!- SUBUNIT: HOMOTETRAMER.
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CC   -!- PTM: PHOSPHORYLATED BY CYCLIC-AMP KINASE. PHOSPHORYLATION PREVENTS
CC       THE LIGAND-INDUCED OPENING OF THE CALCIUM CHANNELS.
CC   -!- CALCIUM APPEARS TO INHIBIT LIGAND BINDING TO THE RECEPTOR, MOST
CC       PROBABLY BY INTERACTING WITH A DISTINCT CALCIUM-BINDING PROTEIN
CC       WHICH THEN INHIBITS THE RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
CC       RETICULUM.
CC   -!- ALTERNATIVE PRODUCTS: ADDITIONAL SUBTYPES OF INSP3R ARISE BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE.
CC   -!- SIMILARITY: TO RYANODINE RECEPTOR.
DR   EMBL; X15373; MMP400.
DR   PIR; S04844; ACMSIT.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION;
KW   ENDOPLASMIC RETICULUM; IONIC CHANNEL; ION TRANSPORT; CALCIUM CHANNEL;
KW   ALTERNATIVE SPLICING.
FT   DOMAIN        1   2273       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   2274   2294       M1 (POTENTIAL).
FT   TRANSMEM   2308   2326       M2 (POTENTIAL).
FT   TRANSMEM   2334   2356       M3 (POTENTIAL).
FT   TRANSMEM   2365   2387       M4 (POTENTIAL).
FT   TRANSMEM   2391   2407       M5 (POTENTIAL).
FT   TRANSMEM   2440   2462       M6 (POTENTIAL).
FT   TRANSMEM   2530   2549       M7 (POTENTIAL).
FT   TRANSMEM   2570   2589       M8 (POTENTIAL).
FT   DOMAIN     2590   2749       CYTOPLASMIC (POTENTIAL).
FT   VARSPLIC    318    332       MISSING (IN INSP3R SI-).
FT   VARSPLIC   1692   1731       MISSING (IN INSP3R SIIABC-).
FT   VARSPLIC   1715   1715       MISSING (IN INSP3R SIIB-).
FT   VARSPLIC   1715   1731       MISSING (IN INSP3R SIIBC-).
FT   MOD_RES    1588   1588       PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   MOD_RES    1755   1755       PHOSPHORYLATION (BY CAPK) (POTENTIAL).
SQ   SEQUENCE   2749 AA;  313193 MW;  22837568 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.99
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
    GTLEPHWSGLLWTAMLISLAIVIALPK
        2310 X    2320


2. US-08-121-713B-30 (1-7)
   IP3R_RAT     INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE

ID   IP3R_RAT       STANDARD;      PRT;  2749 AA.
AC   P29994;
DT   01-APR-1993 (REL. 25, CREATED)
DT   01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 1 RECEPTOR
DE   (INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN P(400)) (TYPE 1 INSP3
DE   RECEPTOR).
GN   INSP3R.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
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RP   SEQUENCE FROM N.A.
RM   90324264
RA   MIGNERY G.A., NEWTON C.L., ARCHER B.T. III, SUEDHOF T.C.;
RL   J. BIOL. CHEM. 265:12679-12685(1990).
CC   -!- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND
CC       MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
CC       THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL
CC       EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-
CC       BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE
CC       PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.
CC   -!- SUBUNIT: HOMOTETRAMER.
CC   -!- PTM: PHOSPHORYLATED BY CYCLIC-AMP KINASE. PHOSPHORYLATION PREVENTS
CC       THE LIGAND-INDUCED OPENING OF THE CALCIUM CHANNELS.
CC   -!- CALCIUM APPEARS TO INHIBIT LIGAND BINDING TO THE RECEPTOR, MOST
CC       PROBABLY BY INTERACTING WITH A DISTINCT CALCIUM-BINDING PROTEIN
CC       WHICH THEN INHIBITS THE RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
CC       RETICULUM.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED.
CC   -!- SIMILARITY: TO RYANODINE RECEPTOR.
DR   EMBL; J05510; RRI145TR.
DR   PIR; A36579; A36579.
KW   RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION;
KW   ENDOPLASMIC RETICULUM; IONIC CHANNEL; ION TRANSPORT; CALCIUM CHANNEL;
KW   ALTERNATIVE SPLICING.
FT   DOMAIN        1   2273       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   2274   2294       M1 (POTENTIAL).
FT   TRANSMEM   2308   2326       M2 (POTENTIAL).
FT   TRANSMEM   2334   2356       M3 (POTENTIAL).
FT   TRANSMEM   2365   2387       M4 (POTENTIAL).
FT   TRANSMEM   2391   2407       M5 (POTENTIAL).
FT   TRANSMEM   2440   2462       M6 (POTENTIAL).
FT   TRANSMEM   2530   2549       M7 (POTENTIAL).
FT   TRANSMEM   2570   2589       M8 (POTENTIAL).
FT   DOMAIN     2590   2749       CYTOPLASMIC (POTENTIAL).
FT   MOD_RES    1589   1589       PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   MOD_RES    1755   1755       PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   VARSPLIC    322    336       MISSING (IN VARIANT).
FT   VARIANT    1372   1372       MISSING (IN ALL, BUT P17 CLONES).
SQ   SEQUENCE   2749 AA;  313132 MW;  22831603 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.99
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
    GTLEPHWSGLLWTAMLISLAIVIALPK
        2310 X    2320


3. US-08-121-713B-30 (1-7)
   DPOE_HUMAN   DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A (EC 2.

ID   DPOE_HUMAN     STANDARD;      PRT;  2257 AA.
AC   Q07864;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
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DE   DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A (EC 2.7.7.7) (DNA
DE   POLYMERASE II SUBUNIT A).
GN   POLE.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 48-51; 874-884 AND 1336-1342.
RM   93252906
RA   KESTI T., FRANTTI H., SYVAOJA J.E.;
RL   J. BIOL. CHEM. 268:10238-10245(1993).
CC   -!- FUNCTION: PARTICIPATES IN DNA REPAIR AND IN CHROMOSOMAL DNA
CC       REPLICATION.
CC   -!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
CC       N PYROPHOSPHATE + DNA(N).
CC   -!- SUBUNIT: CONSISTS OF TWO SUBUNITS (258 KD AND 55 KD).
CC   -!- DOMAIN: THE DNA POLYMERASE ACTIVITY DOMAIN RESIDES IN THE
CC       N-TERMINAL HALF OF THE PROTEIN, WHILE THE C-TERMINUS IS NECESSARY
CC       FOR COMPLEXING SUBUNITS B AND C. THE C-TERMINUS MAY ALSO REGULATE
CC       THE CATALYTIC ACTIVITIES OF THE ENZYME.
CC   -!- IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES: ALPHA, BETA, GAMMA,
CC       DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR DIFFERENT REACTIONS
CC       OF DNA SYNTHESIS.
CC   -!- SIMILARITY: BELONGS TO FAMILY B OF DNA POLYMERASES. HIGH
CC       SIMILARITY WITH YEAST DNA POLYMERASE II.
DR   EMBL; L09561; HSDNPOLCS.
DR   PIR; A46692; A46692.
DR   MIM; 174762; 11TH EDITION.
KW   DNA-DIRECTED DNA POLYMERASE; DNA REPLICATION; DNA REPAIR; DNA-BINDING;
KW   ZINC-FINGER.
FT   ZN_FING    2129   2209       POTENTIAL.
SQ   SEQUENCE   2257 AA;  257967 MW;  19650612 CN;
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Initial Score	=	7	Optimized Score	=	7	Significance =	3.99
Residue Identity	=	28%	Matches	=	2	Mismatches =	5
Gaps	=	0	Conservative Substitutions			=	0

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            X     X
            XWXXXLX
             |   |
   FHSLTISFSRCWEFLLWMDPSNYGGIK
        1880      1890
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4. US-08-121-713B-30 (1-7)
   RRPO_LYCVA RNA POLYMERASE (EC 2.7.7.48).

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ID   RRPO_LYCVA     STANDARD;      PRT;  2210 AA.
AC   P14240;
DT   01-JAN-1990 (REL. 13, CREATED)
DT   01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT   01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)
DE   RNA POLYMERASE (EC 2.7.7.48).
GN   L.
OS   LYMPHOCYTIC CHORIOMENINGITIS VIRUS (STRAIN ARMSTRONG).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; ARENAVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   89204909
RA   SALVATO M.S., SHIMOMAYE E.M., OLDSTONE M.B.A.;
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RL   VIROLOGY 169:377-384(1989).
RN   [2]
RP   SEQUENCE OF 161-387; 424-619 AND 1646-1906 FROM N.A.
RM   88072084
RA   SINGH M.K., FULLER-PACE F.V., BUCHMEIER M.J., SOUTHERN P.J.;
RL   VIROLOGY 161:448-456(1987).
DR   EMBL; J04331; LCVLPY.
DR   EMBL; M18381; LCVLA.
DR   EMBL; M18382; LCVLB.
DR   EMBL; M18383; LCVLC.
DR   PIR; A30181; RRXPLC.
KW   RNA-DIRECTED RNA POLYMERASE.
FT   CONFLICT    164    164       L -> Y (IN REF. 2).
FT   CONFLICT    354    354       Q -> R (IN REF. 2).
FT   CONFLICT    361    361       K -> E (IN REF. 2).
FT   CONFLICT    382    382       H -> D (IN REF. 2).
FT   CONFLICT    552    552       C -> S (IN REF. 2).
FT   CONFLICT   1727   1727       R -> L (IN REF. 2).
SQ   SEQUENCE   2210 AA;  254529 MW;  20447775 CN;
```

Initial Score	=	7	Optimized Score	=	7	Significance =	3.99
Residue Identity	=	28%	Matches	=	2	Mismatches =	5
Gaps	=	0	Conservative Substitutions			=	0

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            X     X
            XWXXXLX
             |   |
   NPKAFKSLKDLWDYMLNYTKGVLEFSI
 1930      1940    X 1950
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5. US-08-121-713B-30 (1-7)
   BIME_EMENI NEGATIVE REGULATOR OF MITOSIS.

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ID   BIME_EMENI     STANDARD;      PRT;  2073 AA.
AC   P24686;
DT   01-MAR-1992 (REL. 21, CREATED)
DT   01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT   01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE   NEGATIVE REGULATOR OF MITOSIS.
GN   BIME.
OS   EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; PLECTOMYCETES; EUROTIALES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   90375468
RA   ENGLE D.B., OSMANI S.A., OSMANI A.H., ROSBOROUGH S., XIANG X.,
RA   MORRIS N.R.;
RL   J. BIOL. CHEM. 265:16132-16137(1990).
CC   -!- FUNCTION: NEGATIVE REGULATOR OF MITOSIS IN E.NIDULANS. THIS
CC       PROTEIN IS PART OF A REGULATORY PATHWAY THAT INCLUDES THE NIMA
CC       PROTEIN KINASE. IT IS REQUIRED TO PREVENT PREMATURE ENTRY INTO
CC       MITOSIS. MUTATIONS TO THIS PROTEIN BOTH CAUSE CELLS TO ENTER
CC       MITOSIS AND PREVENT THEM FROM LEAVING MITOSIS.
DR   EMBL; M59705; ANBIME.
DR   PIR; A37879; BWASBE.
KW   TRANSMEMBRANE; MITOSIS.
FT   DOMAIN      342    353       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   TRANSMEM   1623   1643       POTENTIAL.
FT   TRANSMEM   1685   1703       POTENTIAL.
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FT   TRANSMEM   1746   1764       POTENTIAL.
SQ   SEQUENCE   2073 AA;  229178 MW;  19117395 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.99
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            XWXXXLX
              |   |
   SSSGSYVDTESWESMLEQESGSAGVVA
       850   X   860       870
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6. US-08-121-713B-30 (1-7)
   CCG1_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 250 KD SUBUN

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ID   CCG1_HUMAN     STANDARD;      PRT;  1872 AA.
AC   P21675;
DT   01-MAY-1991 (REL. 18, CREATED)
DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT   01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE   TRANSCRIPTION INITIATION FACTOR TFIID 250 KD SUBUNIT (TBP-ASSOCIATED
DE   FACTOR 250 KD) (P250) (TAFII-250) (CELL CYCLE GENE 1 PROTEIN).
GN   CCG1.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LARYNGEAL CARCINOMA;
RM   91246200
RA   SEKIGUCHI T., NOHIRO Y., NAKAMURA Y., HISAMOTO N., NISHIMOTO T.;
RL   MOL. CELL. BIOL. 11:3317-3325(1991).
RN   [2]
RP   PRELIMINARY SEQUENCE FROM N.A.
RM   89005056
RA   SEKIGUCHI T., MIYATA T., NISHIMOTO T.;
RL   EMBO J. 7:1683-1687(1988).
RN   [3]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RM   93196704
RA   RUPPERT S., WANG E.H., TJIAN R.;
RL   NATURE 362:175-179(1993).
RN   [4]
RP   CHARACTERIZATION.
RM   93196705
RA   HISATAKE K., HASEGAWA S., TAKADA R., NAKATANI Y., HORIKOSHI M.,
RA   ROEDER R.G.;
RL   NATURE 362:179-181(1993).
CC   -!- FUNCTION: MAY PLAY AN ESSENTIAL ROLE IN TFIID ASSEMBLY BY
CC       INTERACTING WITH BOTH TBP AND OTHER TAF, AS WELL AS SERVING TO
CC       LINK THE CONTROL OF TRANSCRIPTION TO THE CELL CYCLE. ESSENTIAL
CC       FOR PROGRESSION OF THE G1 PHASE OF THE CELL CELL CYCLE. POSSESSES
CC       DNA-BINDING ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SUBUNIT: TF2D IS COMPOSED OF TBP AND A VARIETY OF TBP-ASSOCIATED
CC       FACTORS.
CC   -!- PTM: PHOSPHORYLATED BY CASEIN KINASE II IN VITRO.
CC   -!- SIMILARITY: CONTAINS TWO COPIES OF THE BROMODOMAIN.
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CC   -!- SIMILARITY: CONTAINS A HMG BOX.
DR   EMBL; D90359; HSCCG1B.
DR   EMBL; X07024; HSCCG1.
DR   PIR; S03005; S03005.
DR   PIR; A40262; A40262.
DR   MIM; 313650; 11TH EDITION.
DR   PROSITE; PS00633; BROMODOMAIN.
KW   BROMODOMAIN; NUCLEAR PROTEIN; DNA-BINDING; CELL CYCLE; REPEAT;
KW   TRANSCRIPTION REGULATION; PHOSPHORYLATION.
FT   DOMAIN      157    165       PRO-RICH.
FT   DNA_BIND   1195   1273       HMG BOX (POTENTIAL).
FT   DOMAIN     1351   1358       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DOMAIN     1402   1462       BROMODOMAIN.
FT   DOMAIN     1525   1585       BROMODOMAIN.
FT   DOMAIN     1627   1872       ASP/GLU-RICH (ACIDIC TAIL).
SQ   SEQUENCE   1872 AA;  212676 MW;  16805423 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.99
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

            X     X
            XWXXXLX
              |   |
   VAEWRYGPARLWYDMLGVPEDGSGFDY
   340       350   X   360
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7. US-08-121-713B-30 (1-7)
   CA1F_HUMAN COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.

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ID   CA1F_HUMAN     STANDARD;      PRT;  1603 AA.
AC   Q07092;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.
GN   COL16A1.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92335339
RA   PAN T.C., ZHANG R.Z., MATTEI M.G., TIMPL R., CHU M.-L.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 89:6565-6569(1992).
RN   [2]
RP   SEQUENCE OF 421-1603 FROM N.A.
RC   TISSUE=PLACENTA;
RA   YAMAGUCHI N., KIMURA S., MCBRIDE O.W., HORI H., YAMADA Y.,
RA   KANAMORI T., YAMAKOSHI H., NAGAI Y.;
RL   J. BIOCHEM. 112:856-863(1992).
CC   -!- FUNCTION: THE NUMEROUS INTERRUPTIONS IN THE TRIPLE HELIX MAY MAKE
CC       THIS MOLECULE EITHER ELASTIC OR FLEXIBLE.
CC   -!- DOMAIN: THIS SEQUENCE DEFINES EIGHTEEN DIFFERENT DOMAINS, NINE
CC       TRIPLE-HELICAL DOMAINS (COL9 TO COL1) AND TEN NONTRIPLE-HELICAL
CC       DOMAINS (NC10 TO NC1).
CC   -!- DEVELOPMENTAL STAGE: TRANSIENTLY ELEVATED EXPRESSION DURING
CC       GESTATION, AND DECREASE AT TERM.
CC   -!- TISSUE SPECIFICITY: IN THE PLACENTA, WHERE IT IS FOUND IN THE
```

```
CC       AMNION, A MEMBRANOUS TISSUE LINING THE AMNIOTIC CAVITY. WITHIN THE
CC       AMNION, IT IS FOUND IN AN ACELLULAR, RELATIVELY DENSE LAYER OF A
CC       COMPLEX NETWORK OF RETICULAR FIBRES. ALSO LOCATED TO A FIBROBLAST
CC       LAYER BENEATH THIS DENSE LAYER. EXISTS IN TISSUES IN ASSOCIATION
CC       WITH OTHER TYPES OF COLLAGEN.
CC   -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC       UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC   -!- SIMILARITY: BELONGS TO THE FAMILY OF FIBRIL-ASSOCIATED COLLAGENS
CC       WITH INTERRUPTED HELICES (FACIT).
DR   EMBL; M92642; HSCOL16A.
DR   EMBL; S57132; S57132.
DR   PIR; S23810; S23810.
DR   MIM; 120326; 11TH EDITION.
KW   EXTRACELLULAR MATRIX; CONNECTIVE TISSUE; COLLAGEN; HYDROXYLATION;
KW   REPEAT; SIGNAL.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22   1603       COLLAGEN ALPHA 1(XVI) CHAIN.
FT   DOMAIN       22    374       NONHELICAL REGION 10 (NC10).
FT   DOMAIN      375    505       TRIPLE-HELICAL REGION 9 (COL9)
FT                                WITH 3 IMPERFECTIONS.
FT   DOMAIN      506    520       NONHELICAL REGION 9 (NC9).
FT   DOMAIN      521    554       TRIPLE-HELICAL REGION 8 (COL8)
FT                                WITH 1 IMPERFECTION.
FT   DOMAIN      555    571       NONHELICAL REGION 8 (NC8).
FT   DOMAIN      572    630       TRIPLE-HELICAL REGION 7 (COL7)
FT                                WITH 1 IMPERFECTION.
FT   DOMAIN      631    651       NONHELICAL REGION 7 (NC7).
FT   DOMAIN      652    722       TRIPLE-HELICAL REGION 6 (COL6)
FT                                WITH 1 IMPERFECTION.
FT   DOMAIN      723    737       NONHELICAL REGION 6 (NC6).
FT   DOMAIN      738    875       TRIPLE-HELICAL REGION 5 (COL5)
FT                                WITH 3 IMPERFECTIONS.
FT   DOMAIN      876    886       NONHELICAL REGION 5 (NC5).
FT   DOMAIN      887    938       TRIPLE-HELICAL REGION 4 (COL4)
FT                                WITH 2 IMPERFECTIONS.
FT   DOMAIN      939    972       NONHELICAL REGION 4 (NC4).
FT   DOMAIN      973    987       TRIPLE-HELICAL REGION 3 (COL3).
FT   DOMAIN      988   1010       NONHELICAL REGION 3 (NC3).
FT   DOMAIN     1011   1432       TRIPLE-HELICAL REGION 2 (COL2)
FT                                WITH 2 IMPERFECTIONS.
FT   DOMAIN     1433   1471       NONHELICAL REGION 2 (NC2).
FT   DOMAIN     1472   1577       TRIPLE-HELICAL REGION 1 (COL1)
FT                                WITH 2 IMPERFECTIONS.
FT   DOMAIN     1578   1603       NONHELICAL REGION 1 (NC1).
FT   CONFLICT    537    537       R -> P (IN REF. 2).
FT   CONFLICT   1165   1165       S -> P (IN REF. 2).
SQ   SEQUENCE   1603 AA;  157692 MW;  12917962 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.99
Residue Identity =     28%  Matches         =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

           X     X
           XWXXXLX
            |   |
   MWVSWAPGLWLLGLWATFGHGANTG
           10    X   20
```

8. US-08-121-713B-30 (1-7)

PHLX_RABIT PHOSPHOLIPASE ADRAB-B PRECURSOR (EC 3.1.-.-).

```
ID   PHLX_RABIT     STANDARD;      PRT;  1458 AA.
AC   Q05017;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   PHOSPHOLIPASE ADRAB-B PRECURSOR (EC 3.1.-.-).
OS   ORYCTOLAGUS CUNICULUS (RABBIT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; LAGOMORPHA.
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   TISSUE=INTESTINE;
RM   93286138
RA   BOLL W., SCHMID-CHANDA T., SEMENZA G., MANTEI N.;
RL   J. BIOL. CHEM. 268:12901-12911(1993).
CC   -!- FUNCTION: HAS ESTERASE AND PHOSPHOLIPASE A/LYSOPHOSPHOLIPASE
CC       ACTIVITY. CAN CONVERT PHOSPHATIDYLCHOLINE TO FATTY ACIDS AND
CC       GLYCEROPHOSPHOCHOLINE. COULD BE INVOLVED IN UPTAKE OF DIETARY
CC       LIPIDS, POSSIBLY INCLUDING LONG CHAIN RETINYL ESTERS.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE INTESTINE OF ADULT BUT NOT
CC       BABY RABBITS.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. BRUSH BORDER.
CC   -!- TISSUE SPECIFICITY: INTESTINE.
DR   EMBL; Z12841; OCPPHLIP.
DR   PIR; A45665; A45665.
KW   HYDROLASE; REPEAT; SIGNAL.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20   1458       PHOSPHOLIPASE ADRAB-B.
FT   DOMAIN       20   1415       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1416   1439       POTENTIAL.
FT   DOMAIN     1440   1458       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       39   1403       4 X 308-326 AA APPROXIMATE REPEATS.
FT   REPEAT       39    347       1.
FT   REPEAT      362    707       2.
FT   REPEAT      708   1054       3.
FT   REPEAT     1064   1403       4.
SQ   SEQUENCE   1458 AA;  161343 MW;  10794453 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.99
Residue Identity =     28%  Matches         =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

           X     X
           XWXXXLX
            |   |
   SKAHAHAASALWNNMLEPVGQKTTHND
   660       670   X   680
```

9. US-08-121-713B-30 (1-7)
PHA1_PLAFC ERYTHROCYTE-BINDING ANTIGEN EBA-175.

```
ID   EBA1_PLAFC     STANDARD;      PRT;  1426 AA.
AC   P19214;
DT   01-NOV-1990 (REL. 16, CREATED)
DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT   01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE   ERYTHROCYTE-BINDING ANTIGEN EBA-175.
```

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 OS   PLASMODIUM FALCIPARUM (ISOLATE CAMP / MALAYSIA).
 OC   EUKARYOTA; PROTOZOA; APICOMPLEXA; SPOROZOA; COCCIDIA; EUCOCCIDIIDA.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   TISSUE=LATE SCHIZONT;
 RM   90377299
 RA   SIM B.K.L.;
 RL   MOL. BIOCHEM. PARASITOL. 41:293-296(1990).
 DR   EMBL; X52524; PFEBA175.
 DR   PIR; S11561; S11561.
 KW   ANTIGEN.
 FT   DOMAIN      159   1101       ESSENTIAL FOR BINDING TO
 FT                                ERYTHROCYTES.
 FT   VARIANT    1028   1028       E -> V (IN STRAINS FCR3 AND ITG).
 SQ   SEQUENCE   1426 AA;  166155 MW;  10311930 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.99
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XWXXXLX
              |   |
    KEWWNEFREKLWEAMLSEHKNNINNCK
       290    X  300        310


10. US-08-121-713B-30 (1-7)
    KRE5_YEAST   KILLER TOXIN-RESISTANCE PROTEIN 5 PRECURSOR.

 ID   KRE5_YEAST     STANDARD;      PRT;  1365 AA.
 AC   P22023;
 DT   01-AUG-1991 (REL. 19, CREATED)
 DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT   01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
 DE   KILLER TOXIN-RESISTANCE PROTEIN 5 PRECURSOR.
 GN   KRE5.
 OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RM   90258892
 RA   MEADEN P., HILL K., WAGNER J., SLIPETZ D., SOMMER S.S., BUSSEY H.;
 RL   MOL. CELL. BIOL. 10:3013-3019(1990).
 CC   -!- FUNCTION: REQUIRED FOR (1->6)-BETA-D-GLUCAN SYNTHESIS AND NORMAL
 CC       CELL GROWTH.
 CC   -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 DR   EMBL; M33556; SCKRE5.
 DR   PIR; S12202; BVBYK5.
 DR   LISTA; SC00535; KRE5.
 DR   PROSITE; PS00014; ER_TARGET.
 KW   CELL WALL; ENDOPLASMIC RETICULUM; SIGNAL; GLYCOPROTEIN.
 FT   SIGNAL        1     17       POTENTIAL.
 FT   CHAIN        18   1365       KILLER TOXIN-RESISTANCE PROTEIN 5.
 FT   CARBOHYD    115    115       POTENTIAL.
 FT   CARBOHYD    228    228       POTENTIAL.
 FT   CARBOHYD    293    293       POTENTIAL.
 FT   CARBOHYD    457    457       POTENTIAL.
 FT   CARBOHYD    519    519       POTENTIAL.
 FT   CARBOHYD    523    523       POTENTIAL.
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 FT   CARBOHYD    643    643       POTENTIAL.
 FT   CARBOHYD    789    789       POTENTIAL.
 FT   CARBOHYD    870    870       POTENTIAL.
 FT   CARBOHYD   1091   1091       POTENTIAL.
 FT   CARBOHYD   1150   1150       POTENTIAL.
 FT   CARBOHYD   1195   1195       POTENTIAL.
 FT   SITE       1362   1365       PREVENT SECRETION FROM ER.
 SQ   SEQUENCE   1365 AA;  156484 MW;  9856080 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.99
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XWXXXLX
              |   |
    MSGDGYWKEGYWEKMLRENNLEFYSTE
1230      1240      1250


11. US-08-121-713B-30 (1-7)
    YB95_YEAST   HYPOTHETICAL 132.7 KD HELICASE IN ALG7-HIS7 INTERG

 ID   YB95_YEAST     STANDARD;      PRT;  1143 AA.
 AC   P38144;
 DT   01-OCT-1994 (REL. 30, CREATED)
 DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE   HYPOTHETICAL 132.7 KD HELICASE IN ALG7-HIS7 INTERGENIC REGION.
 GN   YBR245C OR YBR1633.
 OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=S288C;
 RA   ALJINOVIC G., POHL F.M., POHL T.M.;
 RL   SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
 CC   -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
 CC   -!- SIMILARITY: TO HELICASES OF THE SNF2/RAD54 FAMILY.
 DR   EMBL; Z36114; SCYBR245C.
 DR   PIR; S46122; S46122.
 KW   HYPOTHETICAL PROTEIN; NUCLEAR PROTEIN; DNA-BINDING; HELICASE;
 KW   ATP-BINDING.
 FT   NP_BIND     235    242       ATP (BY SIMILARITY).
 FT   SITE        338    341       DEGH BOX.
 SQ   SEQUENCE   1143 AA;  132660 MW;  6451971 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.99
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X     X
             XWXXXLX
              |   |
    PARGGCRNTLLWPNMLAIANFHFFKFY
        10    X    20        30


12. US-08-121-713B-30 (1-7)
    SP23_YEAST   SPT23 PROTEIN.
```

```
ID   SP23_YEAST     STANDARD;      PRT;  1082 AA.
AC   P35210;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   SPT23 PROTEIN.
GN   SPT23 OR YKL020C.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   RIEGER M.;
RL   SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE OF 136-752 FROM N.A.
RM   94262317
RA   BURKETT T.J., GARFINKEL D.J.;
RL   YEAST 10:81-92(1994).
CC   -!- FUNCTION: DOSAGE-DEPENDENT SUPPRESSOR OF TY-INDUCED PROMOTER
CC       MUTATIONS. MAY EXERT IT SUPPRESSION EFFECT THROUGH PROTEIN-PROTEIN
CC       INTERACTIONS SINCE DOES NOT PRESENT ANY OF THE MOTIFS GENERALLY
CC       FOUND IN TRANSCRIPTIONAL ACTIVATORS OR DNA BINDING PROTEINS.
CC   -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 738
CC       ONWARD AND IS SHORTER (752 AA) DUE TO A FRAMESHIFT.
CC   -!- SIMILARITY: TO YEAST YIR033W.
DR   EMBL; Z28020; SCYKL020C.
DR   EMBL; L24760; SCSPT23A.
DR   PIR; S37837; S37837.
DR   LISTA; SC01182; SPT23.
FT   CONFLICT    715    715       H -> P (IN REF. 2).
SQ   SEQUENCE   1082 AA;  121337 MW;  5973945 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.99
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
   TKTSIEPDGSLWNRMLTRLNDELPKYE
    920       930  X    940
```

13. US-08-121-713B-30 (1-7)
    PPS3_BACSU PEPTIDE SYNTHETASE 3 (FRAGMENT).

```
ID   PPS3_BACSU     STANDARD;      PRT;   859 AA.
AC   P39847;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   PEPTIDE SYNTHETASE 3 (FRAGMENT).
GN   PPSC OR PPS3.
OS   BACILLUS SUBTILIS.
OC   PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RA   TOGNONI A., GRANDI G.;
```



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RL   SUBMITTED (JUN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
CC       COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
DR   EMBL; Z34883; BSPEPSYN.
DR   SUBTILIST; BG10972; PPSC.
KW   MULTIFUNCTIONAL ENZYME; LIGASE; REPEAT.
FT   NON_TER     859    859
SQ   SEQUENCE   859 AA;  96679 MW;  3839344 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.99
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             XWXXXLX
              |   |
   GATLNTVFQALWGIMLQKVNRSSDAVF
   250       260   X   270
```

14. US-08-121-713B-30 (1-7)
    YLH5_CAEEL PUTATIVE ABC TRANSPORTER C48B4.5 IN CHROMOSOME III

```
ID   YLH5_CAEEL     STANDARD;      PRT;   856 AA.
AC   P34359;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   PUTATIVE ABC TRANSPORTER C48B4.5 IN CHROMOSOME III.
GN   C48B4.5.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RM   94150718
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA   BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA   CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA   FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA   JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
RA   LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA   PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA   SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA   SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA   WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA   WOHLDMAN P.;
RL   NATURE 368:32-38(1994).
CC   -!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC       (ABC TRANSPORTERS).
DR   EMBL; Z29117; CEC48B4.
DR   PIR; S40725; S40725.
DR   WORMPEP; C48B4.5; CE00488.
DR   PROSITE; PS00211; ABC_TRANSPORTER.
KW   HYPOTHETICAL PROTEIN; ATP-BINDING; TRANSPORT.
FT   NP_BIND     563    570       ATP (POTENTIAL).
SQ   SEQUENCE   856 AA;  95999 MW;  3881360 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.99
Residue Identity =    28%  Matches          =      2  Mismatches   =     5
```

Gaps = 0 Conservative Substitutions = 0

```
             X     X
             XWXXXLX
              |   |
    AGIDPKARREVWELLLWCREHSNSALM
         690  X    700
```

15. US-08-121-713B-30 (1-7)
SYFB_BACSU PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.

```
ID   SYFB_BACSU     STANDARD;     PRT;   804 AA.
AC   P17922;
DT   01-NOV-1990 (REL. 16, CREATED)
DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.20) (PHENYLALANINE--
DE   TRNA LIGASE BETA CHAIN).
GN   PHET.
OS   BACILLUS SUBTILIS.
OC   PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RM   91175935
RA   BRAKHAGE A., WOZNY M., PUTZER H.;
RL   BIOCHIMIE 72:725-734(1990).
RN   [2]
RP   ERRATUM.
RM   91234765
RA   BRAKHAGE A., WOZNY M., PUTZER H.;
RL   BIOCHIMIE 73:127-127(1991).
CC   -!- CATALYTIC ACTIVITY: ATP + L-PHENYLALANINE + TRNA(PHE) = AMP +
CC       PYROPHOSPHATE + L-PHENYLALANYL-TRNA(PHE).
CC   -!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
DR   EMBL; X53057; BSPHEST.
DR   PIR; S11731; YFBSB.
DR   SUBTILIST; BG10875; PHET.
KW   AMINOACYL-TRNA SYNTHASE; PROTEIN BIOSYNTHESIS; LIGASE; ATP-BINDING.
SQ   SEQUENCE   804 AA;  87917 MW;  3398444 CN;
```

Initial Score = 7 Optimized Score = 7 Significance = 3.99
Residue Identity = 28% Matches = 2 Mismatches = 5
Gaps = 0 Conservative Substitutions = 0

```
             X     X
             XWXXXLX
              |   |
    TERVAGAVTGLWRKQLWQGEKKPVDFF
     600       610  X    620
```

maryh@stic **stdin**

NeWSprinter20

Fri May 19 11:05:07 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

> O <
O| |O IntelliGenetics
> O <

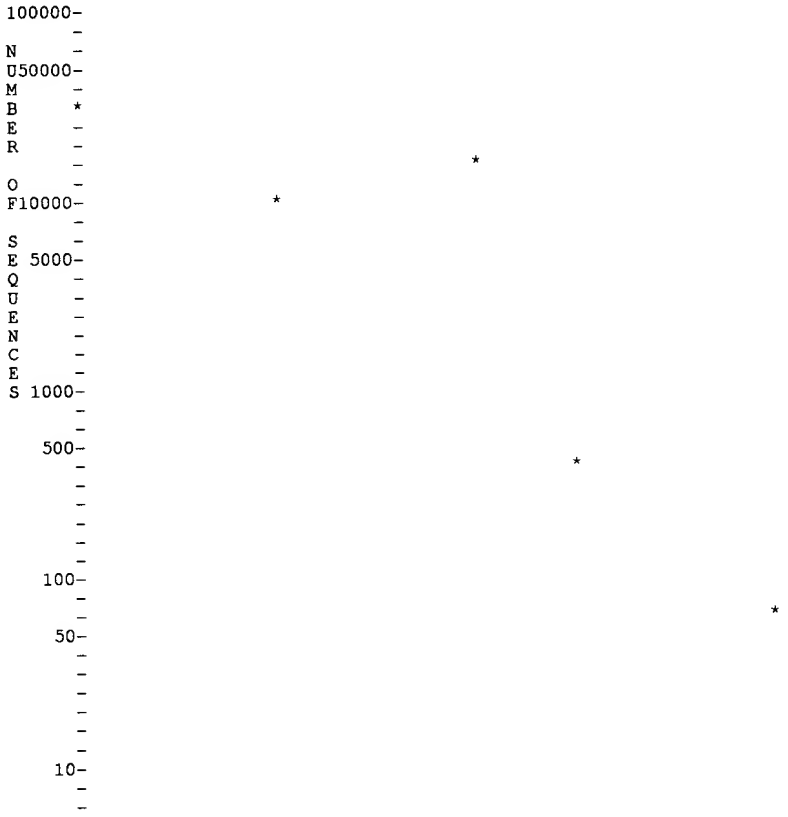
SEQ 33

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

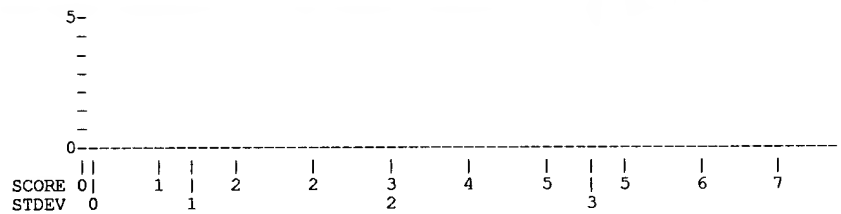
Results file sq33asq.res made by on Fri 19 May 95 8:42:42-PDT.

Query sequence being compared:US-08-121-713B-33 (1-9)
Number of sequences searched: 53402
Number of scores above cutoff: 4011

Results of the initial comparison of US-08-121-713B-33 (1-9) with:
Data bank : A-GeneSeq 18, all entries



Sdata 121713



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	1	1.74

Times:	CPU	Total Elapsed
	00:00:33.96	00:00:34.00

Number of residues: 6354270
Number of sequences searched: 53402
Number of scores above cutoff: 4011

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 3 standard deviations above mean ****					
1. R04198	F gene of simian immunodefici	95	7	7	3.45	0
2. R51074	SphI restriction endonuclease	235	7	7	3.45	0
3. R05934	Bovine beta-1,4-galactosyltra	331	7	7	3.45	0
4. R51687	MVP-5180/91 fragment (gp120/g	351	7	7	3.45	0
5. R44211	Caffeine demethylase.	351	7	7	3.45	0
6. P70668	D-alanine racemase.	389	7	7	3.45	0

7.	R55706	Galactosyltransferase.	398	7	7	3.45	0
8.	R28838	HeLa cell galactosyltransfera	398	7	7	3.45	0
9.	R05932	Human beta-1,4-galactosyltran	400	7	7	3.45	0
10.	R05933	Mouse beta-1,4-galactosyltran	402	7	7	3.45	0
11.	R55130	Rice alpha-amylase coding.	433	7	7	3.45	0
12.	R32987	Rice alpha-amylase.	434	7	7	3.45	0
13.	R10694	Cephalosporin antibiotic bios	437	7	7	3.45	0
14.	R42078	Impatiens Necrotic Spot Virus	449	7	7	3.45	0
15.	R34135	C.roseus TDC with mutated N-t	490	7	7	3.45	0
16.	R34133	Catharanthus roseus tryptopha	500	7	7	3.45	0
17.	R06829	Tryptamine.	500	7	7	3.45	0
18.	R44139	Human FACC.	558	7	7	3.45	0
19.	R06520	Microspore-specific clone L19	584	7	7	3.45	0
20.	R43582	Plant NADPH cytochrome P450 r	712	7	7	3.45	0
21.	R55709	Glycosyltransferase hybrid.	767	7	7	3.45	0
22.	R55708	Glycosyltransferase hybrid.	767	7	7	3.45	0
23.	R04197	Env gene of simian immunodefi	769	7	7	3.45	0
24.	P90954	Yeast topoisomerase I cDNA	769	7	7	3.45	0
25.	R47519	EHV-4 ribonucleotide reductas	789	7	7	3.45	0
26.	R25589	RING4 antigenic peptide trans	808	7	7	3.45	0
27.	R45749	Alpha-DNA polymerase.	882	7	7	3.45	0
28.	R43996	Thermophilic DNA polymerase.	882	7	7	3.45	0
29.	P61082	Complete translation of plasm	898	7	7	3.45	0
30.	P61030	Entire coded sequence from pl	898	7	7	3.45	0
31.	P61056	Translation of plasmid pAU157	899	7	7	3.45	0
32.	R44401	Canine coronavirus 1-71 spike	1101	7	9	3.45	0
33.	R55764	Sequence encoded by the cDNA	1153	7	7	3.45	0
34.	R41668	Human endothelial cell nitric	1203	7	7	3.45	0
35.	R38698	S-PRV-055 TGE virus gp195 gen	1399	7	9	3.45	0
36.	R27818	CCV-6 spike protein.	1443	7	9	3.45	0
37.	R27819	CCVInsavc spike protein.	1451	7	9	3.45	0
38.	R42471	Canine coronavirus 1-71 spike	1452	7	9	3.45	0
39.	R44400	Canine coronavirus 1-71 spike	1452	7	9	3.45	0
40.	R31038	E2 protein of Canine Corona V	1453	7	9	3.45	0
41.	R27820	CCV-C54 spike protein.	1453	7	9	3.45	0
42.	R42478	FECV/FIPV chimeric spike prot	1454	7	9	3.45	0
43.	R42477	FECV/FIPV chimeric spike prot	1454	7	9	3.45	0
44.	R42475	FECV/FIPV chimeric spike prot	1454	7	9	3.45	0
45.	R42474	FECV/FIPV chimeric spike prot	1454	7	9	3.45	0

1. US-08-121-713B-33 (1-9)
R04198 F gene of simian immunodeficiency virus.

```
ID   R04198 standard; protein; 95 AA.
AC   R04198;
DT   12-JUN-1990  (first entry)
DE   F gene of simian immunodeficiency virus.
KW   SIV; simian immunodeficiency virus; AIDS; HIV; vaccine; ss.
OS   SIV.
PN   J01289485-A.
PD   21-NOV-1989.
PF   16-JUN-1988; 119023.
PR   16-JUN-1988; JP-119023.
PA   (TOFU) Toa Nenryo Kogyo KK.
DR   WPI; 90-005176/01.
DR   N-PSDB; Q02829.
PT   DNA complementary to RNA of simian immuno-deficiency virus -
PT   used in vaccines and for diagnosis of AIDS.
PS   Disclosure; Fig 4; 6pp; Japanese.
```



```
CC   F gene derived from RNA of SIV from which vector plasmid pSAH121
CC   may be constructed and incorporated into an E.coli vector. Useful in
CC   developing a vaccine against and in diagnosis of AIDS.
SQ   Sequence   95 AA;
SQ   9 A;  8 R;  6 N;  1 D;  0 B;  4 C;  9 Q;  4 E;  0 Z;  4 G;  1 H;
SQ   5 I;  16 L;  4 K;  1 M;  1 F;  1 P;  5 S;  6 T;  3 W;  4 Y;  3 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.45
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
             |   |   |
    SKSRCMQLTAWLTRLNTWLYNSCLTLLIQ
          10  X     20        30
```

2. US-08-121-713B-33 (1-9)
R51074 SphI restriction endonuclease.

```
ID   R51074 standard; Protein; 235 AA.
AC   R51074;
DT   24-MAY-1994  (first entry)
DE   SphI restriction endonuclease.
KW   Restriction endonuclease; methylase; SphI; fermentation;
KW   Streptomyces phaeochromogenes.
OS   Streptomyces phaeochromogenes.
PN   US5262318-A.
PD   16-NOV-1993.
PF   20-AUG-1992; 932454.
PR   20-AUG-1992; US-932454.
PA   (NEWE ) NEW ENGLAND BIOLABS INC.
PI   Guthrie EP;
DR   WPI; 93-377440/47.
DR   N-PSDB; Q51114.
PT   Sphi restriction endo-nuclease prepn. - comprises cloning SphI
PT   gene to E.coli host and fermentation
PS   Example 1; Columns 25-26; 20pp; English.
CC   A DNA sequence comprising the methylase and SphI restriction
CC   endonuclease genes (Q51114) is used in the construction of a
CC   recombinant vector.  The vector is then used to transform E. coli
CC   RR1 which can then express the restriction endonuclease gene to
CC   produce the enzyme.  The restriction endonuclease gene is cloned
CC   alongside the relevant methylase gene to prevent degradation of
CC   the host cell genome when the restricton endonuclease is produced.
SQ   Sequence   235 AA;
SQ   29 A; 17 R; 9  N; 17 D; 0  B; 8  C; 5  Q; 16 E; 0  Z; 17 G; 4  H;
SQ   8  I; 18 L; 17 K; 5  M; 8  F; 11 P; 13 S; 9  T; 4  W; 6  Y; 14 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.45
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
             |   ||
    PIVLSADQIAWLRQLKMSKRAALVRDYIL
       10     X  20   X    30
```

3. US-08-121-713B-33 (1-9)
R05934 Bovine beta-1,4-galactosyltransferase.

ID R05934 standard; protein; 331 AA.
AC R05934;
DT 22-NOV-1990 (first entry)
DE Bovine beta-1,4-galactosyltransferase.
KW Beta-1,4-galactosyl transferase; sugars; glycoproteins;
KW glycolipids; dyserythropoietic anaemia type II; ds.
OS Bos taurus.
PN WO9007000-A.
PD 28-JUN-1990.
PF 16-NOV-1989; U05128.
PR 13-DEC-1988; US-283732.
PA (JOLL-) LA JOLLA CANCER RES.
PI FUKUDA MN, APPERT HA;
DR WPI; 90-224528/29.
PT New nucleic acid sequences encoding beta-1,4-galactosyl
PT transferase - in bound or soluble forms, and derived
PT polypeptide(s) and antibodies, useful in synthesis and diagnosis.
PS Disclosure; p; English.
CC Derived non-membrane bound peptide product can be collected
CC as a cell secretion from a transformed host. Product is useful
CC in production of sugars, glycoproteins and glycolipids. Abs
CC raised to the product may be used in diagnosis of abnormal
CC conditions such as congenital dyserythropoietic anaemia type II.
SQ Sequence 331 AA;
SQ 14 A; 20 R; 19 N; 17 D; 0 B; 5 C; 16 Q; 11 E; 0 Z; 25 G; 8 H;
SQ 20 I; 32 L; 15 K; 9 M; 13 F; 30 P; 24 S; 13 T; 3 W; 18 Y; 19 V;

Initial Score	=	7	Optimized Score	=	7	Significance	= 3.45
Residue Identity	=	33%	Matches	=	3	Mismatches	= 6
Gaps	=	0	Conservative Substitutions			=	0

```
            X       X
            WXXXLKXXL
               ||  |
   KVAIIIPFRNRQEHLKYWLYYLHPILQRQ
    110       120    X  130
```

4. US-08-121-713B-33 (1-9)
R51687 MVP-5180/91 fragment (gp120/gp41).

ID R51687 standard; Protein; 351 AA.
AC R51687;
DT 07-NOV-1994 (first entry)
DE MVP-5180/91 fragment (gp120/gp41).
KW Human immunodeficiency virus; HIV; antigen; detection; diagnosis;
KW retrovirus; vaccine; lymphocyte; reverse transcriptase;
KW amplification; primer; polymerase chain reaction; PCR.
OS Synthetic.
FH Key Location/Qualifiers
FT Region 1..16
FT /label= gp120
FT Region 17..351
FT /label= gp41
PN EP-591914-A.
PD 13-APR-1994.

PF 05-OCT-1993; 116058.
PR 06-OCT-1992; DE-233646.
PR 22-OCT-1992; DE-235718.
PR 30-DEC-1992; DE-244541.
PR 01-JUN-1993; DE-318186.
PA (BEHW) BEHRINGWERKE AG.
PI Brunn v. A, Eberle J, Gurtler LG, Hauser H-P, Knapp S;
DR WPI; 94-120077/15.
DR N-PSDB; Q58966.
PT New HIV-type immune deficiency virus ECACC V 92092318 - and
PT deriv. cDNA or antigens, useful for diagnosing retroviral
PT infections and vaccines
PS Example 7; Page 13-14; 73pp; German.
CC MVP-5180/91 DNA is obtained by PCR using the primers given
CC in Q58962-65. The primer given in Q58963 is derived from HIV-1
CC BH10 (bases 8129-8109).
CC The obtained fragment is given in Q58966.
SQ Sequence 351 AA;
SQ 24 A; 20 R; 17 N; 14 D; 0 B; 4 C; 29 Q; 13 E; 0 Z; 28 G; 7 H;
SQ 36 I; 49 L; 13 K; 5 M; 3 F; 9 P; 17 S; 20 T; 17 W; 9 Y; 17 V;

Initial Score	=	7	Optimized Score	=	7	Significance	= 3.45
Residue Identity	=	33%	Matches	=	3	Mismatches	= 6
Gaps	=	0	Conservative Substitutions			=	0

```
            X       X
            WXXXLKXXL
               |  ||
   CRLCGAVMQYWLQELKNSATNLLDTIAVS
     310     X 320   X   330
```

5. US-08-121-713B-33 (1-9)
R44211 Caffeine demethylase.

ID R44211 standard; Protein; 351 AA.
AC R44211;
DT 26-MAY-1994 (first entry)
DE Caffeine demethylase.
KW Caffeine demethylase; CDM; Pseudomonas; 3-methyl-7-alkyl-xanthine;
KW 1,3-dimethyl-7-alkyl-xanthine; demethylation; ds.
OS Pseudomonas sp.
PN DE4316882-A.
PD 25-NOV-1993.
PF 19-MAY-1993; 316882.
PR 20-MAY-1992; JP-154380.
PR 27-OCT-1992; JP-312954.
PA (AMAN) AMANO PHARM KK.
PI Imai Y, Koide Y, Nakane S;
DR WPI; 93-378610/48.
DR N-PSDB; Q51766.
PT DNA contg. caffeine de-methylase gene - used in prodn. of
PT 3-methyl-7-alkyl-xanthine cpds. by microbial demethylation of
PT 1,3-di:methyl derivs.
PS Claim 4; Page 16-17; 23pp; German.
CC 3-methyl-7-alkyl-xanthine cpds. can be produced by culturing
CC a transformant contg. the CDM gene in a nutrient contg.
CC 1,3-dimethyl-7-alkyl-xanthine.
CC 3-methyl-7-alkyl-xanthine cpds. are useful as pharmaceutical
CC intermediates.

```
 SQ   Sequence   351 AA;
 SQ   31 A; 19 R; 17 N; 26 D; 0  B; 9  C; 14 Q; 22 E; 0  Z; 11 G; 11 H;
 SQ   15 I; 26 L; 14 K; 5  M; 19 F; 24 P; 27 S; 14 T; 8  W; 14 Y; 25 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.45
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
             |   ||
   ADKVSIQYRKWLREILKEAHQDGAQAFRSA
 310       320       330
```

6. US-08-121-713B-33 (1-9)
P70668 D-alanine racemase.

```
 ID   P70668 standard; protein; 389 AA.
 AC   P70668;
 DT   11-MAR-1991  (first entry)
 DE   D-alanine racemase.
 KW   L-glutamate racemase; D-alanyl-D-alanine ligase.
 OS   Bacillus subtilis.
 PN   GB2177097-A.
 PD   14-JAN-1987.
 PF   17-JUN-1986; 014702.
 PR   18-JUN-1985; US-746437.
 PA   (GENE-) GENENCOR INC.
 PI   Ferrari E;
 DR   WPI; 87-009482/02.
 DR   N-PSDB; N70668.
 PT   Stable maintenance of heterologous DNA in host cell - using host
 PT   cells deficient in ability to synthesise cell wall transformed to
 PT   regain ability
 PS   Disclosure; Fig 2; 13pp; English.
 CC   Protein may be produced in a transformed cell-line defficient in
 CC   D-alanine production. The cell will then express the required sequence
 CC   and a second sequence operably linked to the D-alanine racemase.
 CC   Other sequences which may be used in the same way include those
 CC   encoding L-glutamate racemase or D-alanyl-D-alanine ligase.
 SQ   Sequence   389 AA;
 SQ   37 A; 21 R; 14 N; 18 D; 0  B; 5  C; 8  Q; 29 E; 0  Z; 29 G; 11 H;
 SQ   23 I; 38 L; 30 K; 15 M; 14 F; 15 P; 19 S; 20 T; 4  W; 13 Y; 26 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.45
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
             |   ||
   GTVPVGYADGWLRKLKGTDILVKGKRLKI
 280       290       300
```

7. US-08-121-713B-33 (1-9)
R55706 Galactosyltransferase.

```
 ID   R55706 standard; Protein; 398 AA.
```



```
 AC   R55706;
 DT   18-NOV-1994  (first entry)
 DE   Galactosyltransferase.
 KW   Galactosyltransferase; sialyltransferase; hybrid protein;
 KW   glycosyltransferase; glycoprotein; glycolipid; oligosaccharide;
 KW   HeLa; Escherichia coli; pAD113; glycosylation;
 KW   Saccharomyces cerevisiae.
 OS   Homo sapiens.
 PN   WO9412646-A.
 PD   09-JUN-1994.
 PF   15-NOV-1993; E03194.
 PR   27-NOV-1992; EP-810924.
 PA   (CIBA ) CIBA GEIGY AG.
 PI   Berger EG,  Iwanow SX,  Watzele M;
 DR   WPI; 94-200274/24.
 DR   P-PSDB; Q66889.
 PT   Proteins with glycosyl transferase activity - useful for
 PT   synthesis or modification of glyco-proteins, glyco-lipid(s) and
 PT   oligosaccharide(s)
 PS   Disclosure; Page 32-34; 67pp; English.
 CC   cDNA encoding galactosyltransferase (GT) was isolated from HeLa
 CC   cells, cloned by PCR using the primers given in Q66893-97, and
 CC   expressed in Escherichia coli DH5-alpha using plasmid p4AD113.
 CC   Hybrid proteins (R55708, R55709) comprising membrane-bound or
 CC   soluble derivatives of GT linked to soluble sialyltransferase
 CC   were prepared in Saccharomyces cerevisiae.
 SQ   Sequence   398 AA;
 SQ   26 A; 27 R; 19 N; 21 D; 0  B; 7  C; 20 Q; 11 E; 0  Z; 33 G; 9  H;
 SQ   17 I; 42 L; 11 K; 10 M; 15 F; 35 P; 30 S; 15 T; 3  W; 17 Y; 30 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.45
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
                ||  |
   KVAIIIPFRNRQEHLKYWLYYLHPVLQRQ
    180       190    X  200
```

8. US-08-121-713B-33 (1-9)
R28838 HeLa cell galactosyltransferase enzyme.

```
 ID   R28838 standard; Protein; 398 AA.
 AC   R28838;
 DT   05-APR-1993  (first entry)
 DE   HeLa cell galactosyltransferase enzyme.
 KW   glycosyltransferase; galactosyltransferase; sialyltransferase;
 KW   furosyltransferase; membrane bound; ss.
 OS   Homo sapiens.
 PN   GB2256197-A.
 PD   02-DEC-1992.
 PF   14-APR-1992; 008211.
 PR   31-MAY-1991; EP-810414.
 PR   04-MAR-1992; EP-810167.
 PR   14-APR-1992; GB-008211.
 PA   (CIBA ) CIBA GEIGY AG.
 PI   Berger EG, Meyhack B, Watzele G, Watzele M, Berger E;
 DR   WPI; 92-401159/49.
```

```
DR   N-PSDB; Q31434.
PT   Glycosyltransferase prodn. process - includes transforming yeast
PT   cells with expression cassettes contg. mammalian coding sequences
PT   controlled by yeast promoters
PS   Claim 7; Page 43; 65pp; English.
CC   This sequence represents a galactosyltransferase enzyme from HeLA cells.
CC   (EC 2.4.1.22). It was decoded from the appropriate cDNA. the method
CC   of the invention is used to produce membrane-bound mammalian
CC   glycosyltransferase and variants, using transformed yeasts. It is
CC   less time consuming than natural source isolation and chemical methods.
SQ   Sequence   398 AA;
SQ   26 A; 27 R; 19 N; 21 D; 0  B; 7  C; 20 Q; 11 E; 0  Z; 33 G; 9  H;
SQ   17 I; 42 L; 11 K; 10 M; 15 F; 34 P; 31 S; 15 T; 3  W; 17 Y; 30 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.45
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
                 ||  |
    KVAIIIPFRNRQEHLKYWLYYLHPVLQRQ
     180       190    X  200


9. US-08-121-713B-33 (1-9)
   R05932       Human beta-1,4-galactosyltransferase.

 ID   R05932 standard; protein; 400 AA.
 AC   R05932;
 DT   22-NOV-1990  (first entry)
 DE   Human beta-1,4-galactosyltransferase.
 KW   Beta-1,4-galactosyl transferase; sugars; glycoproteins;
 KW   glycolipids; dyserythropoietic anaemia type II; ds.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   Active-site     112..114
 FT   /label=Potential glycosylation site.
 PN   WO9007000-A.
 PD   28-JUN-1990.
 PF   16-NOV-1989; U05128.
 PR   13-DEC-1988; US-283732.
 PA   (JOLL-) LA JOLLA CANCER RES.
 PI   FUKUDA MN, APPERT HA;
 DR   WPI; 90-224528/29.
 DR   N-PSDB; Q05265.
 PT   New nucleic acid sequences encoding beta-1,4-galactosyl
 PT   transferase - in bound or soluble forms, and derived
 PT   polypeptide(s) and antibodies, useful in synthesis and diagnosis.
 PS   Claim 3; Fig 2; 31pp; English.
 CC   Derived non-membrane bound peptide product can be collected
 CC   as a cell secretion from a transformed host. Product is useful
 CC   in production of sugars, glycoproteins and glycolipids. Abs
 CC   raised to the product may be used in diagnosis of abnormal
 CC   conditions such as congenital dyserythropoietic anaemia type II.
 SQ   Sequence   400 AA;
 SQ   26 A;  27 R;  19 N;  21 D;  0 B;  7 C;  20 Q;  11 E;  0 Z;  34 G;  9 H;
 SQ   18 I;  42 L;  11 K;  10 M; 15 F; 34 P;  30 S;  15 T;  3 W;  18 Y; 30 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.45
```



```
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
                 ||  |
    KVAIIIPFRNRQEHLKYWLYYLHPVLQRQ
      180     X 190   X   200


10. US-08-121-713B-33 (1-9)
    R05933       Mouse beta-1,4-galactosyltransferase.

 ID   R05933 standard; protein; 402 AA.
 AC   R05933;
 DT   22-NOV-1990  (first entry)
 DE   Mouse beta-1,4-galactosyltransferase.
 KW   Beta-1,4-galactosyl transferase; sugars; glycoproteins;
 KW   glycolipids; dyserythropoietic anaemia type II; ds.
 OS   Mus sp.
 PN   WO9007000-A.
 PD   28-JUN-1990.
 PF   16-NOV-1989; U05128.
 PR   13-DEC-1988; US-283732.
 PA   (JOLL-) LA JOLLA CANCER RES.
 PI   FUKUDA MN, APPERT HA;
 DR   WPI; 90-224528/29.
 PT   New nucleic acid sequences encoding beta-1,4-galactosyl
 PT   transferase - in bound or soluble forms, and derived
 PT   polypeptide(s) and antibodies, useful in synthesis and diagnosis.
 PS   Disclosure; p; English.
 CC   Derived non-membrane bound peptide product can be collected
 CC   as a cell secretion from a transformed host. Product is useful
 CC   in production of sugars, glycoproteins and glycolipids. Abs
 CC   raised to the product may be used in diagnosis of abnormal
 CC   conditions such as congenital dyserythropoietic anaemia type II.
 SQ   Sequence   402 AA;
 SQ   25 A;  29 R;  19 N;  22 D;  0 B;  7 C;  19 Q;  10 E;  0 Z;  35 G;  8 H;
 SQ   20 I;  43 L;  18 K;  9 M;  17 F;  34 P;  27 S;  15 T;  3 W;  18 Y;  24 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.45
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
                 ||  |
    KVAIIIPFRNRQEHLKYWLYYLHPILQRQ
    180      190     X 200


11. US-08-121-713B-33 (1-9)
    R55130       Rice alpha-amylase coding.

 ID   R55130 standard; Protein; 433 AA.
 AC   R55130;
 DT   12-JAN-1995  (first entry)
 DE   Rice alpha-amylase coding.
 KW   Virus; recombination; plant virus; alpha trichosanthin; phenotype;
 KW   alpha amylase; alpha haemoglobin; brome mosaic virus; gemini virus;
```

```
KW   rice necrosis virus tobamovirus; gene expression; chinese cucumber.
OS   Oryza sativa.
PN   US5316931-A.
PD   31-MAY-1994.
PF   26-FEB-1988; 160766.
PR   26-FEB-1988; US-160766.
PR   26-FEB-1988; US-160771.
PR   15-JUL-1988; US-219279.
PR   17-FEB-1989; US-310881.
PR   05-MAY-1989; US-347637.
PR   08-JUN-1989; US-363138.
PR   22-OCT-1990; US-600244.
PR   16-JAN-1991; US-641617.
PR   26-JUL-1991; US-737899.
PR   01-AUG-1991; US-739143.
PA   (BIOS-) BIOSOURCE GENETICS CORP.
PI   Dawson WO,  Donson J,  Garger SJ,  Granthan GL,  Grill LK;
PI   Turpen AM, Turpen TH;
DR   WPI; 94-176269/21.
DR   N-PSDB; Q65574.
PT   New recombinant plant viral nucleic acid - capable of systemic
PT   infection and stable expression of non-native nucleic acid in
PT   plant host
PS   Example 4; Columns 53-56; 44pp; English.
CC   The rice alpha-amylase gene may be inserted into a recombinant plant
CC   virus which can then be used to infect plants for the production of
CC   non-native products (in this case alpha-amylase).  Other genes which
CC   may be inserted into the virus are those which control a phenotypic
CC   trait, such as male sterility, or sequences encoding anti-sense RNA
CC   which can be useful to prevent the expression of undesired phenotypic
CC   traits.  The recombinant virus is derived from a plus sense, single
CC   stranded virus selected from tobamovirus, brome mosic virus, rice
CC   necrosis virus or a gemini virus.
SQ   Sequence   433 AA;
SQ   33 A; 17 R; 20 N; 36 D; 0  B; 3  C; 13 Q; 23 E; 0  Z; 47 G; 15 H;
SQ   29 I; 34 L; 20 K; 11 M; 18 F; 21 P; 20 S; 18 T; 15 W; 15 Y; 25 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.45
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

            X       X
            WXXXLKXXL
            |   ||
   NKRVQRELIGWLDWLKMDIGFDAWRLDFA
        190 X     200       210
```

12. US-08-121-713B-33 (1-9)
    R32987 Rice alpha-amylase.

```
ID   R32987 standard; Protein; 434 AA.
AC   R32987;
DT   17-JUN-1993  (first entry)
DE   Rice alpha-amylase.
KW   Recombinant products; commercial production; fermentation;
KW   biosynthesis; natural products; recombinant proteins;
KW   product expression; protein expression; expressed proteins.
OS   Oryza sativa.
PN   WO9303161-A.
```



```
PD   18-FEB-1993.
PF   31-JUL-1992; U06359.
PR   01-AUG-1991; US-739143.
PA   (DAWS/) DAWSON W O.
PA   (DONS/) DONSON J.
PA   (GARG/) GARGER S J.
PA   (GRAN/).
PA   GRANTHAM G L.
PA   (GRIL/) GRILLE L K.
PA   (TURP/) TURPEN A M.
PA   (TURP/).
PA   TURPEN T H.
PI   Dawson WO,  Donson J,  Garger SJ,  Grantham GL,  Grille LK;
PI   Turpenam,  Turpen TH;
DR   WPI; 93-076518/09.
DR   N-PSDB; Q37680.
PT   Recombinant plant viral nucleic acids - used to express a prod.,
PT   e.g. antibody or IL-1 in a plant
PS   Example 4; Page 96; 30pp; English.
CC   This sequence is rice alpha amylase. The coding sequence was inserted
CC   into a recombinant plant viral nucleic acid which was then used to
CC   express a recombinant product (in this case rice alpha-amylase) in a
CC   plant. The plant viral sequence may be from tobacco mosaic, cucumber
CC   green mottle, cowpea mosaic, brome mosaic, broad bean mottle, rice
CC   necrosis, geminiviruses, tomato golden mosaic, Cassava latent and
CC   maize streak viruses.
SQ   Sequence   434 AA;
SQ   34 A; 17 R; 20 N; 36 D; 0  B; 3  C; 13 Q; 23 E; 0  Z; 47 G; 16 H;
SQ   29 I; 34 L; 20 K; 11 M; 18 F; 20 P; 19 S; 18 T; 16 W; 15 Y; 25 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.45
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

            X       X
            WXXXLKXXL
            |   ||
   NKRVQRELIGWLDWLKMDIGFDAWRLDFA
        190 X     200       210
```

13. US-08-121-713B-33 (1-9)
    R10694 Cephalosporin antibiotic biosynthetic enzyme #8.

```
ID   R10694 standard; Protein; 437 AA.
AC   R10694;
DT   27-MAR-1991  (first entry)
DE   Cephalosporin antibiotic biosynthetic enzyme #8.
KW   cephalosporin; antibiotic;
KW   S-(L-alpha-aminoadipyl)-L-cysteinyl-D-; valine synthetase;
KW   isopenicillin N synthetase; isopenicillin N epimerase;
KW   deacetoxycephalosporin C synthetase; beta-lactamase;
KW   deacetoxycephalosporin C hydroxylase.
OS   Lysobacter lactamgenus.
PN   J02291274-A.
PD   03-DEC-1990.
PF   10-JAN-1990; 003762.
PR   01-FEB-1989; JP-024710.
PR   10-JAN-1990; JP-003762.
PA   (TAKE ) TAKEDA CHEMICAL IND KK.
```

```
DR   WPI; 91-018854/03.
DR   N-PSDB; Q10190.
PT   Prepn. of cephalosporin series antibiotics - comprises culturing
PT   transformant of microbe transformed by plasmid contg. new DNA
PT   fragment
PS   Disclosure; Fig 20; 67pp; Japanese.
CC   This protein is encoded by ORF8 of the 23666bp sequence
CC   isolated from L.lactamgenus and comprising the genes for the
CC   cephalosporin biosynthetic enzymes listed in the KEYWORDS. Plasmids
CC   containing at least one of ORF's 1-9 can be used to transform
CC   microbes, such as bacteria or yeast.
CC   See also Q10191-2.
SQ   Sequence   437 AA;
SQ   57 A; 30 R; 20 N; 18 D; 0  B; 4  C; 17 Q; 15 E; 0  Z; 31 G; 1  H;
SQ   23 I; 52 L; 8  K; 11 M; 19 F; 27 P; 24 S; 29 T; 11 W; 17 Y; 23 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.45
Residue Identity =     33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
             |   ||
    PNERLRNVMEWLDFLKVVPPESKISALLG
     290       300    X  310
```

14. US-08-121-713B-33 (1-9)
    R42078 Impatiens Necrotic Spot Virus S Non-structural pro

```
ID   R42078 standard; Protein; 449 AA.
AC   R42078;
DT   29-APR-1994  (first entry)
DE   Impatiens Necrotic Spot Virus S Non-structural protein.
KW   INSV; tospovirus; resistance; pan-handle secondary structure;
KW   plant RNA virus.
OS   Impatiens Necrotic Spot Virus.
PN   EP-566525-A.
PD   20-OCT-1993.
PF   16-MAR-1993; 810190.
PR   19-MAR-1992; GB-006016.
PA   (SANO ) SANDOZ LTD.
PA   (VGRI/) VAN GRINSVEN M Q J M.
PA   (SANO ) SANDOZ PATENT GMBH.
PA   (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.
PA   (SANO ) SANDOZ AG.
PI   De Haan PT,  Gielen JJL,  Goldbach RW,  Peters D,  Van Grinsven MQJ;
PI   Van Grinsven MQJM;
DR   WPI; 93-329814/42.
DR   N-PSDB; Q49956.
PT   Recombinant INSV DNA constructs comprising INSV DNA coding for
PT   transcription into INSV RNA sequences - are used to transform
PT   plants to reduce susceptibility to INSV infection
PS   Example 4; Page 45-46; 64pp; English.
CC   INSV RNA was purified from systemically infected Nicotiana rustica
CC   leaves. The short (S) transcript comprises two genes, one coding for
CC   a non-structural protein and the other (on the complementary strand)
CC   coding for the nucleocapsid protein. The 5'- and 3'-terminal
CC   sequences of the S RNA are capable of hybridising to each other; the
CC   double-stranded structure obtained by such hybridisation is referred
```



```
CC   to as a "pan-handle".
SQ   Sequence   449 AA;
SQ   14 A; 14 R; 30 N; 23 D; 0  B; 5  C; 18 Q; 26 E; 0  Z; 15 G; 10 H;
SQ   30 I; 42 L; 35 K; 13 M; 22 F; 18 P; 55 S; 26 T; 5  W; 17 Y; 31 V;

Initial Score    =      7  Optimized Score  =      7  Significance =  3.45
Residue Identity =     33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
             |   ||
    VLSPTRSVHEWLYTLKPVFNQSQTNNRTV
        190   X   200 X     210
```

15. US-08-121-713B-33 (1-9)
    R34135 C.roseus TDC with mutated N-terminus.

```
ID   R34135 standard; Protein; 490 AA.
AC   R34135;
DT   20-JUL-1993  (first entry)
DE   C.roseus TDC with mutated N-terminus.
KW   Tryptophan decarboxylase; tryptophan analogue; tdc gene.
OS   Catharanthus roseus.
FH   Key             Location/Qualifiers
FT   Protein         4..490
FT   /label= TDC
FT   /note= "mature N-terminus determined by direct
FT   sequencing of isolated TDC"
FT   Misc_difference 2
FT   /note= "Ser in this position in R34133"
FT   Misc_difference 10
FT   /note= "Lys in this position in R34133"
PN   WO9306220-A.
PD   01-APR-1993.
PF   18-SEP-1992; E02175.
PR   20-SEP-1991; EP-202458.
PA   (MOGE-) MOGEN INT NV.
PI   Goddijn OJM,  Hoge JHC,  Schilperoort RA;
DR   WPI; 93-117541/14.
DR   N-PSDB; Q39283.
PT   Selection method for transformed plants - comprises prodn. of
PT   tryptophan analogues in plants and growth in medium deleterious
PT   to non-transformed plant cells
PS   Example 2; Page 32-34; 50pp; English.
CC   An incomplete clone of C.roseus tdc gene was isolated. The missing
CC   sequences were determined by primer extension on polyA+ RNA. (See
CC   Q39281 for the determined nucleotide sequence). An oligonucleotide
CC   was synthesised which encoded the missing bases spanning nucleotide
CC   positions 90 to 125, flanked by a SalI and EcoRI restriction site
CC   and containing an artificially introduced NcoI site. In the
CC   synthetic sequence (see Q39282), there is a point mutation at
CC   position 14 (corresponding to position 93 in Q39281) to create the
CC   NcoI site. Due to an error in DNA synthesis also codon 10 (AAG in
CC   Q39281) was changed to AAT. The resulting changes in encoded amino
CC   acid sequence can be seen by comparing R34133 and R34135.
SQ   Sequence   490 AA;
SQ   32 A; 23 R; 17 N; 28 D; 0  B; 9  C; 11 Q; 30 E; 0  Z; 26 G; 11 H;
SQ   29 I; 54 L; 26 K; 16 M; 21 F; 26 P; 36 S; 32 T; 10 W; 16 Y; 37 V;
```

```
Initial Score     =      7  Optimized Score  =      7  Significance =  3.45
Residue Identity  =    33%  Matches          =      3  Mismatches   =     6
Gaps              =      0  Conservative Substitutions               =     0

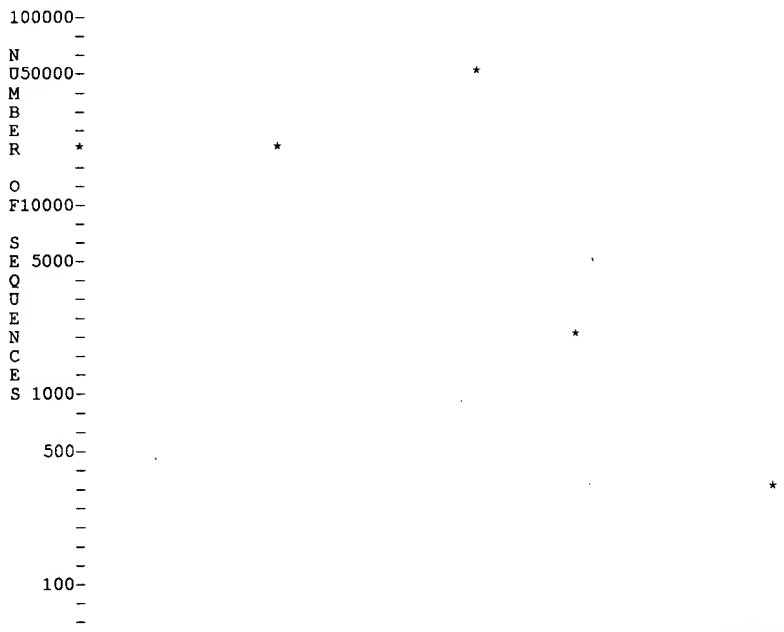
             X       X
             WXXXLKXXL
                ||  |
    FKNWQIATGRKFRSLKLWLILRSYGVVNL
          360 X     370       380
> O <
O| |O  IntelliGenetics
> O <

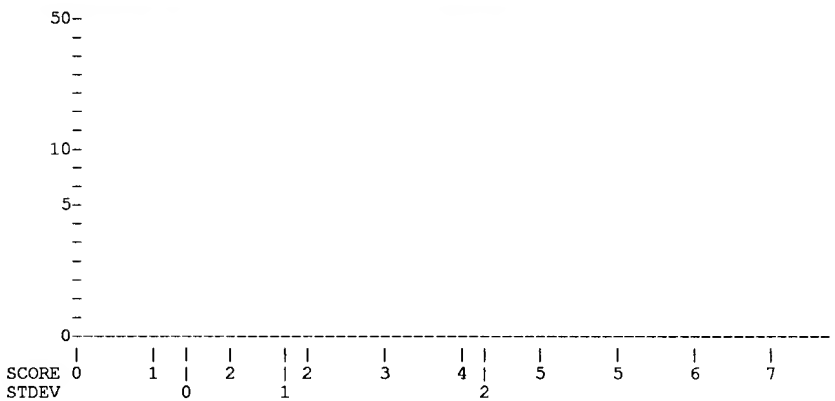
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq33pir.res made by maryh on Fri 19 May 95 10:45:29-PDT.


Query sequence being compared:US-08-121-713B-33 (1-9)
Number of sequences searched:                75511
Number of scores above cutoff:                3819

      Results of the initial comparison of US-08-121-713B-33 (1-9) with:
   Data bank : PIR 43, all entries
```





PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	5	1.66

Times:	CPU	Total Elapsed
	00:01:24.00	00:01:27.00

Number of residues: 22468834
Number of sequences searched: 75511
Number of scores above cutoff: 3819

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 3 standard deviations above mean ****					
1. S33400	Ig heavy chain - mouse	40	7	7	3.01	0
2. S39512	RNA polymerase beta'' - red a	85	7	7	3.01	0
3. JQ1549	V1 protein - Panicum streak v	108	7	7	3.01	0

4.	QQSABE	hypothetical protein B-111 -	111	7	7	3.01	0
5.	S32574	serum amyloid protein SAA - r	122	7	7	3.01	0
6.	JN0029	GSAA1 protein precursor - hum	122	7	7	3.01	0
7.	S23002	traJ protein - Escherichia co	123	7	7	3.01	0
8.	A34172	traJ protein - Escherichia co	123	7	7	3.01	0
9.	S16481	hypothetical protein 1 - Sulf	126	7	7	3.01	0
10.	S22996	traJ protein - Escherichia co	130	7	7	3.01	0
11.	JV0111	probable transcriptional acti	173	7	7	3.01	0
12.	S44695	hypothetical membrane protein	175	7	7	3.01	0
13.	A39414	flavodoxin - Enterobacter agg	177	7	7	3.01	0
14.	RGBY36	cell division control protein	191	7	7	3.01	0
15.	PC1136	purF protein - Lactobacillus	194	7	9	3.01	0
16.	G42148	GTP-binding protein rab16 - r	198	7	7	3.01	0
17.	JQ1964	hypothetical 22.8K protein -	199	7	7	3.01	0
18.	RGECFF	type 1 fimbriae regulatory pr	200	7	7	3.01	0
19.	S15077	Ca2+-transporting ATPase (EC	202	7	9	3.01	0
20.	S29308	hypothetical protein 3 (phaC2	205	7	9	3.01	0
21.	JS0163	Ara protein - Arabidopsis tha	218	7	7	3.01	0
22.	S47101	GTPase - soybean	219	7	7	3.01	0
23.	S16511	probable PRT1 protein - yeast	220	7	7	3.01	0
24.	E42696	thrombin (EC 3.4.21.5) B chai	235	7	7	3.01	0
25.	S47128	HRD238 protein - yeast (Sacch	238	7	7	3.01	0
26.	S31729	arginine transport system pro	238	7	7	3.01	0
27.	S14890	ribosomal protein L17, mitoch	238	7	7	3.01	0
28.	S02063	H+-transporting ATP synthase	238	7	7	3.01	0
29.	S21154	IgE Fc receptor beta chain -	244	7	7	3.01	0
30.	A42806	IgE Fc receptor beta chain -	244	7	7	3.01	0
31.	C40635	indole-3-glycerol-phosphate s	248	7	7	3.01	0
32.	JS0717	hypothetical 29.1K protein (a	259	7	7	3.01	0
33.	TPBPPR	terminal protein - phage PRD1	259	7	7	3.01	0
34.	A24251	lactose synthase (EC 2.4.1.22	261	7	7	3.01	0
35.	S20452	hypothetical protein X - Kleb	271	7	7	3.01	0
36.	JT0613	catechol 1,2-dioxygenase (EC	282	7	7	3.01	0
37.	S28959	acetylglutamate kinase (EC 2.	283	7	7	3.01	0
38.	S27710	hypothetical protein A - Sele	303	7	7	3.01	0
39.	JQ1751	hypothetical 35.5K protein -	303	7	7	3.01	0
40.	B38234	oxoglutarate dehydrogenase (l	308	7	7	3.01	0
41.	NBHUA2	leucine-rich alpha-2-glycopro	312	7	7	3.01	0
42.	S44895	ZK1236.5 protein - Caenorhabd	313	7	7	3.01	0
43.	A24148	N-acetyllactosamine synthase	328	7	7	3.01	0
44.	A35257	replication protein - Neisser	328	7	7	3.01	0
45.	S10256	iron-binding protein precurso	330	7	7	3.01	0

1. US-08-121-713B-33 (1-9)
   S33400 Ig heavy chain - mouse

```
 ENTRY            S33400     #type complete
 TITLE            Ig heavy chain - mouse
 ORGANISM         #formal_name Mus musculus #common_name house mouse
 DATE             08-Dec-1993; #sequence_revision 08-Dec-1993; #text_change
                    08-Dec-1993
 ACCESSIONS       S33400
 REFERENCE        S33391
    #authors      Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
    #journal      Eur. J. Immunol. (1993) 23:206-211
    #title        Optimization of primers for cloning libraries of mouse
                    immunoglobulin genes using the polymerase chain reaction.
    #accession    S33400
       ##status       preliminary
```



```
       ##residues      1-40 ##label KET
       ##cross-references EMBL:X73014
 SUMMARY          #length 40  #molecular-weight 4545  #checksum 4255
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =    37%  Matches          =      3  Mismatches   =     5
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             WXXXLKXXL
             |   ||
    KASGYTFTNYWLHWLKQR
          30 X     40
```

2. US-08-121-713B-33 (1-9)
   S39512 RNA polymerase beta'' - red alga (Cyanidium caldar

```
 ENTRY            S39512     #type complete
 TITLE            RNA polymerase beta'' - red alga (Cyanidium caldarium)
 ORGANISM         #formal_name Cyanidium caldarium
 DATE             07-Oct-1994; #sequence_revision 07-Oct-1994; #text_change
                    07-Oct-1994
 ACCESSIONS       S39512
 REFERENCE        S39512
    #authors      Kostrzewa, M.; Zetsche, K.
    #journal      Plant Mol. Biol. (1993) 23:67-76
    #title        Organization of plastid-encoded ATPase genes and flanking
                    regions including homologues of infB and tsf in the
                    thermophilic red alga Galdieria sulphuraria.
    #accession    S39512
       ##status       preliminary
       ##residues     1-85 ##label KOS
       ##cross-references EMBL:X67814
 SUMMARY          #length 85  #molecular-weight 10114  #checksum 6339
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             WXXXLKXXL
             |   ||
    TKAAFENHIDWLKGLKENVIIGRLIPAGT
  10        20        30
```

3. US-08-121-713B-33 (1-9)
   JQ1549 V1 protein - Panicum streak virus

```
 ENTRY            JQ1549     #type complete
 TITLE            V1 protein - Panicum streak virus
 ORGANISM         #formal_name Panicum streak virus
 DATE             30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                    30-Sep-1993
 ACCESSIONS       JQ1549
 REFERENCE        JQ1549
    #authors      Briddon, R.W.; Lunness, P.; Chamberlin, L.C.L.; Pinner, M.S.;
```

```
                Brundish, H.; Markham, P.G.
   #journal     J. Gen. Virol. (1992) 73:1041-1047
   #title       The nucleotide sequence of an infections insect-transmissible
                  clone of the geminivirus Panicum streak virus.
   #contents    Isolate Kenya
   #accession   JQ1549
      ##molecule_type DNA
      ##residues      1-108 ##label BRI
      ##cross-references EMBL:X60168
SUMMARY         #length 108  #molecular-weight 11866  #checksum 2401
SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =    33%  Matches          =      3  Mismatches   =      6
Gaps             =      0  Conservative Substitutions               =      0

            X       X
            WXXXLKXXL
            |   ||
   FVSVLALYLLWLWVLKDCILLLKAQRGRS
         50        60


4. US-08-121-713B-33 (1-9)
   QQSABE       hypothetical protein B-111 - Staphylococcus aureus

ENTRY           QQSABE     #type complete
TITLE           hypothetical protein B-111 - Staphylococcus aureus plasmid
                  pE194
ORGANISM        #formal_name Staphylococcus aureus
DATE            18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change
                  30-Sep-1993
ACCESSIONS      A04487
REFERENCE       A91790
   #authors     Horinouchi, S.; Weisblum, B.
   #journal     J. Bacteriol. (1982) 150:804-814
   #title       Nucleotide sequence and functional map of pE194, a plasmid
                  that specifies inducible resistance to macrolide,
                  lincosamide, and streptogramin type B antibiotics.
   #cross-references MUID:82167187
   #accession   A04487
      ##molecule_type DNA
      ##residues      1-111 ##label HOR
GENETICS
   #genome      plasmid
SUMMARY         #length 111  #molecular-weight 13305  #checksum 8755
SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =    33%  Matches          =      3  Mismatches   =      6
Gaps             =      0  Conservative Substitutions               =      0

            X       X
            WXXXLKXXL
            |   ||
   VLYPESAKAEWLEYLKELHIQFVVSPLHD
        30  X     40        50


5. US-08-121-713B-33 (1-9)
```



```
   S32574       serum amyloid protein SAA - rabbit

ENTRY           S32574     #type complete
TITLE           serum amyloid protein SAA - rabbit
ORGANISM        #formal_name Oryctolagus cuniculus #common_name domestic
                  rabbit
DATE            02-Dec-1993; #sequence_revision 02-Dec-1993; #text_change
                  02-Dec-1993
ACCESSIONS      S32574
REFERENCE       S32574
   #authors     Mitchell, T.I.; Coon, C.I.; Brinckerhoff, C.E.
   #journal     J. Clin. Invest. (1991) 87:1177-1185
   #title       Serum amyloid A (SAA3) produced by rabbit synovial
                  fibroblasts treated with phorbol esters or interleukin 1
                  induces synthesis of collagenase and is neutralized with
                  specific antiserum.
   #accession   S32574
      ##status       preliminary
      ##residues     1-122 ##label MIT
      ##cross-references EMBL:M64696
SUMMARY         #length 122  #molecular-weight 13806  #checksum 1790
SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =    33%  Matches          =      3  Mismatches   =      6
Gaps             =      0  Conservative Substitutions               =      0

            X       X
            WXXXLKXXL
            |   ||
   FLILGVNSREWLTFLKEAGQGAKDMWRAY
         20        30


6. US-08-121-713B-33 (1-9)
   JN0029       GSAA1 protein precursor - human

ENTRY           JN0029     #type complete
TITLE           GSAA1 protein precursor - human
ORGANISM        #formal_name Homo sapiens #common_name man
DATE            10-Dec-1994; #sequence_revision 10-Dec-1994; #text_change
                  10-Dec-1994
ACCESSIONS      JN0029
REFERENCE       JN0029
   #authors     Sack Jr., G.H.; Talbot Jr., C.C.
   #journal     Gene (1989) 84:509-515
   #title       The human serum amyloid A (SAA)-encoding gene GSAA1:
                  nucleotide sequence and possible
                  autocrine-collagenase-inducer function.
   #accession   JN0029
      ##status       preliminary
      ##residues     1-122 ##label SAC
SUMMARY         #length 122  #molecular-weight 13440  #checksum 2835
SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =    33%  Matches          =      3  Mismatches   =      6
Gaps             =      0  Conservative Substitutions               =      0

            X       X
```

```
            WXXXLKXXL
            |   ||
    SLVLGVSSQGWLTFLKAAGQGAKDMWRAY
           20        30
```

7. US-08-121-713B-33 (1-9)
   S23002 traJ protein - Escherichia coli plasmid RP4

```
 ENTRY            S23002     #type complete
 TITLE            traJ protein - Escherichia coli plasmid RP4
 ORGANISM         #formal_name Escherichia coli
 DATE             31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change
                    02-Aug-1994
 ACCESSIONS       S23002
 REFERENCE        S22992
    #authors      Ziegelin, G.; Pansegrau, W.; Strack, B.; Balzer, D.; Kroeger,
                    M.; Kruft, V.; Lanka, E.
    #journal      DNA Seq. (1991) 1:303-327
    #title        Nucleotide sequence and organization of genes flanking the
                    transfer origin of promiscuous plasmid RP4.
    #cross-references MUID:92190548
    #accession    S23002
       ##molecule_type DNA
       ##residues      1-123 ##label ZIE
       ##cross-references EMBL:X54459
       ##note          the authors did not translate the codon for residue 1
 GENETICS
    #gene         traJ
    #genome       plasmid
 SUMMARY          #length 123  #molecular-weight 13464  #checksum 2336
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
                 ||  |
    LARINGDLGRLGGLLKLWLTDDPRTARFG
          70  X     80        90
```

8. US-08-121-713B-33 (1-9)
   A34172 traJ protein - Escherichia coli plasmid RP4

```
 ENTRY            A34172     #type complete
 TITLE            traJ protein - Escherichia coli plasmid RP4
 ORGANISM         #formal_name Escherichia coli
 DATE             07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
                    23-Mar-1993
 ACCESSIONS       A34172
 REFERENCE        A34172
    #authors      Ziegelin, G.; Fuerste, J.P.; Lanka, E.
    #journal      J. Biol. Chem. (1989) 264:11989-11994
    #title        TraJ protein of plasmid RP4 binds to a 19-base pair invert
                    sequence repetition within the transfer origin.
    #cross-references MUID:89308605
    #accession    A34172
```



```
       ##molecule_type DNA
       ##residues      1-123 ##label ZIE
 GENETICS
    #gene         traJ
    #genome       plasmid
 SUMMARY          #length 123  #molecular-weight 13464  #checksum 2336
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
                 ||  |
    LARINGDLGRLGGLLKLWLTDDPRTARFG
          70  X     80        90
```

9. US-08-121-713B-33 (1-9)
   S16481 hypothetical protein 1 - Sulfolobus solfataricus

```
 ENTRY            S16481     #type complete
 TITLE            hypothetical protein 1 - Sulfolobus solfataricus
 ORGANISM         #formal_name Sulfolobus solfataricus
 DATE             03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
                    03-Feb-1994
 ACCESSIONS       S16481; S14845
 REFERENCE        S16481
    #authors      Ramirez, C.; Matheson, A.T.
    #journal      Mol. Microbiol. (1991) 5:1687-1693
    #title        A gene in the archaebacterium Sulfolobus solfataricus that
                    codes for a protein equivalent to the alpha subunits of the
                    signal recognition particle receptor in eukaryotes.
    #cross-references MUID:92048486
    #accession    S16481
       ##status        preliminary
       ##molecule_type DNA
       ##residues      1-126 ##label RAM
       ##cross-references EMBL:X58538
       ##note          the authors translated the codon GAA for residue 95 as
                        Arg
 SUMMARY          #length 126  #molecular-weight 14744  #checksum 8684
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
             |   ||
    RKFWMIESNSWLKYLKIYKVNYLSQ
         110 X     120
```

10. US-08-121-713B-33 (1-9)
    S22996 traJ protein - Escherichia coli plasmid R751

```
 ENTRY            S22996     #type complete
```

```
TITLE           traJ protein - Escherichia coli plasmid R751
ORGANISM        #formal_name Escherichia coli
DATE            31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change
                  02-Aug-1994
ACCESSIONS      S22996
REFERENCE       S22992
   #authors     Ziegelin, G.; Pansegrau, W.; Strack, B.; Balzer, D.; Kroeger,
                  M.; Kruft, V.; Lanka, E.
   #journal     DNA Seq. (1991) 1:303-327
   #title       Nucleotide sequence and organization of genes flanking the
                  transfer origin of promiscuous plasmid RP4.
   #cross-references MUID:92190548
   #accession   S22996
      ##molecule_type DNA
      ##residues      1-130 ##label ZIE
      ##cross-references EMBL:X54458
GENETICS
   #gene        traJ
   #genome      plasmid
SUMMARY         #length 130  #molecular-weight 14392  #checksum 9839
SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =    33%  Matches          =      3  Mismatches   =      6
Gaps             =      0  Conservative Substitutions               =      0

            X       X
            WXXXLKXXL
                ||  |
   LVRVNGDLGRLGGLLKLWLTDDVRTLQFG
  70        80        90
```

11. US-08-121-713B-33 (1-9)
    JV0111 probable transcriptional activator fecI - Escheric

```
ENTRY           JV0111     #type complete
TITLE           probable transcriptional activator fecI - Escherichia coli
ORGANISM        #formal_name Escherichia coli
DATE            12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
                  18-Jun-1993
ACCESSIONS      JV0111
REFERENCE       JV0111
   #authors     Van Hove, B.; Staudenmaier, H.; Braun, V.
   #journal     J. Bacteriol. (1990) 172:6749-6758
   #title       Novel two-component transmembrane transcription control:
                  regulation of iron dicitrate transport in Escherichia coli
                  K-12.
   #cross-references MUID:91072220
   #contents    Strain K12
   #accession   JV0111
      ##molecule_type DNA
      ##residues      1-173 ##label VAN
GENETICS
   #gene        fecI
   #map_position 93 min
KEYWORDS        membrane protein; transcription activator
SUMMARY         #length 173  #molecular-weight 19480  #checksum 8614
SEQUENCE
```



```
Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =    33%  Matches          =      3  Mismatches   =      6
Gaps             =      0  Conservative Substitutions               =      0

            X       X
            WXXXLKXXL
                ||  |
   SLTFESLYGTHHGWLKSWLTRKLQSAFDA
  10        20        30
```

12. US-08-121-713B-33 (1-9)
    S44695 hypothetical membrane protein YBR116c - yeast (Sac

```
ENTRY           S44695     #type complete
TITLE           hypothetical membrane protein YBR116c - yeast (Saccharomyces
                  cerevisiae)
ALTERNATE_NAMES hypothetical protein YBR0911
ORGANISM        #formal_name Saccharomyces cerevisiae
DATE            27-Jun-1994 #sequence_revision 09-Sep-1994 #text_change
                  09-Sep-1994
ACCESSIONS      S44695; S45984
REFERENCE       S44670
   #authors     Feldmann, H.
   #submission  submitted to the EMBL Data Library, April 1994
   #accession   S44695
      ##molecule_type DNA
      ##residues      1-175 ##label FEL
      ##cross-references EMBL:X78993
REFERENCE       S45927
   #authors     Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
   #submission  submitted to the Protein Sequence Database, August 1994
   #accession   S45984
      ##molecule_type DNA
      ##residues      1-175 ##label FE2
      ##cross-references EMBL:Z35985
GENETICS
   #map_position 2R
KEYWORDS        membrane protein
FEATURE
   120-136          #domain transmembrane #status predicted #label TM1\
   138-158          #domain transmembrane #status predicted #label TM2
SUMMARY         #length 175  #molecular-weight 20215  #checksum 3013
SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =    33%  Matches          =      3  Mismatches   =      6
Gaps             =      0  Conservative Substitutions               =      0

            X       X
            WXXXLKXXL
                ||  |
   TDSLFYQTVFRSCPLKYWLLQAGVSMLIN
        40 X      50        60
```

13. US-08-121-713B-33 (1-9)
    A39414 flavodoxin - Enterobacter agglomerans plasmid pEA3

```
ENTRY           A39414     #type complete
```

```
TITLE            flavodoxin - Enterobacter agglomerans plasmid pEA3
ALTERNATE_NAMES  electron transport protein nifF
ORGANISM         #formal_name Enterobacter agglomerans
DATE             21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change
                   20-Aug-1994
ACCESSIONS       A39414
REFERENCE        A39414
   #authors      Kreutzer, R.; Dayananda, S.; Klingmueller, W.
   #journal      J. Bacteriol. (1991) 173:3252-3256
   #title        Cotranscription of the electron transport protein genes nifJ
                   and nifF in Enterobacter agglomerans 333.
   #cross-references MUID:91217003
   #accession    A39414
      ##molecule_type DNA
      ##residues      1-177 ##label KRE
      ##cross-references GB:M38221
GENETICS
   #gene         nifF
   #genome       plasmid
CLASSIFICATION   #superfamily flavodoxin; flavodoxin homology
KEYWORDS         electron transfer; flavoprotein; FMN
SUMMARY          #length 177  #molecular-weight 19581  #checksum 1188
SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =     33%  Matches          =      3  Mismatches   =      6
Gaps             =      0  Conservative Substitutions               =      0

             X       X
             WXXXLKXXL
             |   ||
   YDLTEERIDSWLEKLKPAVL
   160       170     X


14. US-08-121-713B-33 (1-9)
    RGBY36       cell division control protein CDC36 - yeast (Sacch

ENTRY            RGBY36     #type complete
TITLE            cell division control protein CDC36 - yeast (Saccharomyces
                   cerevisiae)
ALTERNATE_NAMES  start protein CDC36
ORGANISM         #formal_name Saccharomyces cerevisiae
DATE             30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
                   05-May-1994
ACCESSIONS       S12304; A26372
REFERENCE        S05830
   #authors      Barker, D.G.; White, J.H.M.; Johnston, L.H.
   #journal      Nucleic Acids Res. (1985) 13:8323-8337
   #title        The nucleotide sequence of the DNA ligase gene (CDC9) from
                   Saccharomyces cerevisiae: a gene which is cell-cycle
                   regulated and induced in response to DNA damage.
   #cross-references MUID:86093646
   #accession    S12304
      ##molecule_type DNA
      ##residues      1-191 ##label BAR
      ##cross-references EMBL:X03246
REFERENCE        A93635
   #authors      Ferguson, J.; Ho, J.Y.; Peterson, T.A.; Reed, S.I.
   #journal      Nucleic Acids Res. (1986) 14:6681-6697
```



```
   #title        Nucleotide sequence of the yeast cell division cycle start
                   genes CDC28, CDC36, CDC37, and CDC39, and a structural
                   analysis of the predicted products.
   #cross-references MUID:86312926
   #accession    A26372
      ##molecule_type DNA
      ##residues      1-191 ##label FER
      ##cross-references GB:X04287
GENETICS
   #gene         LISTA:CDC36
   #map_position 4L
CLASSIFICATION   #superfamily cell division control protein CDC36
KEYWORDS         cell cycle control
SUMMARY          #length 191  #molecular-weight 22362  #checksum 7370
SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.01
Residue Identity =     33%  Matches          =      3  Mismatches   =      6
Gaps             =      0  Conservative Substitutions               =      0

             X       X
             WXXXLKXXL
                ||  |
   YLELRKRNWRYHKTLKAWLTKDPMMEPIV
  130       140       150


15. US-08-121-713B-33 (1-9)
    PC1136       purF protein - Lactobacillus casei (fragment)

ENTRY            PC1136     #type fragment
TITLE            purF protein - Lactobacillus casei (fragment)
ORGANISM         #formal_name Lactobacillus casei
DATE             30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
                   14-Sep-1994
ACCESSIONS       PC1136; PC2004
REFERENCE        JC1290
   #authors      Gu, Z.M.; Martindale, D.W.; Lee, B.H.
   #journal      Gene (1992) 119:123-126
   #title        Isolation and complete sequence of the purL gene encoding
                   FGAM synthase II in Lactobacillus casei.
   #cross-references MUID:93012962
   #accession    PC1136
      ##molecule_type DNA
      ##residues      1-5,'RLKMKNAGFRC',18-194 ##label GUZ
REFERENCE        JC2024
   #authors      Gu, Z.M.; Martindale, D.W.; Lee, B.H.
   #journal      Gene (1993) 133:147
   #title        Corrigendum: Isolation and complete sequence of the purL gene
                   encoding FGAM synthase II in Lactobacillus casei.
   #accession    PC2004
      ##molecule_type DNA
      ##residues      1-19 ##label GU2
      ##note          this sequence corrects amino terminal sequence errors of
                       purF protein in PC1136
SUMMARY          #length 194  #checksum 5649
SEQUENCE

Initial Score    =      7  Optimized Score  =      9  Significance =  3.01
Residue Identity =     44%  Matches          =      4  Mismatches   =      5
```

```
Gaps            =      0  Conservative Substitutions              =      0

             X       X
             WXXXLKXXL
             |   ||  |
    HLIRRQVGQPWLTQLKTALNEVHGGFAFV
       150   X   160 X     170
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq33spt.res made by  on Fri 19 May 95 9:01:55-PDT.


Query sequence being compared:US-08-121-713B-33 (1-9)
Number of sequences searched:                43470
Number of scores above cutoff:                4864

     Results of the initial comparison of US-08-121-713B-33 (1-9) with:
   Data bank : Swiss-Prot 31, all entries

100000-
      -
N     -
U50000-
M     -
B     -                          *
E     -
R     -
      -
O     -
F10000-              *
      -
S     *
E 5000-
Q     -
U     -
E     -
N     -
C     -                                  *
E     -
S 1000-
      -
      -
   500-
      -
      -
      -                                        *
      -
      -
      -
   100-
      -
      -
    50-
      -
      -
```



```
      -
      -
      -
      -
    10-
      -
      -
     5-
      -
      -
      -
      -
      -
      -
      -                                                              *
      0-------------------------------------------------------------------
       ||     |     ||    ||    |     ||    ||    |     |     |
SCORE 0|     1     2|    3|    4     5|    6|    7     8     9
STDEV -1           0     1           2     3
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	3	5	1.49

Times:	CPU	Total Elapsed
	00:00:45.00	00:00:45.00

Number of residues: 15335248
Number of sequences searched: 43470
Number of scores above cutoff: 4864

Cut-off raised to 2.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% similar sequence to the query sequence was found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. PLSX_ECOLI	PLSX PROTEIN.	346	9	9	4.04	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 2 standard deviations above mean ****					
2. ARRE_RAT	ARRESTIN-E (FRAGMENT).	72	7	7	2.69	0
3. RPOD_GALSU	DNA-DIRECTED RNA POLYMERASE B	85	7	7	2.69	0
4. Y11K_PASVK	HYPOTHETICAL 11.9 KD PROTEIN	108	7	7	2.69	0
5. TRJ6_ECOLI	TRAJ PROTEIN (RELAXOSOME PROT	122	7	7	2.69	0
6. SAA3_RABIT	RABBIT SERUM AMYLOID A (SAA3)	122	7	7	2.69	0
7. SAA3_HUMAN	SERUM AMYLOID A-3 PROTEIN PRE	122	7	7	2.69	0
8. YDP1_SULSO	HYPOTHETICAL 14.7 KD PROTEIN	126	7	7	2.69	0
9. CYT_CYPCA	CYSTATIN PRECURSOR.	129	7	7	2.69	0
10. TRJ5_ECOLI	TRAJ PROTEIN.	130	7	7	2.69	0
11. YZZI_ECOLI	HYPOTHETICAL 15.2 KD PROTEIN	137	7	7	2.69	0
12. YR65_SCHPO	HYPOTHETICAL 15.8 KD PROTEIN	137	7	7	2.69	0
13. FECI_ECOLI	PROBABLE RNA POLYMERASE SIGMA	173	7	7	2.69	0
14. YBW6_YEAST	VERY HYPOTHETICAL 20.2 KD PRO	175	7	7	2.69	0
15. FLAV_ENTAG	FLAVODOXIN.	177	7	7	2.69	0
16. NOT2_YEAST	GENERAL NEGATIVE REGULATOR OF	191	7	7	2.69	0
17. PUR1_LACCA	AMIDOPHOSPHORIBOSYLTRANSFERAS	193	7	9	2.69	0
18. REPY_STAAU	REPLICATION PROTEIN.	199	7	7	2.69	0
19. FIMB_ECOLI	TYPE 1 FIMBRIAE REGULATORY PR	200	7	7	2.69	0
20. YSY2_SYNP7	HYPOTHETICAL 23.0 KD PROTEIN	208	7	7	2.69	0
21. ARA1_ARATH	RAS-RELATED PROTEIN ARA-1.	218	7	7	2.69	0
22. PIGF_HUMAN	PHOSPHATIDYLINOSITOL-GLYCAN B	219	7	7	2.69	0
23. PRT1_HANPO	PUTATIVE PRT1 PROTEIN.	220	7	7	2.69	0
24. ATP6_BACCA	ATP SYNTHASE A CHAIN (EC 3.6.	237	7	7	2.69	0
25. RM08_YEAST	MITOCHONDRIAL 60S RIBOSOMAL P	238	7	7	2.69	0
26. ATP6_THEP3	ATP SYNTHASE A CHAIN (EC 3.6.	238	7	7	2.69	0
27. ARTQ_ECOLI	ARGININE TRANSPORT SYSTEM PER	238	7	7	2.69	0
28. FCEB_HUMAN	HIGH AFFINITY IMMUNOGLOBULIN	244	7	7	2.69	0
29. YN70_YEAST	HYPOTHETICAL 27.5 KD PROTEIN	246	7	7	2.69	0
30. TRPC_SULSO	INDOLE-3-GLYCEROL PHOSPHATE S	248	7	7	2.69	0
31. YAFD_ECOLI	HYPOTHETICAL 29.1 KD PROTEIN	259	7	7	2.69	0
32. TERM_BPPRD	DNA TERMINAL PROTEIN (PROTEIN	259	7	7	2.69	0
33. YPQQ_KLEPN	HYPOTHETICAL PROTEIN IN PQQA	271	7	7	2.69	0
34. ARGB_PORUM	ACETYLGLUTAMATE KINASE (EC 2.	283	7	7	2.69	0
35. YIJE_ECOLI	HYPOTHETICAL 34.1 KD PROTEIN	312	7	7	2.69	0
36. A2GL_HUMAN	LEUCINE-RICH ALPHA-2-GLYCOPRO	312	7	7	2.69	0
37. YO85_CAEEL	HYPOTHETICAL 35.7 KD PROTEIN	313	7	7	2.69	0
38. REPA_NEIGO	REPLICATION PROTEIN.	328	7	7	2.69	0
39. FBP_NEIME	MAJOR FERRIC IRON BINDING PRO	330	7	7	2.69	0
40. FBP_NEIGO	MAJOR FERRIC IRON BINDING PRO	330	7	7	2.69	0
41. COXZ_THEP3	CYTOCHROME C OXIDASE POLYPEPT	356	7	7	2.69	0
42. AROG_BACSU	PHOSPHO-2-DEHYDRO-3-DEOXYHEPT	358	7	7	2.69	0
43. WNT2_MOUSE	WNT-2 PROTEIN PRECURSOR (IRP	360	7	7	2.69	0
44. WNT2_HUMAN	WNT-2 PROTEIN PRECURSOR (IRP	360	7	7	2.69	0
45. CD14_MOUSE	MONOCYTE DIFFERENTIATION ANTI	366	7	7	2.69	0

1. US-08-121-713B-33 (1-9)
   PLSX_ECOLI PLSX PROTEIN.

```
ID   PLSX_ECOLI      STANDARD;      PRT;   346 AA.
AC   P27247;
DT   01-AUG-1992 (REL. 23, CREATED)
DT   01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT   01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE   PLSX PROTEIN.
GN   PLSX.
OS   ESCHERICHIA COLI.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   ENTEROBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RM   93077479
RA   OH W., LARSON T.J.;
RL   J. BACTERIOL. 174:7873-7874(1992).
CC   -!- FUNCTION: NOT KNOWN, PROBABLY INVOLVED IN FATTY ACID OR
CC       PHOSPHOLIPID SYNTHESIS.
DR   EMBL; M96793; ECPLSFABA.
DR   ECOGENE; EG11437; PLSX.
KW   FATTY ACID BIOSYNTHESIS; PHOSPHOLIPID BIOSYNTHESIS.
SQ   SEQUENCE   346 AA;  37100 MW;  592849 CN;

Initial Score    =      9  Optimized Score  =      9  Significance =  4.04
Residue Identity =    44%  Matches          =      4  Mismatches   =     5
Gaps             =      0  Conservative Substitutions              =     0

             X       X
             WXXXLKXXL
             |   ||  |
    SQGEGKKRSWWLLLLKRWLQKSLTRRFSH
      250    X  260  X    270


2. US-08-121-713B-33 (1-9)
   ARRE_RAT     ARRESTIN-E (FRAGMENT).

ID   ARRE_RAT        STANDARD;      PRT;    72 AA.
AC   P37200;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   ARRESTIN-E (FRAGMENT).
GN   EAR.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=PINEAL GLAND;
RM   94140898
RA   CRAFT C.M., WHITMORE D.H., WIECHMANN A.F.;
RL   J. BIOL. CHEM. 269:4613-4619(1994).
CC   -!- TISSUE SPECIFICITY: ADRENAL, CEREBRAL CORTEX, HEART, HYPOTHALAMUS,
CC       INTESTINE, LIVER, LUNG, PITUITARY, RETINA, TESTIS.
CC   -!- SIMILARITY: SIMILARITY IN THE C-TERMINAL WITH ALPHA-TRANSDUCIN
CC       AND OTHER PURINE NUCLEOTIDE-BINDING PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE ARRESTIN FAMILY.
DR   EMBL; U03630; RR03630.
KW   SENSORY TRANSDUCTION.
FT   NON_TER       1       1
SQ   SEQUENCE   72 AA;  8132 MW;  28630 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0
```

```
            X       X
            WXXXLKXXL
            |   ||
   DTNLHISSQCWLKCLKNSKHNVVISSRGG
       10    X   20  X     30
```

3. US-08-121-713B-33 (1-9)
   RPOD_GALSU DNA-DIRECTED RNA POLYMERASE BETA" CHAIN (EC 2.7.7.

```
ID   RPOD_GALSU     STANDARD;      PRT;    85 AA.
AC   P35018;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   DNA-DIRECTED RNA POLYMERASE BETA" CHAIN (EC 2.7.7.6) (FRAGMENT).
GN   RPOC2.
OS   GALDIERIA SULPHURARIA (CYANIDIUM CALDARIUM).
OG   CHLOROPLAST.
OC   EUKARYOTA; PLANTA; PHYCOPHYTA; RHODOPHYTA (RED ALGAE).
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=14-1-1 / ISOLATE 107.79/GOETTINGEN;
RM   94033298
RA   KOSTRZEWA M., ZETSCHE K.;
RL   PLANT MOL. BIOL. 23:67-76(1993).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES.
CC   -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
CC       RNA(N).
CC   -!- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC       SUBUNITS: ALPHA, BETA, BETA', AND BETA".
DR   EMBL; X67814; GSPLSSEQ.
DR   PIR; S39512; S39512.
KW   TRANSCRIPTION; DNA-DIRECTED RNA POLYMERASE; CHLOROPLAST.
FT   NON_TER       1      1
SQ   SEQUENCE   85 AA;  10114 MW;  34876 CN;
```

```
Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0
```

```
            X       X
            WXXXLKXXL
            |   ||
    TKAAFENHIDWLKGLKENVIIGRLIPAGT
  10        20        30
```

4. US-08-121-713B-33 (1-9)
   Y11K_PASVK HYPOTHETICAL 11.9 KD PROTEIN (ORF VI).

```
ID   Y11K_PASVK     STANDARD;      PRT;    108 AA.
AC   Q00336;
DT   01-DEC-1992 (REL. 24, CREATED)
DT   01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 11.9 KD PROTEIN (ORF VI).
```



```
OS   PANICUM STREAK VIRUS (KENYAN ISOLATE).
OC   VIRIDAE; SS-DNA NONENVELOPED VIRUSES; GEMINIVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   92268861
RA   BRIDDON R.W., LUNNESS P., CHAMBERLAIN L.C., BRUNDISH H.,
RA   PINNER M.S., MARKHAM P.G.;
RL   J. GEN. VIROL. 73:1041-1047(1992).
DR   EMBL; X60168; PSGIITDNA.
DR   PIR; JQ1549; JQ1549.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   108 AA;  11866 MW;  63187 CN;
```

```
Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0
```

```
            X       X
            WXXXLKXXL
            |   ||
   FVSVLALYLLWLWVLKDCILLLKAQRGRS
          50        60
```

5. US-08-121-713B-33 (1-9)
   TRJ6_ECOLI TRAJ PROTEIN (RELAXOSOME PROTEIN).

```
ID   TRJ6_ECOLI     STANDARD;      PRT;   122 AA.
AC   P17909;
DT   01-NOV-1990 (REL. 16, CREATED)
DT   01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT   01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE   TRAJ PROTEIN (RELAXOSOME PROTEIN).
GN   TRAJ.
OS   ESCHERICHIA COLI.
OG   PLASMID INCP-BETA RP4.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   ENTEROBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-5 AND 118-122.
RM   89308605
RA   ZIEGELIN G., FUERSTE J.P., LANKA E.;
RL   J. BIOL. CHEM. 264:11989-11994(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HB101;
RM   92190548
RA   ZIEGELIN G., PANSEGRAU W., STRACK B., BALZER D., KROEGER M., KRUFT V.,
RA   LANKA E.;
RL   DNA SEQ. 1:303-327(1991).
RN   [3]
RP   SEQUENCE OF 1-7 FROM N.A.
RM   89184510
RA   LANKA E., FUERSTE J.P.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 86:1771-1775(1989).
CC   -!- FUNCTION: TRANSFER OF PLASMID RP4 DURING BACTERIAL CONJUGATION
CC       REQUIRES THE PLASMID-ENCODED TRAJ PROTEIN, WHICH BINDS TO A 19-
CC       BASE PAIR INVERT SEQUENCE REPETITION WITHIN THE TRANSFER ORIGIN.
CC       TRAJ PROTEIN IS BOUND TO ONLY ONE SIDE OF THE DNA HELIX. THIS
CC       NUCLEOPROTEIN STRUCTURE IS THE INITIAL COMPLEX IN THE PATHWAY TO
```

```
CC       ASSEMBLE A FUNCTIONAL RELAXOSOME.
CC   -!- SUBUNIT: MONOMER.
DR   EMBL; J04942; PRTRAJ.
DR   EMBL; X54459; ECRP4.
DR   EMBL; M25423; PRTRAB.
DR   PIR; A34172; A34172.
DR   PIR; S23002; S23002.
KW   CONJUGATION; DNA-BINDING; PLASMID.
FT   INIT_MET      0       0
SQ   SEQUENCE   122 AA;  13332 MW;  70495 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
                ||  |
    LARINGDLGRLGGLLKLWLTDDPRTARFG
          70 X      80        90
```

6. US-08-121-713B-33 (1-9)
   SAA3_RABIT   RABBIT SERUM AMYLOID A (SAA3) MRNA, COMPLETE CDS.

```
ID   SAA3_RABIT     STANDARD;      PRT;   122 AA.
AC   P35543;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   RABBIT SERUM AMYLOID A (SAA3) MRNA, COMPLETE CDS.
GN   SAA3.
OS   ORYCTOLAGUS CUNICULUS (RABBIT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; LAGOMORPHA.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   91185595
RA   MITCHELL T.I., COON C.I., BRINCKERHOFF C.E.;
RL   J. CLIN. INVEST. 87:1177-1185(1991).
CC   -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC       COMPLEX.
CC   -!- INDUCTION: UPON CYTOKINE STIMULATION.
CC   -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC   -!- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC       EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC       THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC       THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC   -!- SIMILARITY: TO OTHER MAMMALIAN SAAS.
DR   EMBL; M64696; OCSAA3.
DR   PIR; S32574; S32574.
DR   PROSITE; PS00992; SAA.
KW   ACUTE PHASE; PLASMA; HDL; AMYLOID; SIGNAL; MULTIGENE FAMILY.
FT   SIGNAL        1     18       BY SIMILARITY.
FT   CHAIN        19    122       SERUM AMYLOID A-3 PROTEIN.
SQ   SEQUENCE   122 AA;  13806 MW;  64764 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0
```



```
             X       X
             WXXXLKXXL
             |   ||
    FLILGVNSREWLTFLKEAGQGAKDMWRAY
          20        30
```

7. US-08-121-713B-33 (1-9)
   SAA3_HUMAN   SERUM AMYLOID A-3 PROTEIN PRECURSOR.

```
ID   SAA3_HUMAN     STANDARD;      PRT;   122 AA.
AC   P22614;
DT   01-AUG-1991 (REL. 19, CREATED)
DT   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   SERUM AMYLOID A-3 PROTEIN PRECURSOR.
GN   SAA3.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   90128298
RA   SACK G.H. JR., TALBOT C.C. JR.;
RL   GENE 84:509-515(1989).
CC   -!- FUNCTION: PROBABLY A PSEUDOGENE.
CC   -!- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC       EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC       THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC       THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC   -!- SIMILARITY: TO OTHER MAMMALIAN SAAS.
DR   EMBL; X13895; HSSAA1A.
DR   PIR; JN0029; JN0029.
DR   PROSITE; PS00992; SAA.
KW   ACUTE PHASE; PLASMA; HDL; AMYLOID; SIGNAL; MULTIGENE FAMILY.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    122       SERUM AMYLOID A-3 PROTEIN.
SQ   SEQUENCE   122 AA;  13440 MW;  70025 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
             |   ||
    SLVLGVSSQGWLTFLKAAGQGAKDMWRAY
          20        30
```

8. US-08-121-713B-33 (1-9)
   YDP1_SULSO   HYPOTHETICAL 14.7 KD PROTEIN IN DPA 5'REGION (ORF

```
ID   YDP1_SULSO     STANDARD;      PRT;   126 AA.
AC   P27339;
DT   01-AUG-1992 (REL. 23, CREATED)
DT   01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 14.7 KD PROTEIN IN DPA 5'REGION (ORF 1) (AO3).
```

```
 OS   SULFOLOBUS SOLFATARICUS.
 OC   PROKARYOTA; MENDOSICUTES; ARCHAEBACTERIA; SULFOLOBALES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=DSM 1616 / P1;
 RM   92048486
 RA   RAMIREZ C., MATHESON A.T.;
 RL   MOL. MICROBIOL. 5:1687-1693(1991).
 DR   EMBL; X58538; SSDOCK.
 DR   PIR; S14845; S14845.
 DR   PIR; S16481; S16481.
 KW   HYPOTHETICAL PROTEIN.
 SQ   SEQUENCE   126 AA;  14744 MW;  87526 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0

             X       X
             WXXXLKXXL
             |   ||
    RKFWMIESNSWLKYLKIYKVNYLSQ
          110 X     120
```

9. US-08-121-713B-33 (1-9)
   CYT_CYPCA   CYSTATIN PRECURSOR.

```
 ID   CYT_CYPCA      STANDARD;      PRT;   129 AA.
 AC   P35481;
 DT   01-JUN-1994 (REL. 29, CREATED)
 DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE   CYSTATIN PRECURSOR.
 OS   CYPRINUS CARPIO (COMMON CARP).
 OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
 OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   TISSUE=OVARY;
 RA   TSAI Y., HUANG F.L.;
 RL   SUBMITTED (XXX-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
 CC   -!- FUNCTION: CYSTEINE PROTEINASE INHIBITOR.
 CC   -!- SIMILARITY: THIS IS A TYPE 2 CYSTATIN.
 DR   EMBL; L23572; CCCYST.
 DR   HSSP; P01038; 1CEW.
 DR   PROSITE; PS00287; CYSTATIN.
 KW   THIOL PROTEASE INHIBITOR; SIGNAL.
 FT   SIGNAL        1      ?       POTENTIAL.
 FT   CHAIN         ?    129       CYSTATIN.
 FT   ACT_SITE     23     23       REACTIVE SITE (BY SIMILARITY).
 FT   SITE         67     71       SECONDARY AREA OF CONTACT.
 FT   DISULFID     85     94       BY SIMILARITY.
 FT   DISULFID    108    128       BY SIMILARITY.
 SQ   SEQUENCE   129 AA;  14236 MW;  95323 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0
```



```
             X       X
             WXXXLKXXL
             |   ||
    QCKITVWSQPWLNSLKVTENTCM
     110       120    X
```

10. US-08-121-713B-33 (1-9)
    TRJ5_ECOLI   TRAJ PROTEIN.

```
 ID   TRJ5_ECOLI     STANDARD;      PRT;   130 AA.
 AC   P17907;
 DT   01-NOV-1990 (REL. 16, CREATED)
 DT   01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE   TRAJ PROTEIN.
 GN   TRAJ.
 OS   ESCHERICHIA COLI.
 OG   PLASMID INCP-BETA R751.
 OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC   ENTEROBACTERIACEAE.
 RN   [1]
 RP   SEQUENCE FROM N.A.
 RC   STRAIN=HB101;
 RM   92190548
 RA   ZIEGELIN G., PANSEGRAU W., STRACK B., BALZER D., KROEGER M.,
 RA   KRUFT V., LANKA E.;
 RL   DNA SEQ. 1:303-327(1991).
 RN   [2]
 RP   SEQUENCE OF 1-16 FROM N.A.
 RM   89184510
 RA   LANKA E., FUERSTE J.P.;
 RL   PROC. NATL. ACAD. SCI. U.S.A. 86:1771-1775(1989).
 CC   -!- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR POSITIVELY REGULATING THE
 CC       EXPRESSION OF TRANSFER GENES THAT ARE INVOLVED IN THE CONJUGAL
 CC       TRANSFER OF DNA BETWEEN BACTERIAL CELLS.
 CC   -!- SUBCELLULAR LOCATION: OUTER MEMBRANE.
 DR   EMBL; X54458; ECR751.
 DR   EMBL; M25422; PR1TRA.
 DR   PIR; S22996; S22996.
 KW   OUTER MEMBRANE; CONJUGATION; TRANSCRIPTION REGULATION; ACTIVATOR;
 KW   PLASMID.
 SQ   SEQUENCE   130 AA;  14392 MW;  79743 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0

             X       X
             WXXXLKXXL
                ||  |
    LVRVNGDLGRLGGLLKLWLTDDVRTLQFG
   70        80        90
```

11. US-08-121-713B-33 (1-9)
    YZZI_ECOLI   HYPOTHETICAL 15.2 KD PROTEIN IN ICC 3'REGION.

```
 ID   YZZI_ECOLI     STANDARD;      PRT;   137 AA.
 AC   P36653;
```

```
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 15.2 KD PROTEIN IN ICC 3'REGION.
GN   YZZI.
OS   ESCHERICHIA COLI.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   ENTEROBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RA   IMAMURA R., NIKI H., YAMANAKA K., OGURA T., FUJITA N., ISHIHAMA A.,
RA   HIRAGA S.;
RL   SUBMITTED (JUN-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; D16557; ECICC.
DR   ECOGENE; EG12186; YZZI.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   137 AA;  15256 MW;  102300 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
                ||  |
    HGFNSSPRSAKASLLKNWLAEHHPDVEMI
     10        20     X  30
```

12. US-08-121-713B-33 (1-9)
    YR65_SCHPO   HYPOTHETICAL 15.8 KD PROTEIN IN REC6 5'REGION (ORF

```
ID   YR65_SCHPO     STANDARD;      PRT;   137 AA.
AC   P40922;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 15.8 KD PROTEIN IN REC6 5'REGION (ORF137).
OS   SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RM   94274029
RA   LIN Y., SMITH G.R.;
RL   GENETICS 136:769-779(1994).
DR   EMBL; L14773; SPREC6A.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   137 AA;  15776 MW;  107988 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
                ||  |
    KPIKLSLSSNSTPLLKLWLLVAVTWVVLV
    10        20      X 30
```


13. US-08-121-713B-33 (1-9)
    FECI_ECOLI   PROBABLE RNA POLYMERASE SIGMA FACTOR FECI.

```
ID   FECI_ECOLI     STANDARD;      PRT;   173 AA.
AC   P23484;
DT   01-NOV-1991 (REL. 20, CREATED)
DT   01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   PROBABLE RNA POLYMERASE SIGMA FACTOR FECI.
GN   FECI.
OS   ESCHERICHIA COLI.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   ENTEROBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RM   91072220
RA   VAN HOVE B., STAUDENMAIER H., BRAUN V.;
RL   J. BACTERIOL. 172:6749-6758(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RA   BURLAND V.D., PLUNKETT G. III, BLATTNER F.R.;
RL   SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [3]
RP   SIMILARITY TO OTHER ECF SIGMA FACTORS.
RM   94329558
RA   LONETTO M.A., BROWN K.L., RUDD K.E., BUTTNER M.J.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 91:7573-7577(1994).
CC   -!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
CC       ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
CC       THEN IS RELEASED. THIS SIGMA FACTOR REGULATES THE FEC GENES FOR
CC       IRON DICITRATE TRANSPORT (PROBABLE).
CC   -!- SIMILARITY: TO OTHER SIGMA FACTORS THAT DO NOT BELONG TO THE
CC       SIGMA-54 FAMILY. BELONGS TO THE ECF SUBFAMILY.
DR   EMBL; M63115; ECFECIR.
DR   EMBL; U14003; ECUW93.
DR   PIR; JV0111; JV0111.
DR   ECOGENE; EG10291; FECI.
KW   TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
KW   DNA-BINDING; IRON TRANSPORT; TRANSPORT.
FT   DOMAIN       40     52       POLYMERASE CORE BINDING (POTENTIAL).
FT   DNA_BIND    139    158       H-T-H MOTIF (BY SIMILARITY).
SQ   SEQUENCE   173 AA;  19480 MW;  155597 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =    33%  Matches          =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions               =     0

             X       X
             WXXXLKXXL
                ||  |
    SLTFESLYGTHHGWLKSWLTRKLQSAFDA
   10        20        30
```

14. US-08-121-713B-33 (1-9)
    YBW6_YEAST   VERY HYPOTHETICAL 20.2 KD PROTEIN IN LYS2-TKL2 INT

```
ID   YBW6_YEAST     STANDARD;      PRT;   175 AA.
AC   P38268;
DT   01-OCT-1994 (REL. 30, CREATED)
DT   01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT   01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE   VERY HYPOTHETICAL 20.2 KD PROTEIN IN LYS2-TKL2 INTERGENIC REGION.
GN   YBR116C OR YBR0911.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C;
RA   MANNHAUPT G., STUCKA R., EHNLE S., VETTER I., FELDMANN H.;
RL   SUBMITTED (APR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; X78993; SCRACII.
DR   EMBL; Z35985; SCYBR116C.
DR   PIR; S44695; S44695.
KW   HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
FT   TRANSMEM    143    166       POTENTIAL.
SQ   SEQUENCE   175 AA;  20215 MW;  175283 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =     33%  Matches         =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0

             X       X
             WXXXLKXXL
                ||  |
    TDSLFYQTVFRSCPLKYWLLQAGVSMLIN
           40 X      50        60
```

15. US-08-121-713B-33 (1-9)
    FLAV_ENTAG   FLAVODOXIN.

```
ID   FLAV_ENTAG     STANDARD;      PRT;   177 AA.
AC   P28579;
DT   01-DEC-1992 (REL. 24, CREATED)
DT   01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT   01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE   FLAVODOXIN.
GN   NIFF.
OS   ENTEROBACTER AGGLOMERANS.
OG   PLASMID PEA3.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   ENTEROBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=333;
RM   91217003
RA   KREUTZER R., DAYANANDA S., KLINGMUELLER W.;
RL   J. BACTERIOL. 173:3252-3256(1991).
CC   -!- FUNCTION: ELECTRON-TRANSFER PROTEINS THAT FUNCTION IN VARIOUS
CC       ELECTRON TRANSPORT SYSTEMS IN MICRO-ORGANISMS. FUNCTIONALLY
CC       INTERCHANGEABLE WITH FERREDOXIN.
CC   -!- COFACTOR: FMN.
DR   EMBL; M38221; PPNIFF.
DR   PIR; A39414; A39414.
DR   HSSP; P10340; 1OFV.
DR   PROSITE; PS00201; FLAVODOXIN.
```



```
KW   NITROGEN FIXATION; ELECTRON TRANSPORT; FLAVOPROTEIN; FMN; PLASMID.
SQ   SEQUENCE   177 AA;  19581 MW;  159879 CN;

Initial Score    =      7  Optimized Score  =      7  Significance =  2.69
Residue Identity =     33%  Matches         =      3  Mismatches   =     6
Gaps             =      0  Conservative Substitutions              =     0

             X       X
             WXXXLKXXL
             |   ||
    YDLTEERIDSWLEKLKPAVL
    160      170     X
```

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Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

> O <
O| |O IntelliGenetics
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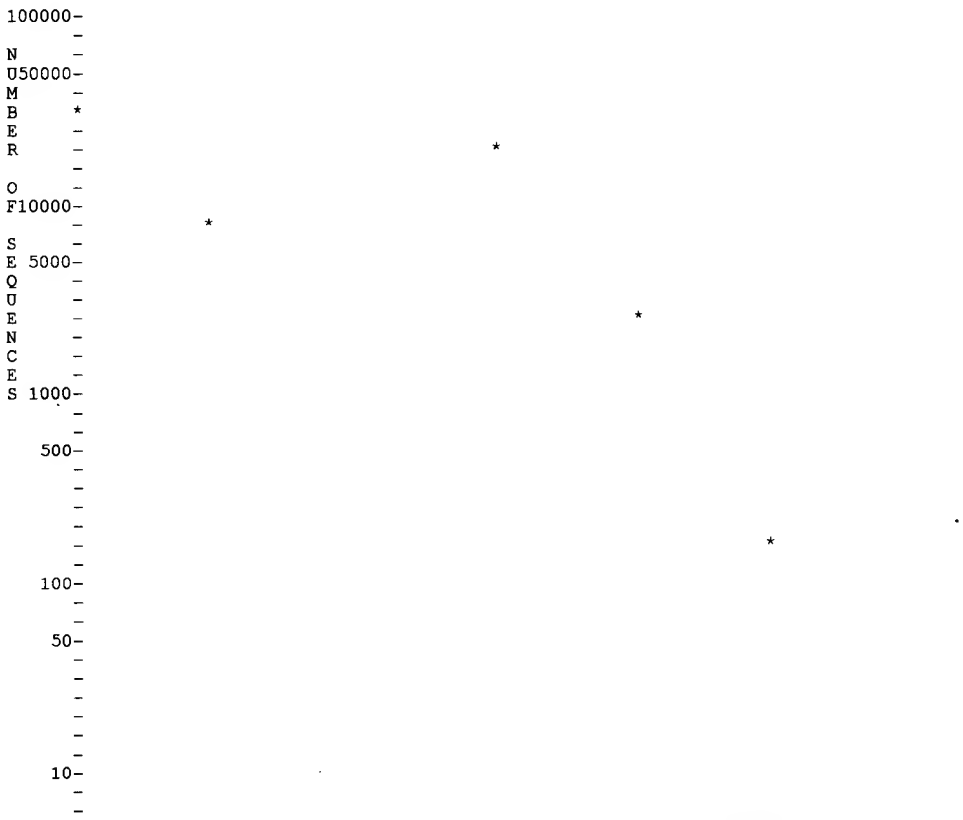
SEQ 43

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

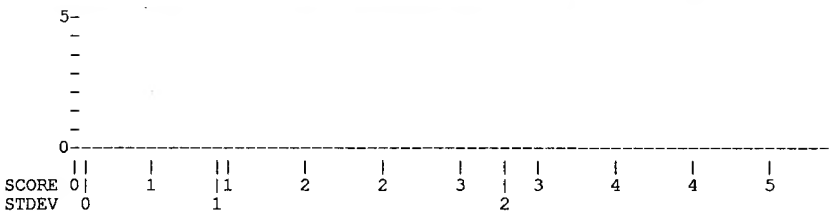
Results file sq43asq.res made by on Fri 19 May 95 8:43:41-PDT.

Query sequence being compared:US-08-121-713B-43 (1-8)
Number of sequences searched: 53402
Number of scores above cutoff: 3795

Results of the initial comparison of US-08-121-713B-43 (1-8) with:
Data bank : A-GeneSeq 18, all entries



Data 121713



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1	2	1.48

Times:	CPU	Total Elapsed
	00:00:31.08	00:00:32.00

Number of residues: 6354270
Number of sequences searched: 53402
Number of scores above cutoff: 3795

Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 2 standard deviations above mean ****					
1. R60334	Blood coagulation inhibiting	5	5	5	2.70	0
2. R15722	Anticoagulant (5).	5	5	5	2.70	0
3. R15730	Anticoagulant (13).	6	5	5	2.70	0
4. R26436	N-terminal auxiliary sequence	8	5	5	2.70	0
5. R26440	N-terminal auxiliary sequence	14	5	5	2.70	0
6. R11153	Hirulog-13.	18	5	5	2.70	0
7. R56242	Fibronectin-derived peptide.	19	5	7	2.70	0

8.	R26193	D-Cha/D-Npa Hirulog-8.	20	5	5	2.70	0
9.	R26192	Hirulog-8.	20	5	5	2.70	0
10.	R26395	Sequence of platelet binding	20	5	5	2.70	0
11.	R11163	Hirulog-27.	20	5	5	2.70	0
12.	R11164	Hirulog-28.	20	5	5	2.70	0
13.	R11158	Hirulog-18b.	20	5	5	2.70	0
14.	R11151	Hirulog-8.	20	5	5	2.70	0
15.	P71352	Synthetic peptide encoding ra	21	5	5	2.70	0
16.	R11156	Hirulog-17.	22	5	5	2.70	0
17.	R11154	Hirulog-15.	22	5	5	2.70	0
18.	R11161	Hirulog-21.	23	5	5	2.70	0
19.	R54698	Cys-7 hirulog derivative - an	24	5	7	2.70	0
20.	R54697	Native hirulog - anticoagulan	24	5	5	2.70	0
21.	R11155	Hirulog-15.	24	5	5	2.70	0
22.	R54699	Cys-20 hirulog derivative - a	25	5	5	2.70	0
23.	R21422	Matrix peptide from bovine te	31	5	5	2.70	0
24.	R05850	Factor VII peptide analogue.	39	5	5	2.70	0
25.	R28993	Encoded by human Gs-alpha com	83	5	5	2.70	0
26.	R51358	Metastasis inhibiting peptide	90	5	7	2.70	0
27.	R25382	Bifunctional inhibitor of pla	96	5	5	2.70	0
28.	R28707	Bifunctional inhibitor of pla	96	5	5	2.70	0
29.	R25151	Bifunctional inhibitor of pla	96	5	5	2.70	0
30.	R28703	Bifunctional inhibitor of pla	96	5	5	2.70	0
31.	R25147	Bifunctional inhibitor of pla	96	5	5	2.70	0
32.	R28708	Bifunctional inhibitor of pla	97	5	5	2.70	0
33.	R28706	Bifunctional inhibitor of pla	97	5	5	2.70	0
34.	R28705	Bifunctional inhibitor of pla	97	5	5	2.70	0
35.	R28704	Bifunctional inhibitor of pla	97	5	5	2.70	0
36.	R13342	NANBH-derived clone GORS22 pr	97	5	5	2.70	0
37.	R25154	Bifunctional inhibitor of pla	98	5	5	2.70	0
38.	R25150	Bifunctional inhibitor of pla	98	5	5	2.70	0
39.	R25153	Bifunctional inhibitor of pla	99	5	5	2.70	0
40.	R25149	Bifunctional inhibitor of pla	99	5	5	2.70	0
41.	R25152	Bifunctional inhibitor of pla	106	5	5	2.70	0
42.	R25148	Bifunctional inhibitor of pla	106	5	5	2.70	0
43.	R07997	Human CD2 cytoplasmic domain.	117	5	5	2.70	0
44.	R47503	Protein derived from G-CSF st	165	5	5	2.70	0
45.	P70247	AA sequence (VII) of a polype	191	5	5	2.70	0

1. US-08-121-713B-43 (1-8)
R60334 Blood coagulation inhibiting peptide.

ID R60334 standard; peptide; 5 AA.
AC R60334;
DT 07-MAR-1995 (first entry)
DE Blood coagulation inhibiting peptide.
KW Blood; fibrin; coagulation; inhibition; thrombin; fibrinogen.
OS Synthetic.
PN J06179696-A.
PD 28-JUN-1994.
PF 19-MAR-1993; 085678.
PR 13-OCT-1992; JP-300380.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (NIHA-) NIPPON HAM KK.
DR WPI; 94-245692/30.
PT New blood coagulation inhibiting peptide(s) having
PT fibrin-agglutination inhibitory activity - useful for the
PT treatment and prevention of thrombosis
PS Claim 1; Page 2; 6pp; Japanese.

CC The blood coagulation inhibiting peptide conprises L-form amino
CC acids and has fibrin agglutination inhibiting activity. Such
CC peptides (see R60327-R60335) were synthesised using a peptide
CC synthesiser (Applied Biosystems Co., 430A) and purified by high
CC pressure liquid chromatography. To 0.2 ml of fibrinogen solution
CC (2.5 mg/ml), 0.2 ml of test peptide solution was added and incubated
CC for 1 minute at 37 deg. Celsius. 0.2 ml of thrombin solution was
CC added and the IC50 was determined according to the method of
CC Kawasaki et al. This peptide had an IC50 of 65 micromolar compared
CC with a control peptide of Gly-Pro-Arg which registered an IC50 of
CC 250 micromolar.
SQ Sequence 5 AA;
SQ 0 A; 1 R; 0 N; 0 D; 0 B; 0 C; 0 Q; 0 E; 0 Z; 2 G; 0 H;
SQ 0 I; 0 L; 0 K; 0 M; 0 F; 2 P; 0 S; 0 T; 0 W; 0 Y; 0 V;

Initial Score = 5 Optimized Score = 5 Significance = 2.70
Residue Identity = 80% Matches = 4 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

```
     X   X
    PXPRPGXC
      ||||
     GPRPG
     X   X
```

2. US-08-121-713B-43 (1-8)
R15722 Anticoagulant (5).

ID R15722 standard; Protein; 5 AA.
AC R15722;
DT 24-JAN-1992 (first entry)
DE Anticoagulant (5).
KW Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc_difference 5
FT /label= G-NH2, G-NH(Ethyl), G-NH(Ethyl)2,
FT G-NH(Butyl)
PN EP-456152-A.
PD 13-NOV-1991.
PF 06-MAY-1991; 107307.
PR 08-MAY-1990; DE-014655.
PA (BEHW) BEHRINGWERKE AG.
PI Stuber W, Fickenscher K;
DR WPI; 91-334142/46.
PT New anticoagulant penta- and hexa:peptide(s) - are
PT Glycine-Proline-Arginine-Proline amino acid derivs. which inhibit
PT agglomeration of fibrin chains but not thrombin
PS Claim 5; Page 8; 8pp; German.
CC The peptides represented in R15718-33 are anticoagulants which are
CC more effective than previously known chemically similar cpds. They
CC can be used for therapeutic and diagnostic purposes.
SQ Sequence 5 AA;
SQ 0 A; 1 R; 0 N; 0 D; 0 B; 0 C; 0 Q; 0 E; 0 Z; 2 G; 0 H;
SQ 0 I; 0 L; 0 K; 0 M; 0 F; 2 P; 0 S; 0 T; 0 W; 0 Y; 0 V;

Initial Score = 5 Optimized Score = 5 Significance = 2.70
Residue Identity = 80% Matches = 4 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

```
     X   X
    PXPRPGXC
      ||||
     GPRPG
     X   X
```

3. US-08-121-713B-43 (1-8)
R15730 Anticoagulant (13).

```
ID   R15730 standard; Protein; 6 AA.
AC   R15730;
DT   24-JAN-1992  (first entry)
DE   Anticoagulant (13).
KW   Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Misc_difference 6
FT   /label= P-NH2, P-NH(Isopropyl)
PN   EP-456152-A.
PD   13-NOV-1991.
PF   06-MAY-1991; 107307.
PR   08-MAY-1990; DE-014655.
PA   (BEHW ) BEHRINGWERKE AG.
PI   Stuber W, Fickenscher K;
DR   WPI; 91-334142/46.
PT   New anticoagulant penta- and hexa:peptide(s) - are
PT   Glycine-Proline-Arginine-Proline amino acid derivs. which inhibit
PT   agglomeration of fibrin chains but not thrombin
PS   Claim 5; Page 8; 8pp; German.
CC   The peptides represented in R15718-33 are anticoagulants which are
CC   more effective than previously known chemically similar cpds.  They
CC   can be used for therapeutic and diagnostic purposes.
SQ   Sequence   6 AA;
SQ   0  A; 1  R; 0  N; 0  D; 0  B; 0  C; 0  Q; 0  E; 0  Z; 3  G; 0  H;
SQ   0  I; 0  L; 0  K; 0  M; 0  F; 2  P; 0  S; 0  T; 0  W; 0  Y; 0  V;
```

Initial Score	=	5	Optimized Score	=	5	Significance =	2.70
Residue Identity	=	66%	Matches	=	4	Mismatches =	2
Gaps	=	0	Conservative Substitutions			=	0

```
     X    X
    PXPRPGXC
      ||||
     GPRPGG
     X    X
```

4. US-08-121-713B-43 (1-8)
R26436 N-terminal auxiliary sequence.

```
ID   R26436 standard; peptide; 8 AA.
AC   R26436;
DT   08-FEB-1993  (first entry)
DE   N-terminal auxiliary sequence.
KW   Negative hydrophobicity; increased renaturation yield.
OS   Synthetic.
PN   EP-500108-A.
PD   26-AUG-1992.
```



```
PF   20-FEB-1992; 102864.
PR   21-FEB-1991; DE-105480.
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
PI   Ambrosius D, Dony C, Rudolph R.
DR   WPI; 92-286227/35.
PT   Increasing renaturation yield of recombinant protein from
PT   prokaryotic host - by expressing it with terminal hydrophilic
PT   aminoacid sequence attached, pref. detachable at specific
PT   cleavage site
PS   Claim 11; Page 14; 18pp; German.
CC   The peptide is used as an auxiliary sequence which can be added to
CC   the N and/or C-terminus of recombinant proteins which exist in at
CC   least partially inactive form and are activated by solubilisation
CC   and/or renaturation techniques. The auxiliary sequence has a ratio
CC   of relative hydrophobicity:number of amino acids of -2.0 kcal/mole
CC   or smaller. Incorporation of the auxiliary sequence increases the
CC   yield during the renaturation process. This method is applied to
CC   recombinant proteins produced in prokaryotic organisms, especially
CC   E. coli. A specific application is production of recombinant
CC   granulocyte-colony stimulating factor (GM-CSF) or its derivatives.
CC   See also R26437-R26444.
SQ   Sequence   8 AA;
SQ   0  A; 1  R; 0  N; 0  D; 0  B; 0  C; 0  Q; 0  E; 0  Z; 0  G; 0  H;
SQ   0  I; 1  L; 0  K; 1  M; 0  F; 4  P; 0  S; 1  T; 0  W; 0  Y; 0  V;
```

Initial Score	=	5	Optimized Score	=	5	Significance =	2.70
Residue Identity	=	66%	Matches	=	4	Mismatches =	2
Gaps	=	0	Conservative Substitutions			=	0

```
     X    X
     PXPRPGXC
     | |||
   MTPLPRPP
     X    X
```

5. US-08-121-713B-43 (1-8)
R26440 N-terminal auxiliary sequence.

```
ID   R26440 standard; peptide; 14 AA.
AC   R26440;
DT   08-FEB-1993  (first entry)
DE   N-terminal auxiliary sequence.
KW   Negative hydrophobicity; increased renaturation yield.
OS   Synthetic.
PN   EP-500108-A.
PD   26-AUG-1992.
PF   20-FEB-1992; 102864.
PR   21-FEB-1991; DE-105480.
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
PI   Ambrosius D, Dony C, Rudolph R.
DR   WPI; 92-286227/35.
PT   Increasing renaturation yield of recombinant protein from
PT   prokaryotic host - by expressing it with terminal hydrophilic
PT   aminoacid sequence attached, pref. detachable at specific
PT   cleavage site
PS   Claim 11; Page 14; 18pp; German.
CC   The peptide is used as an auxiliary sequence which can be added to
CC   the N and/or C-terminus of recombinant proteins which exist in at
CC   least partially inactive form and are activated by solubilisation
```

```
CC   and/or renaturation techniques. The auxiliary sequence has a ratio
CC   of relative hydrophobicity:number of amino acids of -2.0 kcal/mole
CC   or smaller. Incorporation of the auxiliary sequence increases the
CC   yield during the renaturation process. This method is applied to
CC   recombinant proteins produced in prokaryotic organisms, especially
CC   E. coli. A specific application is production of recombinant
CC   granulocyte-colony stimulating factor (GM-CSF) or its derivatives.
CC   See also R26436-R26444.
SQ   Sequence   14 AA;
SQ   0  A; 1  R; 0  N; 0  D; 0  B; 0  C; 0  Q; 2  E; 0  Z; 1  G; 0  H;
SQ   0  I; 2  L; 0  K; 1  M; 0  F; 5  P; 0  S; 2  T; 0  W; 0  Y; 0  V;

Initial Score    =      5  Optimized Score  =      5  Significance =  2.70
Residue Identity =    66%  Matches          =      4  Mismatches   =     2
Gaps             =      0  Conservative Substitutions               =     0

           X    X
           PXPRPGXC
           | |||
    MTPLEEGTPLPRPP
           10   X
```

6. US-08-121-713B-43 (1-8)
   R11153 Hirulog-13.

```
ID   R11153 standard; Protein; 18 AA.
AC   R11153;
DT   21-MAY-1991  (first entry)
DE   Hirulog-13.
KW   Hirudin; thrombin inhibitor.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Modified -site  1
FT   /label= D-Phe
PN   WO9102750-A.
PD   07-MAR-1991.
PF   17-AUG-1990; U04642.
PR   18-AUG-1989; US-395482.
PR   06-JUL-1990; US-549388.
PA   (BIOG-) BIOGEN INC.
PA   (HEAL-) HEALTH RES INC.
PI   Maraganore JM, Fenton JW, Kline T;
DR   WPI; 91-087245/12.
PT   Thrombin inhibitor for therapeutic, prophylactic purposes - used
PT   to treat or prevent vascular disease, inflammatory responses,
PT   carcinoma(s), neuro-degenerative and chronic thromboembolic
PT   diseases
PS   Example 16; Page 50; 125pp; English.
CC   The peptide mimics the action of hirudin and inhibits thrombin. It
CC   is smaller and more potent than hirudin, so less likely to provoke
CC   an immune response. The peptide can be used to prevent/treat
CC   vascular diseases, inflammation, carcinomas and neurodegenerative
CC   diseases.  It can also be used for ex vivo thronbus imaging, for
CC   storing and treating extracorporeal blood and for coating invasive
CC   devices.
CC   See also R11151-R11166.
SQ   Sequence   18 AA;
SQ   0  A; 1  R; 1  N; 1  D; 0  B; 0  C; 0  Q; 4  E; 0  Z; 3  G; 0  H;
SQ   1  I; 1  L; 0  K; 0  M; 2  F; 3  P; 0  S; 0  T; 0  W; 1  Y; 0  V;
```



```
Initial Score    =      5  Optimized Score  =      5  Significance =  2.70
Residue Identity =    57%  Matches          =      4  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

     X     X
    PXPRPGXC
      ||||
     FPRPGGNGDFEEIPEEY
     X     X 10
```

7. US-08-121-713B-43 (1-8)
   R56242 Fibronectin-derived peptide.

```
ID   R56242 standard; peptide; 19 AA.
AC   R56242;
DT   12-JAN-1995  (first entry)
DE   Fibronectin-derived peptide.
KW   Fibronectin; inflammation; antiinflammatory; immunosuppressive;
KW   leukocyte; arthritis; autoimmune disease; graft versus host disease.
OS   Synthetic.
PN   WO9413692-A.
PD   23-JUN-1994.
PF   06-DEC-1993; U11781.
PR   10-DEC-1992; US-990296.
PR   21-OCT-1993; US-139903.
PA   (MINU ) UNIV MINNESOTA.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI   Allen JB,  Furcht LT,  Mccarthy JB,  Wahl SM;
DR   WPI; 94-217799/26.
PT   Fibronectin derived peptide(s) for treating inflammation -
PT   involving leucocyte activation, partic. arthritis and graft
PT   versus host disease
PS   Claim 6; Page 30; 45pp; English.
CC   Chronic inflammation or autoimmune diseases are treated with peptides
CC   corresponding to residues 1906-24 (R56242), 1946-60 (R56243), 1892-99
CC   (R56244), 1961-85 (R56245), 1784-92 (R56246) and 1485-504 (R56247) of
CC   fibronectin.
SQ   Sequence   19 AA;
SQ   0  A; 3  R; 0  N; 0  D; 0  B; 0  C; 0  Q; 2  E; 0  Z; 2  G; 0  H;
SQ   0  I; 0  L; 1  K; 0  M; 0  F; 6  P; 1  S; 0  T; 0  W; 1  Y; 3  V;

Initial Score    =      5  Optimized Score  =      7  Significance =  2.70
Residue Identity =    71%  Matches          =      5  Mismatches   =     2
Gaps             =      0  Conservative Substitutions               =     0

             X     X
             PXPRPGXC
             | ||||
    KPGSPPREVVPRPRPGV
          10  X     X
```

8. US-08-121-713B-43 (1-8)
   R26193 D-Cha/D-Npa Hirulog-8.

```
ID   R26193 standard; peptide; 20 AA.
AC   R26193;
DT   09-FEB-1993  (first entry)
```

```
DE   D-Cha/D-Npa Hirulog-8.
KW   Thrombin; inhibitor; hirudin; metastasis; adult respiratory;
KW   distress; neurodegenerative; Alzheimer's; Parkinson's; intravascular;
KW   coagulation; imaging; reperfusion; tPA.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Misc_difference 1
FT   /note= "D-form of either cyclohexylalanine or
FT   naphthyl alanine"
PN   WO9213952-A.
PD   20-AUG-1992.
PF   03-FEB-1992; U00836.
PR   08-FEB-1991; US-652929.
PA   (BIOJ ) BIOGEN INC.
PI   Bourdon PR, Maraganore JM, Jablonski JM;
DR   WPI; 92-300038/36.
PT   New catalytic site-directed thrombin inhibitors - used for
PT   treatment and prevention of thrombotic disorders,
PT   thrombin-induced inflammation, carcinoma(s), etc.
PS   Example 4; Page 36; 57pp; English.
CC   D-Cha/D-Npa Hirulog-8 are examples of catalytic site directed
CC   thrombin inhibitors.  The inhibitors are designed for optimum
CC   spatial configuration so are more active than hirudin (which
CC   they mimic qualitatively) and can be used at higher doses.  Also
CC   they are less likely to be immunogenic.  Particular applications
CC   include inhibition of metastatic tumours, treatment and prevention
CC   of thrombin-induced inflammation (e.g. in adult respiratory distress
CC   syndrome or reperfusion injury), to treat neurodegenerative diseases
CC   (e.g. Alzheimer's or Parkinson's diseases), to inhibit thrombus
CC   accretion and platelet dependent thrombosis and to treat or prevent
CC   disseminated intravascular coagulation.  The inhibitors can also be
CC   used, in conjunction with a thrombolytic agent, e.g. tPA, to decrease
CC   reperfusion time and increase reocclusion time.  The inhibitors can
CC   also be used in extracorporeal blood circulations, to coat the surface
CC   of invasive devices, and (when coupled to a radioisotope such as iodine
CC   123) for ex vivo imaging of a fibrin or platelet thrombus.
CC   See also R26192-4.
SQ   Sequence   20 AA;
SQ   0  A; 1  R; 1  N; 1  D; 0  B; 0  C; 0  Q; 4  E; 0  Z; 5  G; 0  H;
SQ   1  I; 1  L; 0  K; 0  M; 1  F; 3  P; 0  S; 0  T; 0  W; 1  Y; 0  V;
SQ   1 Others;

Initial Score    =      5  Optimized Score  =      5  Significance =  2.70
Residue Identity =    71%  Matches          =      5  Mismatches   =     2
Gaps             =      0  Conservative Substitutions               =     0

     X     X
    PXPRPGXC
     |||||
     XPRPGGGGNGDFEEIPE
     X     X 10
```

9. US-08-121-713B-43 (1-8)
   R26192 Hirulog-8.

```
ID   R26192 standard; peptide; 20 AA.
AC   R26192;
DT   09-FEB-1993  (first entry)
DE   Hirulog-8.
```



```
KW   Thrombin; inhibitor; hirudin; metastasis; adult respiratory;
KW   distress; neurodegenerative; Alzheimer's; Parkinson's; intravascular;
KW   coagulation; imaging; reperfusion; tPA.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Misc_difference 1
FT   /note= "D-form"
PN   WO9213952-A.
PD   20-AUG-1992.
PF   03-FEB-1992; U00836.
PR   08-FEB-1991; US-652929.
PA   (BIOJ ) BIOGEN INC.
PI   Bourdon PR, Maraganore JM, Jablonski JM;
DR   WPI; 92-300038/36.
PT   New catalytic site-directed thrombin inhibitors - used for
PT   treatment and prevention of thrombotic disorders,
PT   thrombin-induced inflammation, carcinoma(s), etc.
PS   Example 2; Page 33; 57pp; English.
CC   Hirulog-8 is an example of a catalytic site directed thrombin
CC   inhibitor.  The inhibitors are designed for optimum spatial
CC   configuration so are more active than hirudin (which they mimic
CC   qualitatively) and can be used at higher doses.  Also they are less
CC   likely to be immunogenic.  Particular applications include
CC   inhibition of metastatic tumours, treatment and prevention of
CC   thrombin-induced inflammation (e.g. in adult respiratory distress
CC   syndrome or reperfusion injury), to treat neurodegenerative diseases
CC   (e.g. Alzheimer's or Parkinson's diseases), to inhibit thrombus
CC   accretion and platelet dependent thrombosis and to treat or prevent
CC   disseminated intravascular coagulation.  The inhibitors can also be
CC   used, in conjunction with a thrombolytic agent, e.g. tPA, to decrease
CC   reperfusion time and increase reocclusion time.  The inhibitors can
CC   also be used in extracorporeal blood circulations, to coat the surface
CC   of invasive devices, and (when coupled to a radioisotope such as iodine
CC   123) for ex vivo imaging of a fibrin or platelet thrombus.
CC   See also R26193-4.
SQ   Sequence   20 AA;
SQ   0  A; 1  R; 1  N; 1  D; 0  B; 0  C; 0  Q; 4  E; 0  Z; 5  G; 0  H;
SQ   1  I; 1  L; 0  K; 0  M; 2  F; 3  P; 0  S; 0  T; 0  W; 1  Y; 0  V;

Initial Score    =      5  Optimized Score  =      5  Significance =  2.70
Residue Identity =    57%  Matches          =      4  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

     X     X
    PXPRPGXC
      ||||
     FPRPGGGGNGDFEEIPE
     X     X 10
```

10. US-08-121-713B-43 (1-8)
    R26395 Sequence of platelet binding peptide.

```
ID   R26395 standard; peptide; 20 AA.
AC   R26395;
DT   25-JAN-1993  (first entry)
DE   Sequence of platelet binding peptide.
KW   Technetium-99m labelled polypeptide imaging agent;
KW   radiolabeled imaging; radiodiagnostic agent.
OS   Synthetic.
```

```
FH   Key             Location/Qualifiers
FT   Modified_site   1
FT   /label= D-Phe
PN   WO9213572-A.
PD   20-AUG-1992.
PF   07-FEB-1992; U00757.
PR   08-FEB-1991; US-653012.
PA   (DIAT-) DIATECH INC.
PI   Dean RT;
DR   WPI; 92-299767/36.
PT   New technetium-99m labelled polypeptide imaging agents - for
PT   imaging of clots, tumours, infection sites, atherosclerotic and
PT   amyloid plaques or bone, and for visualising organs
PS   Claim 6; Page 13; 19pp; English.
CC   The binding peptide is covalently linked to a 'Cp(aa)Cp' technetium
CC   binding group wherin Cp is a protected cysteine and (aa) is an amino
CC   acid.  The technetium-99m complexes are used to image target sites
CC   within a mammalian body.
SQ   Sequence   20 AA;
SQ   0  A; 1  R; 1  N; 1  D; 0  B; 0  C; 0  Q; 4  E; 0  Z; 5  G; 0  H;
SQ   1  I; 1  L; 0  K; 0  M; 2  F; 3  P; 0  S; 0  T; 0  W; 1  Y; 0  V;

Initial Score    =      5  Optimized Score  =      5  Significance =  2.70
Residue Identity =    57%  Matches          =      4  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

     X     X
    PXPRPGXC
      ||||
     FPRPGGGGNGDFEEIPE
     X     X 10
```

11. US-08-121-713B-43 (1-8)
    R11163 Hirulog-27.

```
ID   R11163 standard; Protein; 20 AA.
AC   R11163;
DT   21-MAY-1991  (first entry)
DE   Hirulog-27.
KW   Hirudin; thrombin inhibitor.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Modified -site  1
FT   /label= D-Phe
FT   Modified -site  3
FT   /label= OTHER
FT   /note= "Arg-(CO-CH2)"
PN   WO9102750-A.
PD   07-MAR-1991.
PF   17-AUG-1990; U04642.
PR   18-AUG-1989; US-395482.
PR   06-JUL-1990; US-549388.
PA   (BIOG-) BIOGEN INC.
PA   (HEAL-) HEALTH RES INC.
PI   Maraganore JM, Fenton JW, Kline T;
DR   WPI; 91-087245/12.
PT   Thrombin inhibitor for therapeutic, prophylactic purposes - used
PT   to treat or prevent vascular disease, inflammatory responses,
PT   carcinoma(s), neuro-degenerative and chronic thromboembolic
```



```
PT   diseases
PS   Example 26; Page 67; 125pp; English.
CC   The peptide mimics the action of hirudin and inhibits thrombin. It
CC   is smaller and more potent than hirudin, so less likely to provoke
CC   an immune response. The peptide can be used to prevent/treat
CC   vascular diseases, inflammation, carcinomas and neurodegenerative
CC   diseases.  It can also be used for ex vivo thronbus imaging, for
CC   storing and treating extracorporeal blood and for coating invasive
CC   devices.
CC   See also R11151-R11166.
SQ   Sequence   20 AA;
SQ   0  A; 1  R; 1  N; 1  D; 0  B; 0  C; 0  Q; 4  E; 0  Z; 5  G; 0  H;
SQ   1  I; 1  L; 0  K; 0  M; 2  F; 3  P; 0  S; 0  T; 0  W; 1  Y; 0  V;

Initial Score    =      5  Optimized Score  =      5  Significance =  2.70
Residue Identity =    57%  Matches          =      4  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

     X     X
    PXPRPGXC
      ||||
     FPRPGGGGNGDFEEIPE
     X     X 10
```

12. US-08-121-713B-43 (1-8)
    R11164 Hirulog-28.

```
ID   R11164 standard; Protein; 20 AA.
AC   R11164;
DT   21-MAY-1991  (first entry)
DE   Hirulog-28.
KW   Hirudin; thrombin inhibitor.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Modified -site  1
FT   /label= D-Phe
FT   Modified -site  3
FT   /label= OTHER
FT   /note= "Arg-(CH2N)"
PN   WO9102750-A.
PD   07-MAR-1991.
PF   17-AUG-1990; U04642.
PR   18-AUG-1989; US-395482.
PR   06-JUL-1990; US-549388.
PA   (BIOG-) BIOGEN INC.
PA   (HEAL-) HEALTH RES INC.
PI   Maraganore JM, Fenton JW, Kline T;
DR   WPI; 91-087245/12.
PT   Thrombin inhibitor for therapeutic, prophylactic purposes - used
PT   to treat or prevent vascular disease, inflammatory responses,
PT   carcinoma(s), neuro-degenerative and chronic thromboembolic
PT   diseases
PS   Example 27; Page 68; 125pp; English.
CC   The peptide mimics the action of hirudin and inhibits thrombin. It
CC   is smaller and more potent than hirudin, so less likely to provoke
CC   an immune response. The peptide can be used to prevent/treat
CC   vascular diseases, inflammation, carcinomas and neurodegenerative
CC   diseases.  It can also be used for ex vivo thronbus imaging, for
CC   storing and treating extracorporeal blood and for coating invasive
```

```
CC   devices.
CC   See also R11151-R11166.
SQ   Sequence   20 AA;
SQ   0  A; 1  R; 1  N; 1  D; 0  B; 0  C; 0  Q; 4  E; 0  Z; 5  G; 0  H;
SQ   1  I; 1  L; 0  K; 0  M; 2  F; 3  P; 0  S; 0  T; 0  W; 1  Y; 0  V;

Initial Score    =      5  Optimized Score  =      5  Significance =  2.70
Residue Identity =    57%  Matches          =      4  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

     X     X
    PXPRPGXC
      ||||
     FPRPGGGGNGDFEEIPE
     X     X 10
```

13. US-08-121-713B-43 (1-8)
    R11158 Hirulog-18b.

```
ID   R11158 standard; Protein; 20 AA.
AC   R11158;
DT   21-MAY-1991  (first entry)
DE   Hirulog-18b.
KW   Hirudin; thrombin inhibitor.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Modified -site  1
FT   /label= D-Phe
FT   Modified -site  3
FT   /label= OTHER
FT   /note= "beta-homoarginine"
PN   WO9102750-A.
PD   07-MAR-1991.
PF   17-AUG-1990; U04642.
PR   18-AUG-1989; US-395482.
PR   06-JUL-1990; US-549388.
PA   (BIOG-) BIOGEN INC.
PA   (HEAL-) HEALTH RES INC.
PI   Maraganore JM, Fenton JW, Kline T;
DR   WPI; 91-087245/12.
PT   Thrombin inhibitor for therapeutic, prophylactic purposes - used
PT   to treat or prevent vascular disease, inflammatory responses,
PT   carcinoma(s), neuro-degenerative and chronic thromboembolic
PT   diseases
PS   Example 21; Page 52; 125pp; English.
CC   The peptide mimics the action of hirudin and inhibits thrombin. It
CC   is smaller and more potent than hirudin, so less likely to provoke
CC   an immune response. The peptide can be used to prevent/treat
CC   vascular diseases, inflammation, carcinomas and neurodegenerative
CC   diseases.  It can also be used for ex vivo thronbus imaging, for
CC   storing and treating extracorporeal blood and for coating invasive
CC   devices.
CC   See also R11151-R11166.
SQ   Sequence   20 AA;
SQ   0  A; 1  R; 1  N; 1  D; 0  B; 0  C; 0  Q; 4  E; 0  Z; 5  G; 0  H;
SQ   1  I; 1  L; 0  K; 0  M; 2  F; 3  P; 0  S; 0  T; 0  W; 1  Y; 0  V;

Initial Score    =      5  Optimized Score  =      5  Significance =  2.70
Residue Identity =    57%  Matches          =      4  Mismatches   =     3
```



```
Gaps             =      0  Conservative Substitutions               =     0

     X     X
    PXPRPGXC
      ||||
     FPRPGGGGNGDFEEIPE
     X     X 10
```

14. US-08-121-713B-43 (1-8)
    R11151 Hirulog-8.

```
ID   R11151 standard; peptide; 20 AA.
AC   R11151;
DT   21-MAY-1991  (first entry)
DE   Hirulog-8.
KW   Hirudin; thrombin inhibitor; Hirulog-9; Hirulog-11; Hirulog-12.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Modified -site  1
FT   /label= D-Phe
PN   WO9102750-A.
PD   07-MAR-1991.
PF   17-AUG-1990; U04642.
PR   18-AUG-1989; US-395482.
PR   06-JUL-1990; US-549388.
PA   (BIOG-) BIOGEN INC.
PA   (HEAL-) HEALTH RES INC.
PI   Maraganore JM, Fenton JW, Kline T;
DR   WPI; 91-087245/12.
PT   Thrombin inhibitor for therapeutic, prophylactic purposes - used
PT   to treat or prevent vascular disease, inflammatory responses,
PT   carcinoma(s), neuro-degenerative and chronic thromboembolic
PT   diseases
PS   Example 4; Page 39; 125pp; English.
CC   The peptide mimics the action of hirudin and inhibits thrombin. It
CC   is smaller and more potent than hirudin, so less likely to provoke
CC   an immune response. The peptide can be used to prevent/treat
CC   vascular diseases, inflammation, carcinomas and neurodegenerative
CC   diseases.  It can also be used for ex vivo thronbus imaging, for
CC   storing and treating extracorporeal blood and for coating invasive
CC   devices.  The same sequence but with a D-Pro at posn. 4 replacing
CC   the L-Pro is designated Hirulog-9; Hirulog-8 with the Tyr at posn.
CC   19 modified to 3,5-diiodoTyr is known as Hirulog-11, and modified
CC   to Tyr(OSO3) as Hirulog-12.
CC   See also R11152-R11166.
SQ   Sequence   20 AA;
SQ   0  A; 1  R; 1  N; 1  D; 0  B; 0  C; 0  Q; 4  E; 0  Z; 5  G; 0  H;
SQ   1  I; 1  L; 0  K; 0  M; 2  F; 3  P; 0  S; 0  T; 0  W; 1  Y; 0  V;

Initial Score    =      5  Optimized Score  =      5  Significance =  2.70
Residue Identity =    57%  Matches          =      4  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

     X     X
    PXPRPGXC
      ||||
     FPRPGGGGNGDFEEIPE
     X     X 10
```

15. US-08-121-713B-43 (1-8)
P71352 Synthetic peptide encoding rabies virus coat glyco

```
 ID   P71352 standard; protein; 21 AA.
 AC   P71352;
 DT   01-JAN-1980  (first entry)
 DE   Synthetic peptide encoding rabies virus coat glycoprotein antigenic
 DE   determinant.
 KW   Rabies virus; glycoprotein; coat protein; vaccine; antigen;
 KW   immunogen; mammal; ss.
 OS   Synthetic.
 FH   Key             Location/Qualifiers
 FT   Misc_difference 12
 FT   /label= N or T
 FT   Misc_difference 20
 FT   /label= N or K
 PN   WO8700179-A.
 PD   15-JAN-1987.
 PF   03-JUL-1986; U01424.
 PR   03-JUL-1985; US-752222.
 PR   12-DEC-1986; US-941163.
 PA   (SALK ) SALK INST FOR BIOL STUD.
 PI   Patrick JW, Heinemann SF, Boss BD, Cowan WM;
 DR   WPI; 87-021980/03.
 PT   Synthetic peptide-based anti-rabies compsns. - having an amino
 PT   acid sequence of a segment of the rabies virus coat glyco:protein
 PS   Claim 2; Page 53; 58pp; English.
 CC   When this peptide is conjugated to a carrier protein which is
 CC   immunogenic in a mammal, it is capable of raising an immune
 CC   response against rabies virus, and may therefore be used as a
 CC   potential anti-rabies vaccine.  The peptide may also be used in the
 CC   treatment, prophylaxis and diagnosis of rabies.  See also P71350-1
 CC   P71353-55.
 SQ   Sequence   21 AA;
 SQ   1  A; 3  R; 0  N; 1  D; 0  B; 1  C; 0  Q; 0  E; 0  Z; 3  G; 0  H;
 SQ   1  I; 0  L; 1  K; 0  M; 1  F; 3  P; 2  S; 2  T; 0  W; 0  Y; 0  V;
 SQ   2 Others;

Initial Score    =      5  Optimized Score  =      5  Significance =  2.70
Residue Identity =    66%  Matches          =      4  Mismatches   =     2
Gaps             =      0  Conservative Substitutions               =     0

      X    X
    PXPRPGXC
      ||||
      PRPGTPCDIFTXSRGK
      X    X  10
> 0 <
0| |0  IntelliGenetics
> 0 <

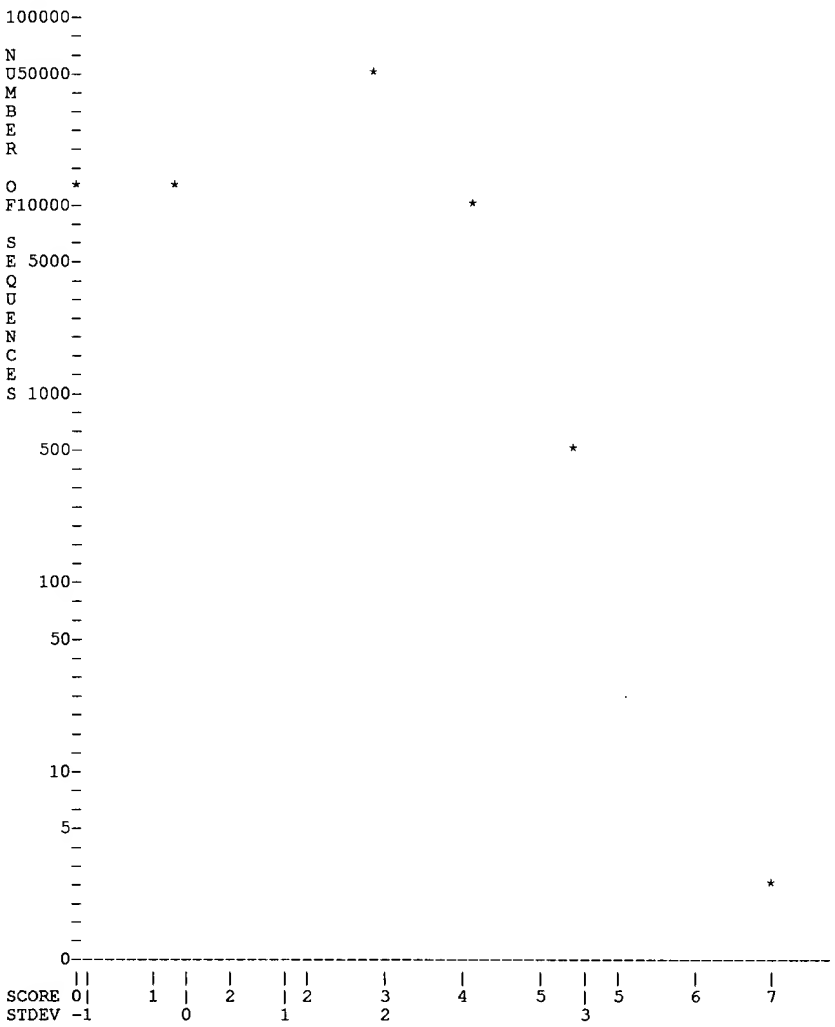
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq43pir.res made by  on Fri 19 May 95 8:49:14-PDT.


Query sequence being compared:US-08-121-713B-43 (1-8)
Number of sequences searched:                75511
```


Number of scores above cutoff: 4067

Results of the initial comparison of US-08-121-713B-43 (1-8) with:
Data bank : PIR 43, all entries



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	6
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	4	1.29

Times:	CPU	Total Elapsed
	00:01:12.06	00:01:13.00

Number of residues:	22468834
Number of sequences searched:	75511
Number of scores above cutoff:	4067

Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 3 standard deviations above mean ****					
1. A27797	class I histocompatibility an	356	7	7	3.86	0
2. JQ0532	OP protein - Kennedya yellow	753	7	7	3.86	0
	**** 2 standard deviations above mean ****					
3. S33300	probable substance P - smalle	11	5	5	2.32	0
4. A37196	bradykinin-potentiating pepti	13	5	5	2.32	0
5. XAVI9B	angiotensin-converting enzyme	13	5	5	2.32	0
6. S40139	T cell receptor J-alpha wnI.2	24	5	5	2.32	0
7. S27042	acetylcholinesterase (EC 3.1.	47	5	5	2.32	0
8. A36589	bactenecin 7 - bovine	59	5	7	2.32	0
9. B41573	acetylcholinesterase (EC 3.1.	72	5	5	2.32	0
10. E48059	oncoprotein zL-Myc - zebra fi	77	5	5	2.32	0
11. A61552	progesterone receptor, form B	91	5	5	2.32	0
12. S39448	guanylate kinase (EC 2.7.4.8)	98	5	5	2.32	0
13. B38277	hypothetical hydroxyproline-r	100	5	5	2.32	0
14. A42452	V1 protein - tobacco yellow d	102	5	5	2.32	0
15. S20822	hypothetical protein 103 - ph	103	5	7	2.32	0
16. S15151	hypothetical protein 103 - ph	103	5	7	2.32	0
17. S02365	hypothetical protein - Rhizob	113	5	5	2.32	0
18. S48846	GTP cyclohydrolase I (EC 3.5.	114	5	5	2.32	0

19. PN0139	lutropin beta chain - minke w	118	5	5	2.32	0
20. PN0141	lutropin beta chain - sperm w	118	5	5	2.32	0
21. S34165	keratin type II, hair - sheep	123	5	7	2.32	0
22. S20178	hypothetical protein (IFM1 3'	125	5	5	2.32	0
23. JU0068	homeotic protein CHox1 - chic	126	5	5	2.32	0
24. B48662	hypothetical protein repA4 -	128	5	5	2.32	0
25. QQECB1	hypothetical protein RepA4 -	128	5	5	2.32	0
26. QQECBR	hypothetical protein RepA4 -	128	5	5	2.32	0
27. S12371	hsp protein - human	130	5	5	2.32	0
28. A26839	ORF1 protein - Escherichia co	134	5	7	2.32	0
29. S01387	U1 snRNP protein C - human	159	5	5	2.32	0
30. A44263	U1-specific snRNP C protein -	159	5	5	2.32	0
31. S09404	Mannose 6-phosphate receptor	163	5	7	2.32	0
32. S14549	DNA-directed RNA polymerase (	165	5	5	2.32	0
33. JC2081	granulocyte colony-stimulatin	165	5	5	2.32	0
34. A42361	DNA-directed RNA polymerase (	165	5	5	2.32	0
35. JH0656	hypothetical 18.3K protein (n	168	5	5	2.32	0
36. S36749	transcription factor HES-3 -	175	5	5	2.32	0
37. S24298	chorion protein - silkworm	178	5	5	2.32	0
38. S37398	adenine phosphoribosyltransfe	182	5	5	2.32	0
39. JK0219	somatotropin - African elepha	190	5	5	2.32	0
40. KIPGGU	guanylate kinase (EC 2.7.4.8)	197	5	5	2.32	0
41. S39447	guanylate kinase (EC 2.7.4.8)	198	5	5	2.32	0
42. S14456	XA-1 protein - African clawed	198	5	5	2.32	0
43. S32545	Guanylate kinase - pig	199	5	5	2.32	0
44. S43041	guanylate kinase (EC 2.7.4.8)	207	5	5	2.32	0
45. KIECGU	guanylate kinase (EC 2.7.4.8)	207	5	5	2.32	0

1. US-08-121-713B-43 (1-8)
   A27797 class I histocompatibility antigen HLA alpha chain

ENTRY A27797 #type complete
TITLE class I histocompatibility antigen HLA alpha chain (clone RS5) precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 18-Oct-1989 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1993
ACCESSIONS A27797
REFERENCE A27797
#authors Srivastava, R.; Chorney, M.J.; Lawrance, S.K.; Pan, J.; Smith, Z.; Smith, C.L.; Weissman, S.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:4224-4228
#title Structure, expression, and molecular mapping of a divergent member of the class I HLA gene family.
#cross-references MUID:87231978
#accession A27797
##molecule_type DNA
##residues 1-356 ##label SRI
##cross-references GB:M16714
GENETICS
#introns 21/3; 110/3; 202/1; 294/1; 333/1; 343/3
SUMMARY #length 356 #molecular-weight 39484 #checksum 7384
SEQUENCE

Initial Score	= 7	Optimized Score	= 7	Significance	= 3.86
Residue Identity	= 62%	Matches	= 5	Mismatches	= 3
Gaps	= 0	Conservative Substitutions		=	0

X X

```
            PXPRPGXC
            | ||||
    TLLLLLSEARPLPRPGRGSHSLKYIPLS
        10    X   20 X      30
```

2. US-08-121-713B-43 (1-8)
   JQ0532 OP protein - Kennedya yellow mosaic virus

```
 ENTRY            JQ0532     #type complete
 TITLE            OP protein - Kennedya yellow mosaic virus
 ORGANISM         #formal_name Kennedya yellow mosaic virus
 DATE             31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                    31-Dec-1993
 ACCESSIONS       JQ0532
 REFERENCE        JQ0532
    #authors      Ding, S.; Keese, P.; Gibbs, A.
    #journal      J. Gen. Virol. (1990) 71:925-931
    #title        The nucleotide sequence of the genomic RNA of kennedya yellow
                    mosaic tymovirus-Jervis Bay isolate: relationships with
                    potex- and carlaviruses.
    #contents     Strain Jervis Bay isolate
    #accession    JQ0532
       ##molecule_type mRNA
       ##residues      1-753 ##label DIN
 SUMMARY          #length 753  #molecular-weight 82427  #checksum 9812
 SEQUENCE

Initial Score    =      7  Optimized Score  =      7  Significance =  3.86
Residue Identity =    62%  Matches          =      5  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

            X      X
            PXPRPGXC
            | ||||
    AASSQSSSILPLPRPGNRPGVLPGPKVR
  260       270       280
```

3. US-08-121-713B-43 (1-8)
   S33300 probable substance P - smaller spotted catshar

```
 ENTRY            S33300     #type complete
 TITLE            probable substance P - smaller spotted catshar
 ORGANISM         #formal_name Scyliorhinus canicula #common_name smaller
                    spotted catshark, smaller spotted dogfish
 DATE             08-Dec-1993; #sequence_revision 08-Dec-1993; #text_change
                    08-Dec-1993
 ACCESSIONS       S33300
 REFERENCE        S33300
    #authors      Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.
    #journal      Eur. J. Biochem. (1993) 214:469-474
    #title        Primary structures and biological activities of
                    substance-P-related peptides from the brain of the dogfish,
                    Scyliorhinus canicula.
    #accession    S33300
       ##status       preliminary
       ##residues     1-11 ##label WAU
 SUMMARY          #length 11  #molecular-weight 1278  #checksum 4938
 SEQUENCE
```



```
Initial Score    =      5  Optimized Score  =      5  Significance =  2.32
Residue Identity =    57%  Matches          =      4  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

     X     X
    PXPRPGXC
      ||||
     KPRPGQFFGLM
     X     X 10
```

4. US-08-121-713B-43 (1-8)
   A37196 bradykinin-potentiating peptide 1 - island jararac

```
 ENTRY            A37196     #type complete
 TITLE            bradykinin-potentiating peptide 1 - island jararaca
 ORGANISM         #formal_name Bothrops insularis #common_name island jararaca
 DATE             14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change
                    05-Aug-1994
 ACCESSIONS       A37196
 REFERENCE        A37196
    #authors      Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
    #journal      J. Protein Chem. (1990) 9:221-227
    #title        Primary structure and biological activity of bradykinin
                    potentiating peptides from Bothrops insularis snake venom.
    #cross-references MUID:90351557
    #accession    A37196
       ##status       preliminary
       ##molecule_type protein
       ##residues     1-13 ##label CIN
 KEYWORDS         pyroglutamic acid
 FEATURE
    1                 #modified_site pyrrolidone carboxylic acid (Gln) #status
                        experimental
 SUMMARY          #length 13  #molecular-weight 1388  #checksum 7017
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.32
Residue Identity =    50%  Matches          =      4  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

      X      X
      PXPRPGXC
        ||||
    QGGWPRPGPEIPP
      X     10
```

5. US-08-121-713B-43 (1-8)
   XAVI9B angiotensin-converting enzyme inhibitor V-9 - jara

```
 ENTRY            XAVI9B     #type complete
 TITLE            angiotensin-converting enzyme inhibitor V-9 - jararaca
 ORGANISM         #formal_name Bothrops jararaca #common_name jararaca
 DATE             #sequence_revision 13-Jul-1981 #text_change 08-Dec-1994
 ACCESSIONS       A01253
 REFERENCE        A90356
    #authors      Ondetti, M.A.; Williams, N.J.; Sabo, E.F.; Pluscec, J.;
                    Weaver, E.R.; Kocy, O.
```

```
    #journal       Biochemistry (1971) 10:4033-4039
    #title         Angiotensin-converting enzyme inhibitors from the venom of
                     Bothrops jararaca. Isolation, elucidation of structure, and
                     synthesis.
    #cross-references MUID:72118526
    #accession     A01253
       ##molecule_type protein
       ##residues      1-13 ##label OND
       ##note          the structure of the peptide was confirmed by synthesis
 COMMENT     This peptide also potentiates bradykinin by inhibiting the kinases
               that inactivate it.
 CLASSIFICATION   #superfamily bradykinin-potentiating peptide
 KEYWORDS         pyroglutamic acid
 FEATURE
    1                 #modified_site pyrrolidone carboxylic acid (Gln) #status
                        experimental
 SUMMARY          #length 13  #molecular-weight 1388  #checksum 7017
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.32
Residue Identity =    50%  Matches          =      4  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

      X      X
      PXPRPGXC
        ||||
    QGGWPRPGPEIPP
      X     10
```

6. US-08-121-713B-43 (1-8)
   S40139 T cell receptor J-alpha wnI.2 - human

```
 ENTRY            S40139     #type complete
 TITLE            T cell receptor J-alpha wnI.2 - human
 ORGANISM         #formal_name Homo sapiens #common_name man
 DATE             07-Dec-1994; #sequence_revision 07-Dec-1994; #text_change
                    07-Dec-1994
 ACCESSIONS       S40139
 REFERENCE        S40133
    #authors      Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
    #submission   submitted to the EMBL Data Library, February 1993
    #accession    S40139
       ##status       preliminary
       ##residues     1-24 ##label PLA
       ##cross-references EMBL:X71025
 SUMMARY          #length 24  #molecular-weight 2380  #checksum 3180
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.32
Residue Identity =    50%  Matches          =      4  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

    X      X
    PXPRPGXC
      ||||
    VSPRPGAAGNKLTFGGGT
    X       10
```


7. US-08-121-713B-43 (1-8)
   S27042 acetylcholinesterase (EC 3.1.1.7) - rat

```
 ENTRY            S27042     #type complete
 TITLE            acetylcholinesterase (EC 3.1.1.7) - rat
 ORGANISM         #formal_name Rattus norvegicus #common_name Norway rat
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S27042
 REFERENCE        S27042
    #authors      Legay, C.; Bon, S.; Massoulie, J.
    #journal      FEBS Lett. (1993) 315:163-166
    #title        Expression of a cDNA encoding the glycolipid-anchored form of
                    rat acetylcholinesterase.
    #accession    S27042
       ##status       preliminary
       ##residues     1-47 ##label LEG
 SUMMARY          #length 47  #molecular-weight 4960  #checksum 5424
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.32
Residue Identity =    50%  Matches          =      4  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

            X      X
            PXPRPGXC
              ||||
    CTCPSPAHGEAAPRPGPALSLSLLFFLF
          20        30
```

8. US-08-121-713B-43 (1-8)
   A36589 bactenecin 7 - bovine

```
 ENTRY            A36589     #type complete
 TITLE            bactenecin 7 - bovine
 ORGANISM         #formal_name Bos primigenius taurus #common_name cattle
 DATE             12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change
                    24-Jun-1993
 ACCESSIONS       A36589
 REFERENCE        A36589
    #authors      Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.;
                    Romeo, D.
    #journal      J. Biol. Chem. (1990) 265:18871-18874
    #title        Amino acid sequences of two proline-rich bactenecins.
                    Antimicrobial peptides of bovine neutrophils.
    #cross-references MUID:91035404
    #accession    A36589
       ##status       preliminary
       ##molecule_type protein
       ##residues     1-59 ##label FRA
 SUMMARY          #length 59  #molecular-weight 6910  #checksum 9841
 SEQUENCE

Initial Score    =      5  Optimized Score  =      7  Significance =  2.32
Residue Identity =    62%  Matches          =      5  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

            X      X
            PXPRPGXC
```

```
              | ||||
    RLPRPRPRPLPFPRPGPRPIPRPLPFPR
    10        20     X  30
```

9. US-08-121-713B-43 (1-8)
   B41573 acetylcholinesterase (EC 3.1.1.7) - mouse (fragmen

```
 ENTRY            B41573     #type fragment
 TITLE            acetylcholinesterase (EC 3.1.1.7) - mouse (fragment)
 ORGANISM         #formal_name Mus musculus #common_name house mouse
 DATE             30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                    23-Jun-1993
 ACCESSIONS       B41573
 REFERENCE        A41573
    #authors      Li, Y.; Camp, S.; Rachinsky, T.L.; Getman, D.; Taylor, P.
    #journal      J. Biol. Chem. (1991) 266:23083-23090
    #title        Gene structure of mammalian acetylcholinesterase. Alternative
                    exons dictate tissue-specific expression.
    #cross-references MUID:92078174
    #accession    B41573
       ##status        preliminary
       ##molecule_type DNA
       ##residues      1-72 ##label LIA
       ##cross-references GB:M76540
 KEYWORDS         carboxylic ester hydrolase
 SUMMARY          #length 72  #checksum 2652
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.32
Residue Identity =    50%  Matches          =      4  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             PXPRPGXC
              ||||
    CTCPSPAHGEAAPRPGPDLALSLLFFLF
       10    X  20  X     30
```

10. US-08-121-713B-43 (1-8)
    E48059 oncoprotein zL-Myc - zebra fish (fragment)

```
 ENTRY            E48059     #type fragment
 TITLE            oncoprotein zL-Myc - zebra fish (fragment)
 ORGANISM         #formal_name Brachydanio rerio #common_name zebra fish
 DATE             21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change
                    18-Nov-1994
 ACCESSIONS       E48059
 REFERENCE        A48059
    #authors      Schreiber-Agus, N.; Horner, J.; Torres, R.; Chiu, F.C.;
                    DePinho, R.A.
    #journal      Mol. Cell. Biol. (1993) 13:2765-2775
    #title        Zebra fish myc family and max genes: differential expression
                    and oncogenic activity throughout vertebrate evolution.
    #cross-references MUID:93233639
    #accession    E48059
       ##status        preliminary
       ##molecule_type mRNA; DNA
       ##residues      1-77 ##label SCH
```



```
       ##cross-references NCBIP:129812
       ##note          sequence extracted from NCBI backbone
       ##note          sequence not compared to nucleotide translation
 SUMMARY          #length 77  #checksum 9459
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.32
Residue Identity =    50%  Matches          =      4  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             PXPRPGXC
              ||||
    SPSRTLDGDWLFPRPGDRWVGAAEGLTC
       20    X  30  X     40
```

11. US-08-121-713B-43 (1-8)
    A61552 progesterone receptor, form B - chicken (fragments

```
 ENTRY            A61552     #type fragments
 TITLE            progesterone receptor, form B - chicken (fragments)
 ORGANISM         #formal_name Gallus gallus #common_name chicken
 DATE             15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change
                    15-Oct-1994
 ACCESSIONS       A61552
 REFERENCE        A61552
    #authors      Simpson, R.J.; Grego, B.; Govindan, M.V.; Gronemeyer, H.
    #journal      Mol. Cell. Endocrinol. (1987) 52:177-184
    #title        Peptide sequencing of the chick oviduct progesterone receptor
                    form B.
    #accession    A61552
       ##status        preliminary
       ##molecule_type protein
       ##residues      1-91 ##label SIM
 SUMMARY          #length 91  #checksum 8063
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.32
Residue Identity =    50%  Matches          =      4  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             PXPRPGXC
              ||||
    VDAGPGAPGPSQPRPGAARPGPEDDAGP
          10 X      20
```

12. US-08-121-713B-43 (1-8)
    S39448 guanylate kinase (EC 2.7.4.8) - bovine

```
 ENTRY            S39448     #type complete
 TITLE            guanylate kinase (EC 2.7.4.8) - bovine
 ORGANISM         #formal_name Bos primigenius taurus #common_name cattle
 DATE             20-May-1994; #sequence_revision 20-May-1994; #text_change
                    20-May-1994
 ACCESSIONS       S39448
 REFERENCE        S39448
    #authors      Gaidarov, I.O.; Suslov, O.N.; Abdulaev, N.G.
```

```
    #journal      FEBS Lett. (1993) 335:81-84
    #title        Enzymes of the cyclic GMP metabolism in bovine retina. I.
                    Cloning and expression of the gene for guanylate kinase.
    #accession    S39448
       ##status        preliminary
       ##residues      1-98 ##label GAI
 SUMMARY          #length 98  #molecular-weight 10747  #checksum 8606
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.32
Residue Identity =    50%  Matches          =      4  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             PXPRPGXC
              ||||
    GSIFSVSHTTRDPRPGEENGKDYYFVTR
         20   X    30        40


13. US-08-121-713B-43 (1-8)
    B38277       hypothetical hydroxyproline-rich glycoprotein (clo

 ENTRY            B38277     #type fragment
 TITLE            hypothetical hydroxyproline-rich glycoprotein (clone MG1.6a)
                    - Chlamydomonas reinhardtii (fragment)
 ORGANISM         #formal_name Chlamydomonas reinhardtii
 DATE             31-May-1991 #sequence_revision 31-May-1991 #text_change
                    30-Sep-1993
 ACCESSIONS       B38277
 REFERENCE        A38277
    #authors      Adair, W.S.; Apt, K.E.
    #journal      Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7355-7359
    #title        Cell wall regeneration in Chlamydomonas: accumulation of
                    mRNAs encoding cell wall hydroxyproline-rich glycoproteins.
    #cross-references MUID:91017504
    #accession    B38277
       ##status        preliminary
       ##molecule_type mRNA
       ##residues      1-100 ##label ADA
       ##note          sequence not compared to nucleotide translation
 SUMMARY          #length 100  #checksum 4244
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.32
Residue Identity =    50%  Matches          =      4  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             PXPRPGXC
              ||||
    RPLQPERLVRAPPRPGPAPRQQQLPLP
         80   X    90        100


14. US-08-121-713B-43 (1-8)
    A42452       V1 protein - tobacco yellow dwarf virus (strain Au

 ENTRY            A42452     #type complete
 TITLE            V1 protein - tobacco yellow dwarf virus (strain Australia)
```



```
 ORGANISM         #formal_name tobacco yellow dwarf virus
 DATE             15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change
                    08-Apr-1994
 ACCESSIONS       A42452
 REFERENCE        A42452
    #authors      Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.;
                    Thomas, J.E.
    #journal      Virology (1992) 187:633-642
    #title        The nucleotide sequence of the infectious cloned DNA
                    component of tobacco yellow dwarf virus reveals features of
                    geminiviruses infecting monocotyledonous plants.
    #accession    A42452
       ##molecule_type DNA
       ##residues      1-102 ##label MOR
       ##cross-references GB:M81103
 SUMMARY          #length 102  #molecular-weight 11178  #checksum 6879
 SEQUENCE

Initial Score    =      5  Optimized Score  =      5  Significance =  2.32
Residue Identity =    50%  Matches          =      4  Mismatches   =     4
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             PXPRPGXC
             |  |||
    TTTEIGFGNTPLRRPGEGNPNGGPV
     80        90    X  100


15. US-08-121-713B-43 (1-8)
    S20822       hypothetical protein 103 - phage Pf1

 ENTRY            S20822     #type complete
 TITLE            hypothetical protein 103 - phage Pf1
 ORGANISM         #formal_name phage Pf1
 DATE             22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
                    22-Nov-1993
 ACCESSIONS       S20822
 REFERENCE        S20696
    #authors      Hill, D.F.; Short, N.J.; Perham, R.N.; Petersen, G.B.
    #submission   submitted to the EMBL Data Library, March 1990
    #accession    S20822
       ##status        preliminary
       ##residues      1-103 ##label HIL
       ##cross-references EMBL:X52107
 SUMMARY          #length 103  #molecular-weight 11154  #checksum 8403
 SEQUENCE

Initial Score    =      5  Optimized Score  =      7  Significance =  2.32
Residue Identity =    62%  Matches          =      5  Mismatches   =     3
Gaps             =      0  Conservative Substitutions               =     0

             X      X
             PXPRPGXC
             | ||||
    NHGRQSLLPTPNPRPGLRLLCVLVRKAG
          10 X      20
```